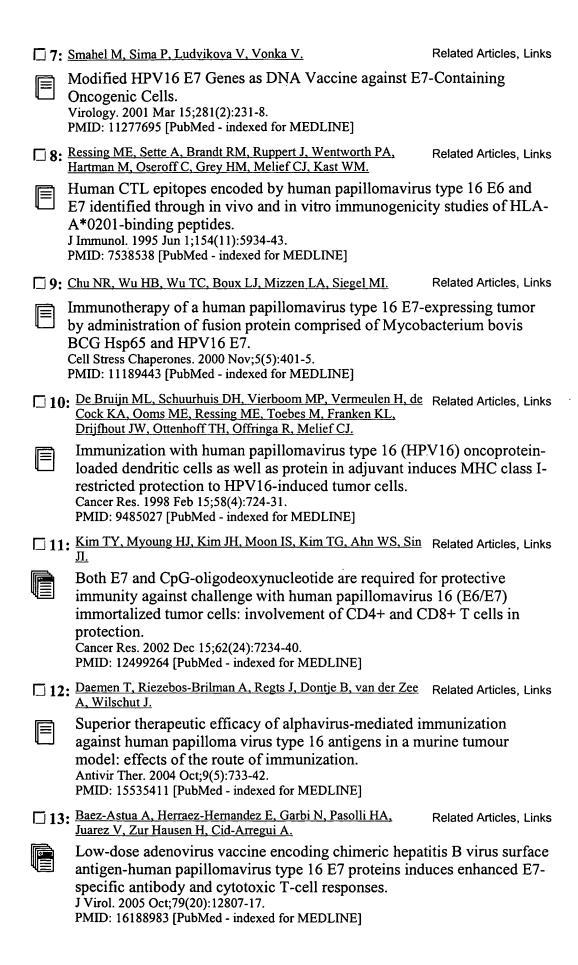
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	□ 5:	Chu NR, Wu F	IB, Wu T, E	Boux LJ, Sieg	el MI, Mizze	n LA.	Relate	ed Articles	, Links
		Immunother tumour by a bovis bacille Clin Exp Immo PMID: 109311	dministrat Calmette anol. 2000 A	ion of fusion -Guerin (B Aug;121(2):2	on protein o CG) hsp65 16-25.	comprising and HPV	g Mycoł		
	□ 6:	Cassetti MC, M Eiben GL, Sm	AcElhiney S ith LR, Kast	P, Shahabi V WM.	, Pullen JK,	Le Poole IC	. Relate	ed Articles	, Links
		Antitumor e particles end Vaccine. 2004 PMID: 146703	oding mu Jan 2;22(3-	tated HPV 1 4):520-7.	6 E6 and 1	E7 genes.	s virus re	eplicon	

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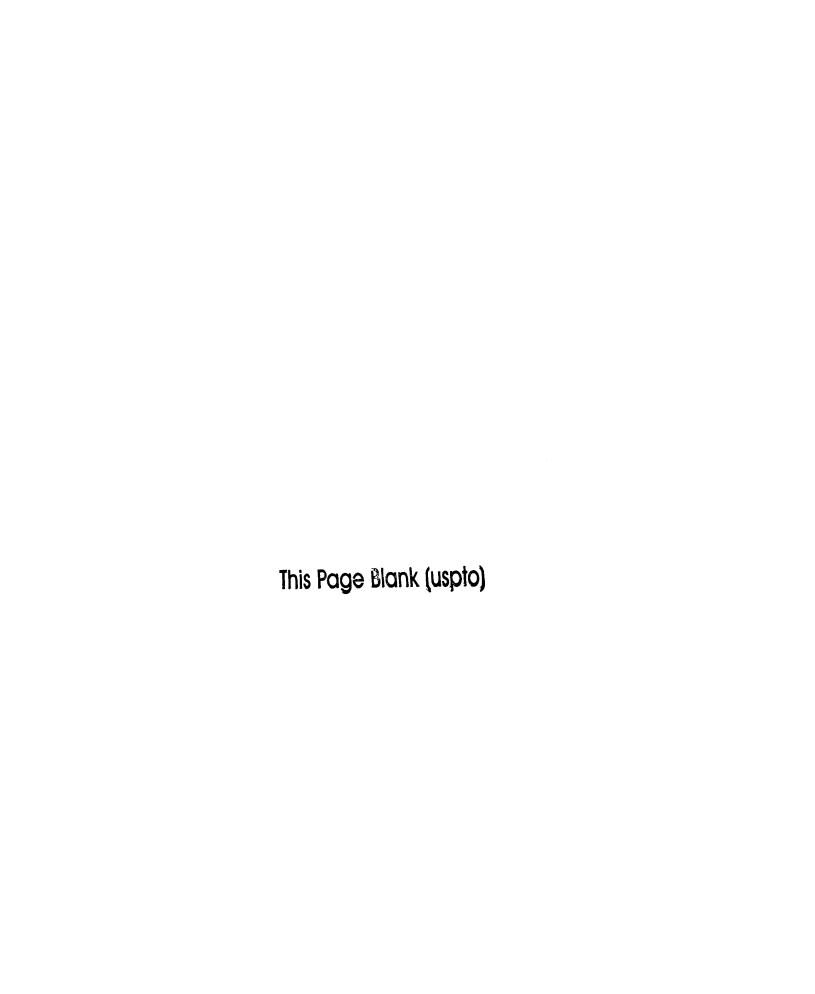
□ 14:	Lasaro MO, Diniz MO, Reyes-Sandoval A, Ertl HC, Ferreira LC.	Related Articles, Links
	Anti-tumor DNA vaccines based on the expression of la papillomavirus-16 E6/E7 oncoproteins genetically fuse glycoprotein D from herpes simplex virus-1. Microbes Infect. 2005 Dec;7(15):1541-50. Epub 2005 Sep 9. PMID: 16213178 [PubMed - indexed for MEDLINE]	
□ 15:	Sun Q, Tang SC, Pater MM, Pater A.	Related Articles, Links
	Different HPV16 E6/E7 oncogene expression patterns reconstructed from HPV16-immortalized human endoc genital keratinocytes. Oncogene. 1997 Nov 13;15(20):2399-408. PMID: 9395236 [PubMed - indexed for MEDLINE]	-
□16:	Azoury-Ziadeh R, Herd K, Fernando GJ, Frazer IH, Tindle RW.	Related Articles, Links
	T-helper epitopes identified within the E6 transforming cervical cancer-associated human papillomavirus type Viral Immunol. 1999;12(4):297-312. PMID: 10630789 [PubMed - indexed for MEDLINE]	
□17:	Indrova M, Reinis M, Bubenik J, Jandlova T, Bieblova J, Vonka V, Velek J.	Related Articles, Links
	Immunogenicity of dendritic cell-based HPV16 E6/E7 CTL activation and protective effects. Folia Biol (Praha). 2004;50(6):184-93. PMID: 15709713 [PubMed - indexed for MEDLINE]	peptide vaccines:
□ 18:	Fernando GJ, Murray B, Zhou J, Frazer IH.	Related Articles, Links
	Expression, purification and immunological characterizatransforming protein E7, from cervical cancer-associate papillomavirus type 16. Clin Exp Immunol. 1999 Mar;115(3):397-403. PMID: 10193409 [PubMed - indexed for MEDLINE]	
□ 19:	Peng S, Ji H, Trimble C, He L, Tsai YC, Yeatermeyer J, Boyd DA, Hung CF, Wu TC.	Related Articles, Links
	Development of a DNA vaccine targeting human papil oncoprotein E6. J Virol. 2004 Aug;78(16):8468-76. PMID: 15280455 [PubMed - indexed for MEDLINE]	lomavirus type 16
□ 20:	Kadish AS, Ho GY, Burk RD, Wang Y, Romney SL, Ledwidge R, Angeletti RH.	Related Articles, Links
	Lymphoproliferative responses to human papillomaviruproteins E6 and E7: outcome of HPV infection and ass J Natl Cancer Inst. 1997 Sep 3;89(17):1285-93. PMID: 9293919 [PubMed - indexed for MEDLINE]	
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Search Results - Record(s) 1 through 3 of 3 returned.

☐ 1. Document ID: CN 1160463 C, CN 1381583 A

L4: Entry 1 of 3

File: DWPI

Aug 4, 2004

DERWENT-ACC-NO: 2003-258260

DERWENT-WEEK: 200612

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TITLE: Human papillomavirus E6/E7 fusion gene and its efficient expression carrier

and fusion protein vaccine

INVENTOR: ZHAO, Q

PRIORITY-DATA: 2002CN-0117143 (April 24, 2002)

PATENT-FAMILY:

 PUB-NO
 PUB-DATE
 LANGUAGE
 PAGES
 MAIN-IPC

 CN 1160463 C
 August 4, 2004
 000
 C12N015/62

 CN 1381583 A
 November 27, 2002
 000
 C12N015/62

INT-CL (IPC): $\underline{A61}$ \underline{K} $\underline{48/00}$; $\underline{A61}$ \underline{P} $\underline{35/00}$; $\underline{C07}$ \underline{K} $\underline{19/00}$; $\underline{C12}$ \underline{N} $\underline{15/62}$; $\underline{C12}$ \underline{N} $\underline{15/63}$

Full Title Citation Front Review Classification Date Reference <u>Seguences Attachments</u> Claims KMC Draw De

☐ 2. Document ID: NZ 505108 A, WO 9933868 A2, AU 9924191 A, ZA 9811848 A, EP 1040123 A2, BR 9814487 A, CZ 200002376 A3, AU 729336 B, HU 200100526 A2, JP 2001527091 W

L4: Entry 2 of 3

File: DWPI

Oct 25, 2002

DERWENT-ACC-NO: 1999-405485

DERWENT-WEEK: 200274

COPYRIGHT 2006 DERWENT INFORMATION LTD

TITLE: Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to induce

immune response to HPV

INVENTOR: DALEMANS, W L J; GERARD, C M G

PRIORITY-DATA: 1997GB-0027262 (December 24, 1997)

PATENT-FAMILY:

 PUB-NO
 PUB-DATE
 LANGUAGE
 PAGES
 MAIN-IPC

 NZ 505108 A
 October 25, 2002
 000
 A61K039/02

 WO 9933868 A2
 July 8, 1999
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 C07K014/00



Record List Display Page 2 of 3

AU 9924191 A	July 19, 1999		000	
ZA 9811848 A	July 26, 2000		063	C07K000/00
EP 1040123 A2	October 4, 2000	E	000	C07K014/00
BR 9814487 A	October 10, 2000		000	C07K014/00
CZ 200002376 A3	November 15, 2000		000	C07K014/01
AU 729336 B	February 1, 2001		000	C07K014/00
HU 200100526 A2	June 28, 2001		000	A61K039/12
JP 2001527091 W	December 25, 2001		093	C07K014/025

INT-CL (IPC): $\underline{A61}$ K $\underline{38/16}$; $\underline{A61}$ K $\underline{39/00}$; $\underline{A61}$ K $\underline{39/02}$; $\underline{A61}$ K $\underline{39/09}$; $\underline{A61}$ K $\underline{39/102}$; $\underline{A61}$ K $\underline{39/385}$; $\underline{A61}$ K $\underline{39/39}$; $\underline{A61}$ P $\underline{35/00}$; $\underline{C07}$ K $\underline{0/00}$; $\underline{C07}$ K $\underline{14/01}$; $\underline{C07}$ K $\underline{14/025}$; $\underline{C07}$ K $\underline{14/285}$; $\underline{C07}$ K $\underline{14/315}$; $\underline{C07}$ K $\underline{19/00}$; $\underline{C12}$ N $\underline{15/09}$

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Document ID: DE 69824013 T2, WO 9910375 A2, AU 9892639 A, ZA 9807591 A, NO 200000850 A, EP 1007551 A2, BR 9812139 A, CZ 200000634 A3, CN 1276833 A, HU 200004327 A2, AU 732946 B, MX 2000001813 A1, KR 2001023193 A, JP 2001513986 W, US 6342224 B1, NZ 502632 A, US 20020182221 A1, EP 1007551 B1, DE 69824013 E, ES 2221198 T3

L4: Entry 3 of 3

File: DWPI

Jun 2, 2005

DERWENT-ACC-NO: 1999-190587

DERWENT-WEEK: 200537

COPYRIGHT 2006 DERWENT INFORMATION LTD

TITLE: Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for

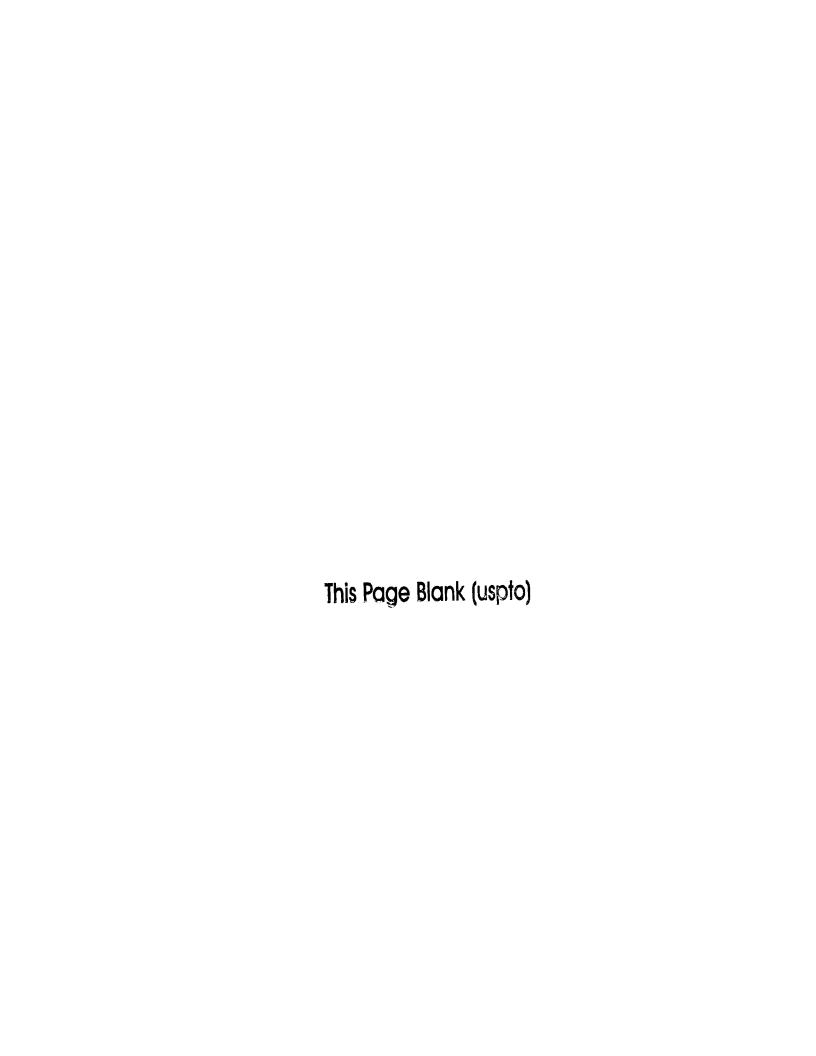
treatment or prophylaxis of HPV induced lesions

INVENTOR: BRUCK, C; DELISSE, A E F ; GERARD, C M G ; LOMBARDO-BENCHEIKH, A ; SILVA, T C ; CABEZON, S T ; CABEZON SILVA, T ; FERNANDE DELISSE, A E ; GHISLAINE GERARD, C

PRIORITY-DATA: 1997GB-0017953 (August 22, 1997)

PATENT-FAMILY:

PUB-NO	PUB-DATE	LANGUAGE	PAGES	MAIN-IPC
DE 69824013 T2	June 2, 2005		000	C07K014/025
WO 9910375 A2	March 4, 1999	E	095	C07K014/00
AU 9892639 A	March 16, 1999		000	C07K014/00
ZA 9807591 A	April 26, 2000		096	C07K000/00
NO 200000850 A	April 14, 2000		000	C07K019/00
EP 1007551 A2	June 14, 2000	E	000	C07K014/00
BR 9812139 A	July 18, 2000		000	C07K014/00
CZ 200000634 A3	January 17, 2001		000	C07K014/00
CN 1276833 A	December 13, 2000		000	C12N015/62
HU 200004327 A2	March 28, 2001		000	C07K014/00
AU 732946 B	May 3, 2001		000	C07K014/00
MX 2000001813 A1	October 1, 2000		000	C07K014/00
KR 2001023193 A	March 26, 2001		000	C12N015/62



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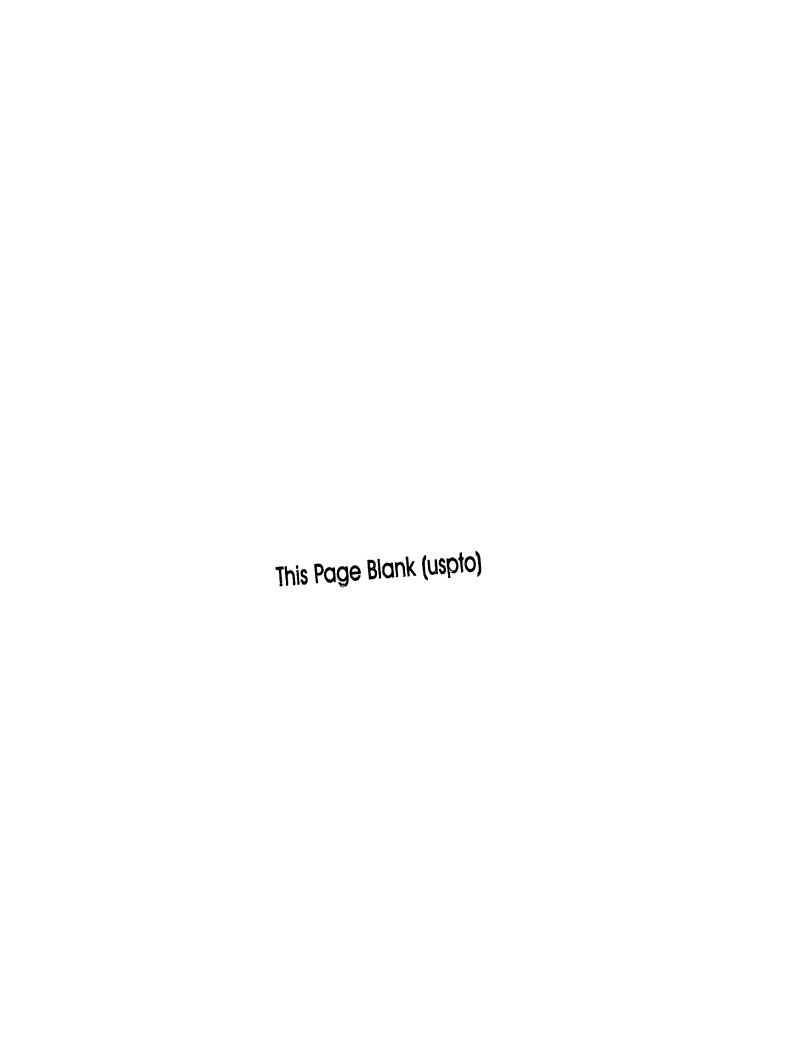
JP 2001513986 W	September 11, 2001		131	C12N015/09
US 6342224 B1	January 29, 2002		000	A61K039/00
NZ 502632 A	March 28, 2002		000	C07K014/285
US 20020182221 A1	December 5, 2002		000	A61K039/12
EP 1007551 B1	May 19, 2004	E	000	C07K014/025
DE 69824013 E	June 24, 2004		000	C07K014/025
ES 2221198 T3	December 16, 2004		000	C07K014/025

NZ 502632 A , US 20020182221 A1 INT-CL (IPC): A61 K 9/107; A61 K 38/02; A61 K 39/00; A61 K 39/12; A61 K 39/145; A61 K 39/39; A61 P 35/00; A61 P 37/00; C07 H 14/00; C07 H 21/04; C07 K 0/00; C07 K 1/00; C07 K 14/00; C12 N 1/15; C12 N 1/19; C12 N 1/20; C12 N 1/21; C12 N 1/20; C12 N

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☐ 1. Document ID: US 6558670 B1

L10: Entry 1 of 6

File: USPT

May 6, 2003

US-PAT-NO: 6558670

DOCUMENT-IDENTIFIER: US 6558670 B1

TITLE: Vaccine adjuvants .

DATE-ISSUED: May 6, 2003

INVENTOR-INFORMATION:

STATE ZIP CODE NAME CITY

Court St Etienne Friede; Martin BE BE

Hermand; Philippe Court St Etienne

US-CL-CURRENT: $\underline{424}/\underline{184.1}$; $\underline{424}/\underline{278.1}$, $\underline{424}/\underline{283.1}$, $\underline{514}/\underline{25}$

Full Title Citation Front Review Classification Date Reference Sample Lie Line Claims

☐ 2. Document ID: US 6544518 B1

L10: Entry 2 of 6 File: USPT Apr 8, 2003

COUNTRY

US-PAT-NO: 6544518

DOCUMENT-IDENTIFIER: US 6544518 B1

TITLE: Vaccines

DATE-ISSUED: April 8, 2003

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Friede; Martin Farnham GB Garcon; Nathalie Wavre BE Gerard; Catherine Marie Ghislaine Rhode Saint Genese BE Hermand; Philippe Court-Saint-Etienne BE

US-CL-CURRENT: 424/184.1; 424/208.1, 424/228.1, 424/229.1, 424/231.1, 424/249.1, <u>424/278.1</u>, <u>424/283.1</u>, <u>514/25</u>

Record List Display Page 2 of 4

Full Title Citation Front Review Classification Date Reference Sequences Attachments: Claims KMC Draw. De

☐ 3. Document ID: US 6342224 B1

L10: Entry 3 of 6

File: USPT

Jan 29, 2002

US-PAT-NO: 6342224

DOCUMENT-IDENTIFIER: US 6342224 B1

TITLE: Recombinant papillomavirus vaccine and method for production and treatment

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP	CODE	COUNTRY	
Bruck; Claudine	Rixensart				BE	
Silva; Teresa Cabezon	Lenkebeek				BE	
Fernande Delisse; Anne-Marie Eva	Gosselies				BE	
Ghislaine Gerard; Catherine Marie	Rhode Saint Genese				BE	
Lombardo-Bencheikh; Angela	Wavre				BE	

US-CL-CURRENT: 424/192.1; 424/185.1, 424/186.1, 424/204.1, 435/252.3, 435/320.1, 435/325, 435/69.3, 435/69.7, 530/350, 536/23.4, 536/23.72

Full	Title	Citation	Front	Review	Classification	Date	Reference	HERENS ALTERNITATES	Claims	KWIC	Draw, De

☐ 4. Document ID: US 6306397 B1

L10: Entry 4 of 6

File: USPT

Oct 23, 2001

US-PAT-NO: 6306397

DOCUMENT-IDENTIFIER: US 6306397 B1

TITLE: Variants of human papilloma virus antigens

DATE-ISSUED: October 23, 2001

INVENTOR-INFORMATION:

CITY STATE ZIP CODE COUNTRY NAME Edwards; Stirling John Northcote ΑU AU Cox; John Cooper Bullengarook ΑU Webb; Elizabeth Ann Eltham Frazer; Ian St. Lucia ΑU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/204.1, 435/235.1, 435/69.1, 435/69.7, 536/23.1, 536/23.72, 536/24.3

Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KMC Draw. De



☐ 5. Document ID: US 6303128 B1

L10: Entry 5 of 6

File: USPT

Oct 16, 2001

US-PAT-NO: 6303128

DOCUMENT-IDENTIFIER: US 6303128 B1

TITLE: Method for protein expression

DATE-ISSUED: October 16, 2001

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Webb; Elizabeth Ann Eltham AU Edwards; Stirling John Northcote AU

US-CL-CURRENT: $\underline{424}/\underline{199.1}$; $\underline{424}/\underline{192.1}$, $\underline{435}/\underline{235.1}$, $\underline{435}/\underline{320.1}$, $\underline{435}/\underline{325}$, $\underline{435}/\underline{69.1}$,

<u>435/69.7</u>

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DOCUMENT-IDENTIFIER: US 6004557 A

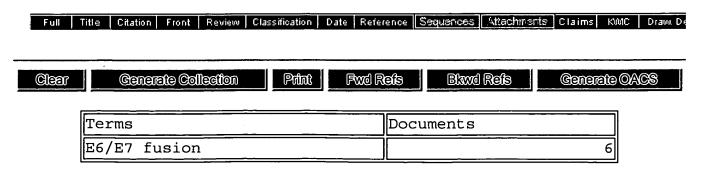
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DATE-ISSUED: December 21, 1999

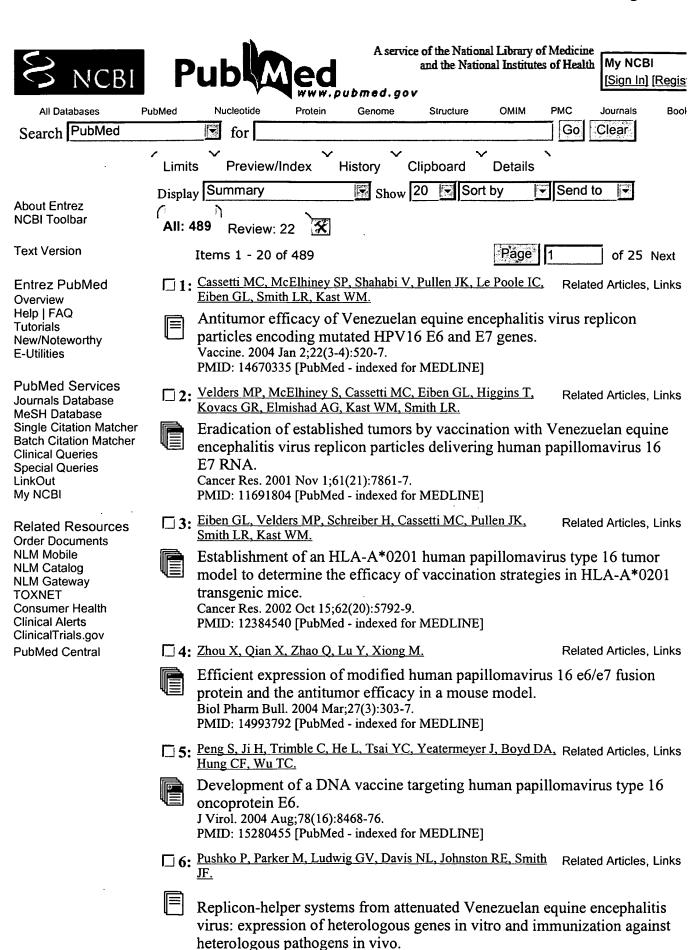
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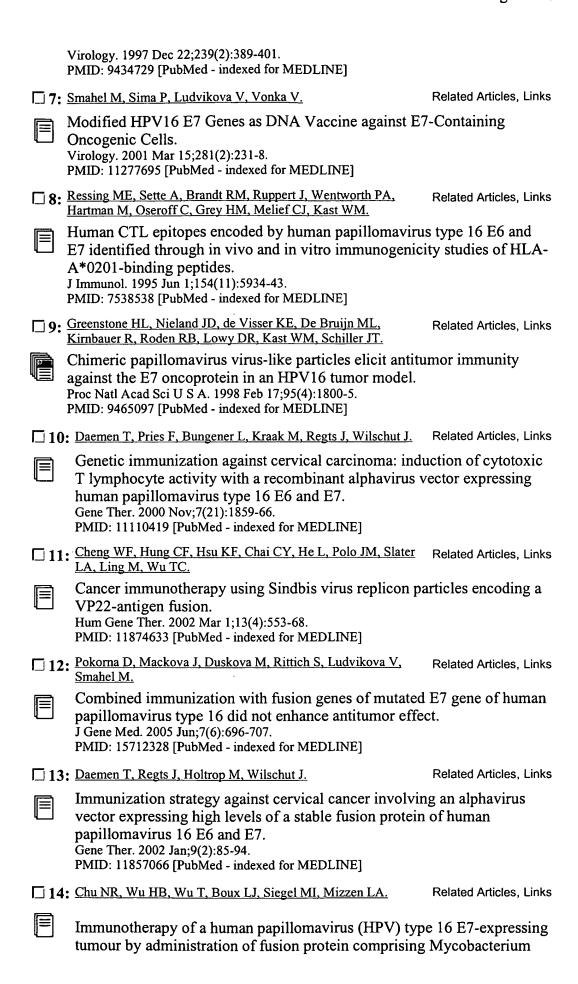
NAME CITY STATE ZIP CODE COUNTRY

Edwards; Stirling John Caburg AU
Cox; John Cooper Bullengarook AU
Webb; Elizabeth Ann Eltham AU
Frazer; Ian St. Lucia. AU



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bovis bacille Calmette-Guerin (BCG) hsp65 and HPV16 E7. Clin Exp Immunol. 2000 Aug;121(2):216-25. PMID: 10931134 [PubMed - indexed for MEDLINE] 15: Azoury-Ziadeh R, Herd K, Fernando GJ, Frazer IH, Tindle RW. Related Articles, Links T-helper epitopes identified within the E6 transforming protein of cervical cancer-associated human papillomavirus type 16. Viral Immunol. 1999;12(4):297-312. PMID: 10630789 [PubMed - indexed for MEDLINE] 16: Melero I, Singhal MC, McGowan P, Haugen HS, Blake J, Related Articles, Links Hellstrom KE, Yang G, Clegg CH, Chen L. Immunological ignorance of an E7-encoded cytolytic T-lymphocyte epitope in transgenic mice expressing the E7 and E6 oncogenes of human papillomavirus type 16. J Virol. 1997 May;71(5):3998-4004. PMID: 9094677 [PubMed - indexed for MEDLINE] 17: Daemen T, Riezebos-Brilman A, Regts J, Dontje B, van der Zee Related Articles, Links A, Wilschut J. Superior therapeutic efficacy of alphavirus-mediated immunization against human papilloma virus type 16 antigens in a murine tumour model: effects of the route of immunization. Antivir Ther. 2004 Oct;9(5):733-42. PMID: 15535411 [PubMed - indexed for MEDLINE] 18: Wakabayashi MT, Da Silva DM, Potkul RK, Kast WM. Related Articles, Links Comparison of human papillomavirus type 16 L1 chimeric virus-like particles versus L1/L2 chimeric virus-like particles in tumor prevention. Intervirology. 2002;45(4-6):300-7. PMID: 12566713 [PubMed - indexed for MEDLINE] 19: Indrova M, Reinis M, Bubenik J, Jandlova T, Bieblova J, Vonka Related Articles, Links V, Velek J. Immunogenicity of dendritic cell-based HPV16 E6/E7 peptide vaccines: CTL activation and protective effects. Folia Biol (Praha). 2004;50(6):184-93. PMID: 15709713 [PubMed - indexed for MEDLINE] [20: Lasaro MO, Diniz MO, Reyes-Sandoval A, Ertl HC, Ferreira LC. Related Articles, Links Anti-tumor DNA vaccines based on the expression of human papillomavirus-16 E6/E7 oncoproteins genetically fused with the glycoprotein D from herpes simplex virus-1. Microbes Infect. 2005 Dec;7(15):1541-50. Epub 2005 Sep 9. PMID: 16213178 [PubMed - indexed for MEDLINE] of 25 Next Items 1 - 20 of 489 Display Summary Show 20 Sort by Send to

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☐ 1. Document ID: US 6558670 B1

L10: Entry 1 of 6

File: USPT

May 6, 2003

US-PAT-NO: 6558670

DOCUMENT-IDENTIFIER: US 6558670 B1

TITLE: Vaccine adjuvants

DATE-ISSUED: May 6, 2003

INVENTOR-INFORMATION:

NAME CITY

STATE ZIP CODE (

COUNTRY

Friede; Martin Hermand; Philippe Court St Etienne Court St Etienne

BE

BE

US-CL-CURRENT: <u>424/184.1</u>; <u>424/278.1</u>, <u>424/283.1</u>, <u>514/25</u>

Full Title Citation Front Review Classification Date Reference <u>Sequences Attachments</u> Claims KMC Draw. De

☐ 2. Document ID: US 6544518 B1

L10: Entry 2 of 6

File: USPT

Apr 8, 2003

US-PAT-NO: 6544518

DOCUMENT-IDENTIFIER: US 6544518 B1

TITLE: Vaccines

DATE-ISSUED: April 8, 2003

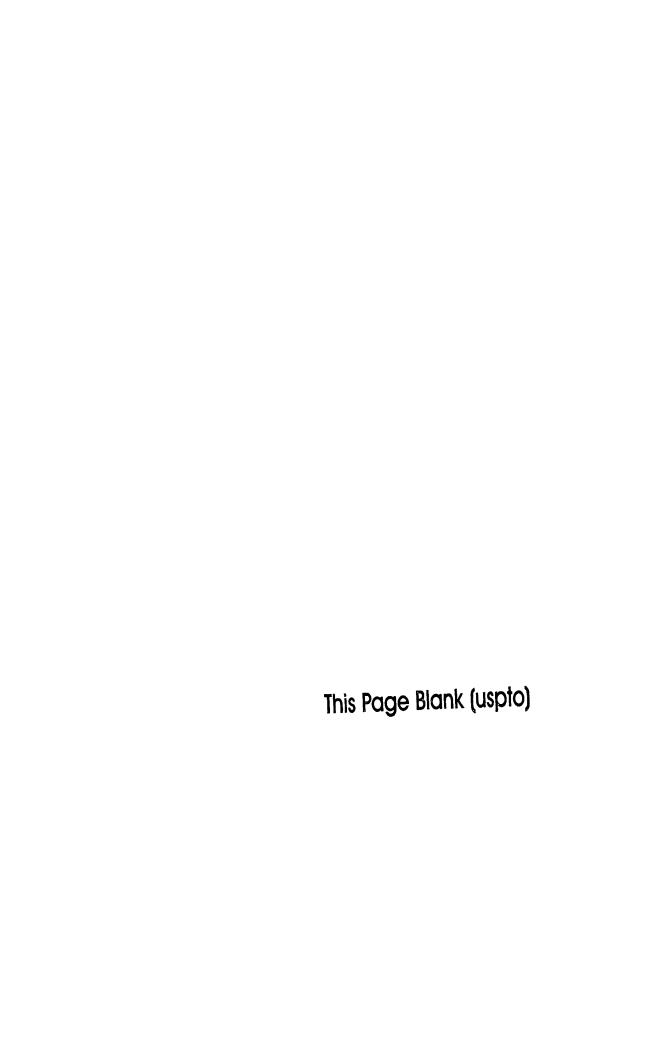
INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Friede; Martin Farnham GB
Garcon; Nathalie Wavre BE
Gerard; Catherine Marie Ghislaine Rhode Saint Genese BE
Hermand; Philippe Court-Saint-Etienne BE

US-CL-CURRENT: 424/184.1; 424/208.1, 424/228.1, 424/229.1, 424/231.1, 424/249.1,

424/278.1, 424/283.1, 514/25



Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KWIC Draw De

☐ 3. Document ID: US 6342224 B1

L10: Entry 3 of 6

File: USPT

Jan 29, 2002

US-PAT-NO: 6342224

DOCUMENT-IDENTIFIER: US 6342224 B1

TITLE: Recombinant papillomavirus vaccine and method for production and treatment

DATE-ISSUED: January 29, 2002

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP	CODE	COUNTRY
Bruck; Claudine	Rixensart				BE
Silva; Teresa Cabezon	Lenkebeek				BE
Fernande Delisse; Anne-Marie Eva	Gosselies				BE
Ghislaine Gerard; Catherine Marie	Rhode Saint Genese				BE
Lombardo-Bencheikh; Angela	Wavre				BE

US-CL-CURRENT: $\underline{424}/\underline{192.1}$; $\underline{424}/\underline{185.1}$, $\underline{424}/\underline{186.1}$, $\underline{424}/\underline{204.1}$, $\underline{435}/\underline{252.3}$, $\underline{435}/\underline{320.1}$, $\underline{435}/\underline{69.3}$, $\underline{435}/\underline{69.7}$, $\underline{530}/\underline{350}$, $\underline{536}/\underline{23.4}$, $\underline{536}/\underline{23.72}$

Full	Title	Citation	Front	Review	Classification	Date	Reference	《 相符》的自治	Claims	KWIC	Draw, De
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☐ 4. Document ID: US 6306397 B1

L10: Entry 4 of 6

File: USPT

Oct 23, 2001

US-PAT-NO: 6306397

DOCUMENT-IDENTIFIER: US 6306397 B1

TITLE: Variants of human papilloma virus antigens

DATE-ISSUED: October 23, 2001

INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY
Edwards; Stirling John Northcote AU
Cox; John Cooper Bullengarook AU
Webb; Elizabeth Ann Eltham AU
Frazer; Ian St. Lucia AU

US-CL-CURRENT: 424/192.1; 424/186.1, 424/204.1, 435/235.1, 435/69.1, 435/69.7, 536/23.1, 536/23.72, 536/24.3

Full Title Citation Front Review Classification Date Reference Sequences Attachments Claims KWIC Draw De

☐ 5. Document ID: US 6303128 B1

L10: Entry 5 of 6

File: USPT

Oct 16, 2001

US-PAT-NO: 6303128

DOCUMENT-IDENTIFIER: US 6303128 B1

TITLE: Method for protein expression

DATE-ISSUED: October 16, 2001

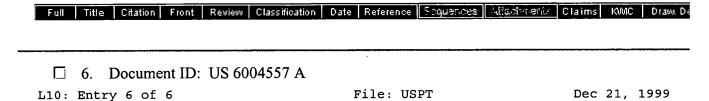
INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Webb; Elizabeth Ann Eltham AU
Edwards; Stirling John Northcote AU

US-CL-CURRENT: 424/199.1; 424/192.1, 435/235.1, 435/320.1, 435/325, 435/69.1,

<u>435/69.7</u>



US-PAT-NO: 6004557

DOCUMENT-IDENTIFIER: US 6004557 A

TITLE: Variants of human papillomavirus antigens

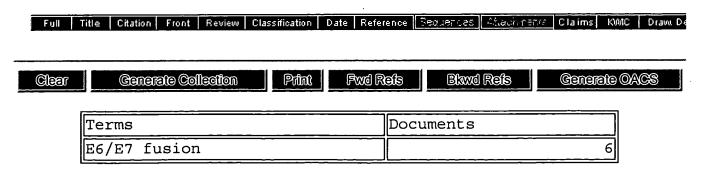
DATE-ISSUED: December 21, 1999

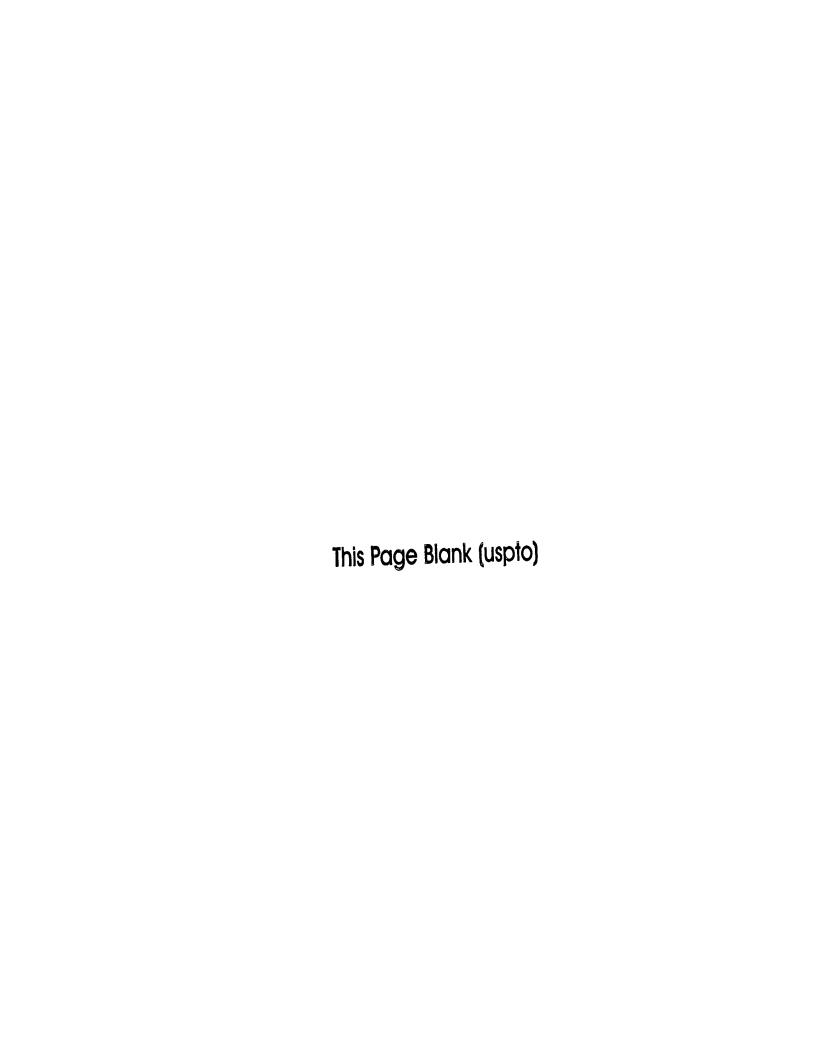
INVENTOR-INFORMATION:

NAME CITY STATE ZIP CODE COUNTRY

Edwards; Stirling John Caburg AU
Cox; John Cooper Bullengarook AU
Webb; Elizabeth Ann Eltham AU
Frazer; Ian St. Lucia. AU

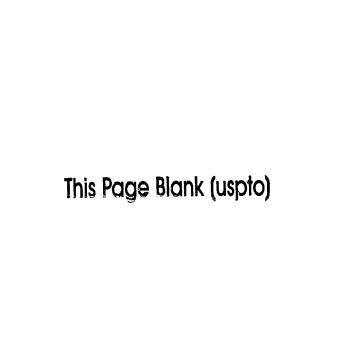
US-CL-CURRENT: $\underline{424}/\underline{192.1}$; $\underline{424}/\underline{186.1}$, $\underline{424}/\underline{199.1}$, $\underline{424}/\underline{204.1}$, $\underline{435}/\underline{235.1}$, $\underline{435}/\underline{320.1}$, $\underline{435}/\underline{69.7}$, $\underline{536}/\underline{23.1}$, $\underline{536}/\underline{23.72}$, $\underline{536}/\underline{24.3}$





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Previous Page Next Page Go to Doc#



WEST Search History

Hide Items Restore Clear Cancel

DATE: Thursday, June 15, 2006

Hide?	Set Name	Query	<u>Hit Count</u>
	DB = USR	PT; PLUR=YES; OP=A	DJ
	L10	E6/E7 fusion	6
	L9	US-6342224-B1.did.	1
	L8	US-6342224-B1.did.	1
DB=EPAB; PLUR=YES; OP=ADJ			
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DB=DWPI; PLUR=YES; OP=ADJ			
	L4	E6/E7 fusion	3
DB=PGPB; PLUR=YES; OP=ADJ			
	L3	E6/E7 fusion	12
	L2	E6/E7 fuion	0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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AAY25378
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AAY25634
AED52634
AED527366
AD044068
AD0427366
AD0427366
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AAR42361
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AAW557721
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Biocceleration
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Aay02634
Aag42640
Ad642068
Ada27366
Ada92544
Ada14293
Aae38618
Aar22767
Aar42361
Aay58476
Aay5847721
Aab98421
Aab98421
Aau72607
Aab67546
Aab86332
Aau177713
Aau10810
Abb82375
                                                                                                                                                           Ado44070
Aed13079
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                                                                                                                                                                                 Description
Amino aci

HPV16 E7

HPV fusion

Prot.D1/3

Fusion pr

Amino aci

HPV-16 L2

HUMAN PAP

HUMAN PAP

HUMAN PAP

HUMAN PAP

HUMAN PAP

Wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
 888889999999189448239323982333800999999911
       AAO16630
AAD7190076
ADF18632
ADD749005
ADD749005
ADD7469083
ADD7469083
ADD769083
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ADD798615
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ADD79
AGOJEGGO Human pap
AdG09516 Human pap
AdG109516 Amino aci
Add10632 Human pap
AdG10632 Human pap
AdM32916 Amino aci
Adn4003 Amino aci
Ad044073 Amino aci
Ad044073 Amino aci
Ad044073 Amino aci
Ad044073 Amino aci
Ad0415532 Human pap
Adv59383 HPV16 E7
Aea40816 Anti-apop
Aeb11989 HPV16 E7
Aec98392 HPV prote
Aec98871 HPV 16 E7
Aed63360 HPV16 E7
Aed63360 HPV16 E7
Add992615 HPV fusio
Aay02631 Furbino aci
Aab31616 Amino aci
Aab31616 Amino aci
Aay1380 HPV fusio
Aay02631 Furbino Br
Aed52644 Fusion pr
Aed52644 Fusion pr
Aed92636 Amino aci
Aay41380 Amino aci
Aay25371 Human pap
Aer47005 Human pap
Aer47005 Human pap
Aer47005 Human pap
Aer40815 Amino aci
Aab31610 Amino aci
Aab31611 Amino aci
Aab31611 Amino aci
Aab31614 Amino aci
Aab31615 Amino aci
Aab31617 Amino aci
Aab31618 Amino aci
Aab31618 Amino aci
Aab31611 Amino aci
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Adf09516 Human I
Adf18632 Human I
Adf18632 Human I
Adf190076 Human I
Adm12916 Amino a
Adm49005 Human I
Adw1532 Human I
Adw1532 Human I
Adw15932 Human I
Adw16016 Anti-al
Aea40816 Anti-al
Aeb11989 HPV16
Aec98871 HPV 16
Aec19871 HPV 16
Aed13078 HPV16
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RESULT 1
AD044070
ID AD044070
ID AD044070
AXX AD04
AXX B6 F
KW E6 F
KW Cerv
KW anal
XXX Gene
OS Synt
XXX Gene
OS Synt
XXX Gene
OS Synt
XX WO2(
PN W02(
PN W02(
AM
XXX O3-(
PR 03-(
PR 03-(
AM
XXX O1-)
CC CAN
XXX O2-(
PR 03-(
CXX O2-(
CX O2-(
CXX O2
                                                                                                                                                                                                    The present sequence represents a fusion protein, comprising E7 and E6 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion CC protein is designated E7E6PentM, and comprises an E7 amino terminus CC (where residues 24, 26 and 91 have been replaced with glycine) and an E6 CC (arboxy terminus (where residues 63 and 106 have been replaced with CC glycine). E7E6PentM is representative of fusion proteins of the CC invention. The specification describes human papillomavirus E6 and E7 CC polypeptides, where the E7 polypeptide has mutations at any one or more CC of the amino acids corresponding to amino acids 24, 26 or 91 of the CC sequence given in AD044073 and the E6 polypeptide has no mutations or has CC mutations at any one or more of the amino acids corresponding to amino CC cacids 63 or 106 of there sequence given in AD044072. The polypeptides of CC the invention are useful for treating or preventing human papillomavirus CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins CC and nucleic acids encoding the fusion proteins are useful for generating CC immune responses against HPV. They are also useful for treating lower CC gastrointesting liver cancers.
                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97
98
99
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type 16. Synthetic.
                                                                                                                          Sequence 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 22; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-316328/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cervical cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a fusion protein designated E7E6PentM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75-76; 101pp; English.
                                                                                                                                                                                 tract cancers, e.g. anal cancer, and other system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune response;
                             99.4%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9999
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ADE21865
ADO05276
Score 514; DB 8; Length 248; Pred. No. 3.9e-57; O; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Abb82376 Modified
Ade21865 HPV-16 E7
Ado05276 Human pap
Adu66377 Human pap
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RESULT 2
ADDITO 19
ID ADDI
ACC AEDI
ACC AEDI
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XX AEDI
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                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel vaccine composed of an antigen protein and a second protein as an s-(methyl mercury)-1-cysteine (CMH class II) ligand. The second protein is taken from a group including human Lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures. The viral antigens can be for hepatitis B (HBV), human papillomavirus (HBV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-Barr virus (EBV), Cytomegalovirus (CMV), and their combinations. The bacterial antigens can be intracellular bacteria of tuberculosis, leprosy and listeria. A vaccine of the invention has virucide, and antibacterial
                                                                                                                                                                                                                                                                                                                                                                      Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Therapeutic vaccine, for viral and bacterial conditions, comprises antigen protein and a viral or bacterial protein, coupled together stable hydrogen or covalence bonds in biological media.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AED13077.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPV16 E7 variant protein sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                activity. The present sequence represents the HPV16 variant E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 1; 51pp; French.
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                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYGYGQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                        99.2%;
                                                                                                                                                                                                                                     Score 513; DB 9; Lo
Pred. No. 1.6e-57;
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RESULT 4
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonuclectide. The products of the invention can be used to induce arimmune response in a patient to an HPV antigen. They can also be used f preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-405485/34.
N-PSDB; AAX78794.
                   Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy; tumour; lesion; benign; malignant; virus; infection.
                                                                                                                    17-OCT-2003
22-JUN-1999
                                                                                                                                                                                  AAY02634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                            Prot.D1/3-E7-mut(C24G, E26Q)/HPV16 protein.
                                                                                                                                                                                                                      AAY02634 standard; protein;
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                                                                                                                                                                                                                                                                                                                            174
                                                                                                                                                                                                                                                                                                                                                                                                           114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                  51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYGYQQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 513; DB 2;
Pred. No. 4.6e-57;
0; Mismatches 3
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RESULT 5
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus.
Haemophilus influenza
Chimeric.
                                                                                            Haemophilus influenzae; strain Human papillomavirus type 16. Synthetic.
                                                                                                                                              Fusion protein; vaccine; papilloma; virucide; uterine cervix tumor; E7;
                                                                                                                                                                                                           29-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 8; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1999
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                       Misc-difference
                                               Misc-difference
                                                                                                                                                                                 Fusion protein D1/3-E7-His(HPV16), C137G/E139Q
                                                                                                                                                                                                                                                          AED52640
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                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYGYQQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       220 AA;
                                                                                                                                                                                                                                                        standard; protein;
                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cabezon Silva T,
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                       /note= "Wild-type Cys substituted by Gly" 139
                                              Location/Qualifiers
           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                  99.2%;
          "Wild-type Glu substituted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Delisse AEF,
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 513; DB 2;
Pred. No. 4.6e-57;
0; Mismatches 3
                                                                                                                                             cytostatic; papillomavirus infection; mutein; D protein.
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (cLyth) or thioredoxin. The present sequence represents a mutated HPV-H. influenzae D protein, fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-MAR-2005.
Smith L,
                                                                                                             03-OCT-2002; 2002US-0415929P
                                                                                                                                                                  02-OCT-2003; 2003WO-US031726
                                                                                                                                                                                                                              15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus type 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a fusion protein
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                                                        (AMHP ) WYETH HOLDINGS CORP
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Cassetti MC
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96.9%;
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Pred. No. 4.6e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                           gastrointestinal tract cancer;
penile cancer; vulvar cancer.
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14-FEB-2002; 14-FEB-2002; 14-FEB-2002;

2002US-0356118P. 2002US-0356119P. 2002US-0356123P. 2002US-0356113P. 2003WO-US004516

14-FEB-2002; 14-FEB-2003; 21-AUG-2003 WO2003068804-A2 Human papillomavirus cell line; American Type Culture Collection PTA-4047; ATCC-4047; baculoviruses; viral recombinant protein; virus-like particle; v diagnostic reagent; human papillomavirus type 16; HPV-16; L2/E7/

vaccine;

protein.

type 16

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RESULT 7
ADA27366
ID ADA2
XX ADA22
XX ADA2
XX ADA2
XX CPL
DT 20-N
DE HPV-
XX Cell
EW diag
KW diag
KW diag
KW diag
XX Huma
OS Huma
OS Huma
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OS 114-F
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                     HPV-16 L2/E7/E2 fusion protein SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                           20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADA27366 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system, including penile and vulvar cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; 805
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Pred. No. 5.3e-57;
" "" matches 3;
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2002US-0356133P. 2002US-0356135P.

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14-FEB-2002;
14-FEB-2002;
14-FEB-2002;
14-FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes a cell line comprising a cell that is a clone, derivative, mutant and/or transfectant of a cell line designated American Type Culture Collection (ATCC) PTA-4047. The cell upon culture grows continuously and retains the identifying characteristics of the cell line designated ATCC-4047. Also described is a process of making a cell line. The insect cell line suseful in replicating baculoviruses, as a host substrate for baculovirus plaque assays, as a source of insect proteins, acts as depot for cell transfection to produce recombinant baculoviruses, and in expressing viral recombinant proteins.

Extracellular and intracellular viral recombinant proteins and virus-like particles expressed from the cell line are useful as pharmaceutical compositions, vaccines or diagnostic reagents. The present sequence represents a human papillomavirus type 16 (HPV-16) L2/E7/E2 fusion protein, which is used in the exemplification of the present invention.
                                                                                                                                                                      codon optimised; viral capsid protein; virus-like particle; VLP;
antigenic; human papillomavirus infection; virucide; vaccine;
gene therapy; human papillomavirus type 16; dysplasia; infection
                                                                                                                                                                                                                                                                                              HPV-16 L2/E7/E2 fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADA92544 standard; protein; 805
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        baculoviruses to produce large amounts of recombin medical, pharmaceutical and veterinary importance.
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14-FEB-2002;
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14-FEB-2002;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New insect cell line designated ATCC PTA-4047, useful
                                                     Human papillomavirus type 16
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DB; ADA27374.
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                                                                                                                                             protein.
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2002US-0356151P.
2002US-0356154P.
2002US-0356154P.
2002US-0356156P.
2002US-0356156P.
2002US-0356161P.
2002US-0356161P.
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96.9%;
                                                                                                                                                                                                                                                                                              amino acid sequence
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Pred. No. 2.4e-56;
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                                                                                                                                                                                                                                                                                              SEQ
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                                                                                                                                                                                                                                                                                                 NO: 9
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                                                                                                                                                                      infection; HPV-16;
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The present invention describes a codon optimised polynucleotide encoding CC a viral capsid protein that self assembles into a virus-like particle CC (VLP) that exhibits conformational antigenic epitopes capable of raising CC neutralising antibodies, where the VLP is expressed from a host cell comprising the above codon optimised polynucleotide operably liked to a eukaryotic or prokaryotic control element, capable of replication in prokaryotic and/or CC eukaryotic host; (2) a host cell comprising the vector; (3) a cc multiplicity of VLPs that exhibit conformational antigenic epitopes, and CC papillomavirus related disease or disorder, comprising a CC multiplicity of VLPs that exhibit conformational antigenic epitopes, and CC acarrier, diluent or adjuvant; (4) a diagnostic kit for detecting a papillomavirus related disease or disorder, comprising a CC papillomavirus infection, comprising a multiplicity of VLPs that exhibit conformational antigenic epitopes, and cetection agent comprising a construction of the comprising a construction of the comprising a construction of the comprising a construction agent comprising a construction of the comprising a construction of construction of construction of construction of construction construction and construction construction of construction of construction and construction of constr
14 FEB-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New codon optimized polynucleotide encoding a viral capsid protein that self assembles into a virus-like particle, useful for diagnosing, preventing or treating human papillomavirus infections or associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-FEB-2003;
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2002US-0356150P.
2002US-0356151P.
2002US-0356154P.
2002US-0356154P.
2002US-0356156P.
2002US-0356157P.
2002US-0356167P.
2002US-0356162P.
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2002US-0356126P.
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WO2003068933-A2

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ADA14293
ADA
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14-FEB-2002;
14-FEB-2002;
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14-FEB-
14-FEB-
The present invention describes a method for purifying a recombinant extracellular or intracellular virus-like particle (VLP). The method comprises harvesting a cell suspension comprising cells containing a plurality of VLPs to produce a harvested supernatant, optionally the disrupting the harvested cells to produce cell lysates containing the VLP, clarifying the harvested supernatant, concentrating the containing the concentration, disfiltering the concentrated supernatant, and recovering the purified recombinant VLP. Also described: (1) a cell line designate
                                                                                                                                                                                                                                                                                                      Purifying a recombinant human papillomavirus (HPV) L1, useful for diagnosing, preventing or treating HPV infections, comprises clarifying, concentrating and diafiltering cells containing HPV particles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             purification; recombinant extracellular virus-like particle; Virecombinant intracellular virus-like particle; Virecombinant intracellular virus-like particle; virus-like particle; Virus-like particle; Virucide; vaccine; gene therapy, human papillomavirus; HPV; infection; dysplasia; HPV-16; fusion protein.
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                                                                                                                                                                                                                                                        Disclosure;
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2002US-0356156P.
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14-FEB-2002;
14-FEB-2002;
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Pred. No. 2.4e-56;
0; Mismatches 3
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The peptide is the sequence of the human papillomavirus HPV 16 E7 nucleoprotein. Peptides corresponding to regions (pref. epitopic regions) of HPV 16 E7 were synthesised by standard Merrifield synthesis. Examples of such peptides are E7 1-10, 29-50 or 70-81. Compositions contg. these
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21-SEP-1992
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                                                                                                     Immunogenic peptide(s) derived from E6 or E7 region of HI recombinant cells encoding them, useful in treatment and cervical warts or cancer resulting from HPV infection.
                                                                                                                                                                                                                                                       26-SEP-1990;
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Pred. No. 2.4e-56;
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prophylaxis
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RESULT 12
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                                                                                                                                                                                                                         The sequence is that of the human papillomavirus type 16 E7 protein. protein sequence was aligned with that of bovine papillomavirus type See also AAR42360. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                                                                                                          Use of papilloma-virus E7 protein or fragments for the therapy of papilloma-virus disease - for the regression of tumours e.g. removal of warts from udders or mouth of milking cows or for treatment of horses of warts from udders or mouth of milking cows or for treatment of horses of warts from udders or mouth of milking cows or for treatment of horses of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic
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21-MAY-1994
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Pred. No. 2.2e-57;
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Pred. No. 2.
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                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Evaluation of proliferative state of cells transformed with human papilloma virus - by determining cyclin-dependent kinase activity induced by E7 onco-protein.
                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98
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N-PSDB; AAV16717.
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                                                                                                                                                                                                                                                  The invention relates to a novel assay for identifying compounds which inhibit viral replication and pathogenesis by increasing proteasomal degradation of viral components or molecules induced by viral infection. The method comprises reacting a compound with proteasomal protein (20% proteasomes separately with or without 19% and 11% complexes), viral gene product, and protein or peptide substrates, measuring protease activity; and identifying the compound as an inhibitor if the protease activity of the assay system is increased. The assays of the invention can be used to identify compounds which inhibit viral replication and pathogenesis, and modulate and/or regulate proteasome activity. Compounds which increase proteasomal degradation of viral components or molecules induced by viral infection are of value in the treatment of viral disease. Compounds which modulate proteasomal nuclease activity have use in the treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-JUN-1998;
13-JUN-1998;
13-JUN-1998;
13-JUN-1998;
                                                                                                                                                               Sequence
                                                                                                                                                                                                        inflammatory disease, and AIDS in HIV infected patients. The methods may also be used to generate resistance to bacterial or viral damage. Sequences AAY58472-Y58474 represent examples of viral proteins which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPV B7 oncoprotein; proteasome activity; degradation; virus component; viral infection; inflammatory disease; anti-inflammatory; anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-106109/09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus (HPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY58474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY58474 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 8; 35pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                regulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel assay methods for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRID-) BRIDGEHEAD TECHNOLOGIES
              13
                                                           1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                    95;
                                                                                                                                                                                             proteasomal
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  proteosomal
                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Petit F,
                                                                                                                                                                8
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nicolas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98GB-00012760
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98GB-00012759.
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98GB-00012757.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-GB001840
                                                                                                                                                                                             function
                                                                                                                   99.0%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kloetzel P, P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E7 oncoprotein.
                                                                                                   0;
                                                                                                   Score 512; DB
Pred. No. 2.2e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jarrousse A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compounds which modulate and/or
                                                                                                                   DB 3;
.2e-57;
                                                                                                                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gautier
                                                                                                    Indels
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                                                                                                    0
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                                                                                                   Gaps
                                          60
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RESULT 15
AXY57721
ID AXY57
AC AAY57
AC CACPI
KW CCACPI
XX CWEDI
XX CWEDI
XX WPI;
DR WPI;
DR WPI;
DR WPI;
DR WPI;
CC The I
CC The
RESULT 16
AAB98421
ID AAB98
XX
AC AAB98
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genital warts such as condylomata acuminata. However, the type and severity of disease caused by the papillomavirus is dependent on the strain causing the infection. The present sequence represents the human papillomavirus 16 E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a fusion protein comprising 2 amino acids sequences from 2 different papillomavirus specific (PVS) proteins. The fusion protein may be administered for preventing and treating papillomavirus infections in humans and animals. Papillomaviruses are implicated in the pathology of malignant tumour formation in the anogenital tract (of these tumours, cervical cancer is the most frequent (500000 cases/year) and in the formation of precursor lesions of cervical intrapithalial neoplasia ((IN)). Papillomaviruses also cause benign
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pusion proteins comprising papillomavirus specific proteins useful for vaccinating against malignant tumors of the anogenital tract such as cervical carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus; HPV; L1 fusion protein; vaccine; cytostatic; viral capsomere; virucide; dermatological; malignant tumour formation; cervical cancer; cervical intraepithelial neoplasia; genital wart;
                               AAB98421;
                                                                                      AAB98421 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-063092/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burger A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 34; 46pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus 16 E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MEDI-) MEDIGENE GMBH.
                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                           μ
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                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hallek M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98CA-02229955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98CA-02229955
                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98
                                                                                          98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 512; DB 3;
Pred. No. 2.2e-57;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 98
                                                                                                                                                                                                                                        98
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                                                                                                                                                                                                                                                                                                                                                               60
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RESULT 17
AAU01718
ID AAU01
XX
AC AAU01

AAU01718 standard; protein; 98 AA

AAU01718;

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                                                                                                                                                                                                                                        The present invention describes an isolated prepared human papillomavirus (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine (C production. Peptides and corresponding nucleic acid compositions from the C present invention are useful for stimulating an immune response to HPV by stimulating the production of CTL or HTL responses, specifically in the C manifested symptoms e.g. genital warts or neoplastic growth. The peptides (C manifested symptoms e.g. genital warts or neoplastic CTLs following (C can also be used in a tetramer staining assay to assess peripheral blood (C mononuclear cells for the presence of antigen-specific CTLs following (C exposure to a pathogen or immunogen, and as reagents to evaluate immune (C compositions are useful for removing warts or treating HPV infections. (C The epitopes for inclusion in an epitope-base vaccine may be selected (C from conserved regions of viral or tumour-associated antigens, which (C epitope-base vaccines. An additional advantage is the ability to combine (C epitopes achieving enhanced immunogenicity, the major benefit of the (C vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent (C invention
                                                                                                                                                Query Match
Best Local
                                                                                                                                 Matches
                                                                                                                                                                                               Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       An isolated human papilloma virus (HPV) epitope, useful in vaccines for treating HPV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-DEC-1999; 99US-0172705P
15-AUG-2000; 2000US-00641528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-DEC-2000; 2000WO-US033549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV; epitope; T cell; identification; vaccine; infection; genital wart; neoplastic growth; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 21; 756pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-381497/40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIM-) EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              papillomavirus protein HPV16 E7
61
                             19
                                                                                                                                 95;
                                                                                                                                                Similarity
                                                                                MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                           MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sidney J,
                                                                                                                                                                                                 Ŗ,
                                                                                                                               Conservative
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                                                                                                                                                96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Southwood S,
                                                                                                                               Score 512; DB 4; L
Pred. No. 2.2e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chesnut R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Celis
                                                                                                                                                                Length 98;
                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Grey HM;
                                                                                                                                 <u>.</u>
                                                                                                                                 Gaps
                                                                  60
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cc cyroplasmic translocation domain of a Pseudomonas excretion (CC or a granulocyte-macrophage colony stimulating factor (GM-CSF); and (b) a CC second polypeptide domain containing an antigenic polypeptide. A CC composition comprising the chimeric polypeptide is useful for inducing an immune response such as a cytotoxic T cell response. The nucleic acid or cyrotoxic response to the composition is administered as naked DNA by gene gun or equivalent, or by liposomal CC composition. These are thus useful for vaccinating a mammal against composition by inducing an immune response to a pathogen. Preferably they care useful for vaccinating a mammal against the compositions and methods are useful for stimulating or enhancing the compositions and methods are useful for stimulating or enhancing the capid molecules and vaccination methods, yield potent antigen. The climeric nucleic capid molecules and vaccination methods, yield potent antigen-specific commune response that is at least 40 fold more potent than conventional CC DNA vaccines. The vaccines are safe and useful for administration to immunogenicity
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                                                                                                                                                                                                                             Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The sequence represents the amino acid sequence of human papilloma virus-16 (HPV-16) E7 antigen used in construction of a chimeric polypeptide comprising: (a) a first polypeptide domain containing a carboxy terminal fragment of a heat shock protein (HSP), an Flt-3 ligand (FL), a cytoplasmic translocation domain of a Pseudomonas exotoxin A (ETA dII),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New chimeric polypeptide, useful as anti-tumor vaccines, comprises carboxy terminal fragment of heat shock protein, Flt-3 ligand or cytoplasmic translocation domain of Pseudomonas exotoxin A and antigenic
                                                                                                                                                                                                                           Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20-OCT-1999; 99US-00421608.
09-FEB-2000; 2000US-00501097.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF; chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A; ET antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine; immunotherapy; HPV-16; E7 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 39; 110pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papilloma virus-16 (HPV-16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2001
                                     61
                                                                                                                                                    95;
                                                                                                                                                                    Similarity
                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                         MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQABPDRAHYNIVTFCCK
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                    99.0%;
                                                                                                                                              Score 512; DB Pred. No. 2.2e 0; Mismatches
                                                                                                                                                  <u>..</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E7 antigen
                                                                                                                                                                    DB 4; Length 98; .2e-57;
                                                                                                                                                ω
•-
                                                                                                                                                  Indels
                                                                                                                                                <u>,</u>
                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ETA dII;
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ш

1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60

Matches

Local Similarity 95;

Conservative

<u>,</u>

Indels

٥,

Gaps

60

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RESULT 18
AAU72607
ID AAU72
                                                                            Creambent kinase-2 (CDK2) kinase (I) activity, comprising measuring (I) contivity on CDK2 substrate in the presence of human papillomavirus (HPV) CC E7 or its fragment, and in the presence of human papillomavirus (HPV) CC E7 or its fragment, and in the presence and absence of test compound. The clear compound is identified as inhibitor of E7-induced (I) activity when CC decreased phosphorylation of CDK2 substrate is detected. The method is useful for identifying an antivirate is detected. The method is cleantifying an inhibitor of E7-induced CDK2 kinase activity. This CC measuring viral proliferation in the presence and absence of identified inhibitor as an antiviral agent when CC decreased proliferation in the presence and absence of identified CC identified inhibitors are useful for reducing HPV E7-induced kinase activity or for ameliorating HPV proliferation by inhibiting E7-induced CC compared to viral proliferation in the absence of the inhibitor. The CC identified inhibitors are useful for reducing HPV E7-induced kinase complex. The inhibitors identified by inhibiting E7-induced CC prosence complex. The inhibitors identified by inhibiting E7-induced CC control of the inhibitors identified by inhibiting E7-induced cCC control of medicament for ameliorating viral infection e.g. HPV CC infection, adenoviral infection or similar virus 40 (SV40) infection. The CC correct os field.)
                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus; HPV; E7; cyclin E; cyclin A; virucide; E7-induced cyclin-dependent kinase-2; CDK2 kinase; HPV infecadenoviral infection; simian virus 40 infection; SV40.
                                                                          Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying E7-induced cyclin-dependent kinase-2 activity inhibitor, comprises identifying test compounds which reduce cyclin-dependent kina-2 substrate phosphorylation in presence of human papillomavirus E7 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                06-AUG-2003
26-FEB-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 12-13; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fisher C, He W;
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25-AUG-2000; 2000US-00648215.
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(HEWW/) HE W.
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(first entry)
                 99.0%;
Score 512; DB 4; I
Pred. No. 2.2e-57;
0; Mismatches 3;
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RESULT 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The specification describes a method for identifying inhibitors of E7-induced CDK2 kinase activity. The method comprises measuring CDK2 kinase activity on a CDK2 substrate in presence of human papillomavirus (HPV) E7 (or fragment), in presence and absence of a test compound and measuring phosphorylation of substrate. The method is useful for identifying an inhibitor of E7-induced CDK2 kinase activity. The identified inhibitor is useful for reducing or inhibiting HPV proliferation in an individual. Inhibitors of E7 binding to the CDK2 complex are useful in preparing medicament for ameliorating viral infection e.g. HPV infection, adenoviral or SV40 infection. The present sequence represents a papillomavirus E7 fragment, which is used in the method of the invention. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying inhibitors of human papilloma virus E7 protein-induced increase in CDK2 kinase activity for use as antiviral agent, by me kinase activity on CDK2 substrate in presence of E7 protein, test
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11-SEP-2003
29-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a E7 fragment that activates CDK2.
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                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                               Score 512; DB 4;
Pred. No. 2.2e-57;
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RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes a fusion protein comprising cell import and/or export signal sequences and an antigen which is suitable for immunizing an individual against a disease, together with a DNA that codes for said protein. The invention also relates to the use of the protein (II) and its encoding DNA (I) for immunizing an individual against diseases, in particular against infection-induced auto-immune and tumor diseases. This sequence represents a fragment of the human papillomavirus E7 protein used in the preparation of the fusion constructs described in the method
Calreticulin; CRT; endoplasmic reticulum chaperone polypeptide; cytostatic; vaccine; human papillomavirus 16; HPV 16; B7; DNA vaccine; enhanced antigen-specific immune response; cytotoxic T lymphocyte; tumour; cancer; cervical cancer.
                                                                      Human papillomavirus 16 (HPV16), E7
                                                                                                  05-JUN-2002
                                                                                                                                                        AAU77713
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 4; 23pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Identifying inhibitors and activators of eukaryotic potassium channels, for use as therapeutic agents, comprises using a transformed yeast cell that does not express endogenous channels.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion protein; VP22; E7; cell import signal; cell export signal; antigen; immunization; infection-induced auto-immune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                        98
                                                                                                                                                       standard; protein;
                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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Pred. No. 2.2e-57;
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Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polypeptide comprising a first polypeptide domain comprising and a second polypeptide domain comprising at least one antigenic peptide e.g. calreticulin (CRT) and a second polypeptide domain comprising at least one antigenic peptide e.g. Human papillomavirus 16 (HPV 16) E7. The nucleic acid is useful as a vaccine (DNA vaccine) for inducing enhanced antigen-specific immune responses, particularly those mediated by cytotoxic T lymphocytes. The nucleic acid and compositions comprising the nucleic acid is also useful for inhibiting the growth of tumours and cancers e.g. cervical cancer. This is the amino acid sequence of the human papillomavirus type 16 (HPV 16) early gene 7 (E7) used in the creation of a DNA vaccine
                                                                                                                    Human papillomavirus 16; HPV 16; cancer; squamous cell carcinoma; adenocarcinoma; koilocytosis; hyperkerotosis; intraepithelial neo; intraepithelial lesion; dysplasia; head cancer; neck cancer; small cell lung cancer; melanoma; oncogene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acids encoding a fusion polypeptide comprising an endoplasmic reticulum chaperone polypeptide linked to an antigenic polypeptide, useful as a vaccine for inducing antigen-specific immune responses.
                                                            Key
                                                                                                                                                                                                                                29-AUG-2003
14-FEB-2002
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                                                                                         Human papillomavirus type 16
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                                              Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
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(first entry)
 /label= E7 peptide_epitope_1
/note= "This region is specifically referred to in claim
2"
                                                            Location/Qualifiers
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                                                                                                                                                                                              E7 coding region.
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RESULT 23
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08-JAN-2003

(first entry)

ABB82375

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                                                                                                                                                                                                                                      CC soluble in aqueous solution and has a lysine or cysteine residue near the comming the proposal proposal proposal proposal process and formany glycine and asparagine residues. The peptides and diagnostic comethod are used to diagnose HPV infection, especially infection since HPV 16 cc oncogenic HPV by using peptides derived from the E2 region, since HPV 16 cc and 18 are the main HPV genetic types associated with cancers, and cy resence of antibodies to E2 protein is known to provide evidence of HPV 16 cc infection. They are also useful to diagnose HPV associated malignancy or premalignancy, especially carcinoma by using peptides derived from the E6 co r E7 regions, since E6 and E7 are thought to be tumour-specific cor antigens. The peptides and diagnostic method are especially useful to diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix) cc diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix) cc diagnose cervical carcinoma (e.g. adenocarcinoma of the uterine cervix) cc diagnose of malignant cancers. They are also used to detect head and neck cancers, small cell lung cancers, penal and anal squamous cell carcinomas cc and melanoma. This is the amino acid sequence of the E7 early coding cregion of HPV 16, an oncoprotein that destabilies cell cycle control cc through its interaction with the cyclin-dependent kinase inhibitor corotein, p21, described in the method of the invention. (Updated on 29-cc AUG-2003 to standardise OS field)
                                                                                                                                                         Matches
                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New peptides derived from E2, E6 or E7 early coding regions of human papillomavirus 16 and 18, useful in diagnosis of human papillomavirus infection and associated malignancy e.g. cervical carcinoma.
                                                                                                                                                                                                                                    Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a novel peptide derived from the E2, early coding region of human papillomavirus (HPV) 16 and 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hu YX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-APR-2000; 2000US-0194796P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-APR-2001; 2001WO-US011233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 3; 28pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-OCT-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (IMPA-) IMPACT DIAGNOSTICS INC.
                                                                                                                                                         Local Similarity
                                     61
61
                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60...80
/label= E7 peptide_epitope_2
/note= "This region is specifically referred to 2"
                                                                                                                                                                          96.9%;
                                                                                                                                                         0;
                                                                                                                                                       Score 512; DB 5; 1
Pred. No. 2.2e-57;
0; Mismatches 3;
                                                                                                                                                                                             Length 98;
                                                                                                                                                         Indels
                                                                                                                                                         0
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                                                                                                                                                         Gaps
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RESULT 24
AAO16630
ID AAO16
XX
AC AAO16
XX
DT 15-MP
XX
XX
DE Human
XX
KW Epitc
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                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to a nucleic acid molecule that encodes a fusion CC polypeptide, comprising a first nucleic acid sequence encoding a CC polypeptide, optionally, fused in frame with the nucleic acid, a linker nucleic acid encoding a linker peptide, and a nucleic acid, a linker CC nucleic acid encoding a linker peptide, and a nucleic acid that is linked in frame to them, and that encodes an antigenic peptide or polypeptide. CC The nucleic acid molecule, polypeptides and vectors are useful as CC vaccines for enhancing immune responses, primarily cycotoxic T CC lymphocytes (CTL) responses to specific antigens such as tumour or viral CC antigens, and for inhibiting growth or preventing re-growth of a tumour. CC The packaging cell line is useful for generating alphavirus replicon CC particles without contamination from replicon-competent virus. The pathogenic organisms include viruses such as human papilloma virus (HPV), hepatitis B virus, hepatitis C virus, human immunodeficiency virus, the patitis B virus, and bacteria that grow intracellularly such as mycobacteria CC and listeria. The present sequence represents a wild-type HPV E-7 protein
                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule encoding an antigenic fusion polypeptide useful as vaccines for enhancing or inducing immune responses, primarily cytotoxic T lymphocytes (CTL) responses to specific antigens such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunogenicity; hepatotropic; ar E7 protein.
                               Human papillomavirus E7 antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-740856/80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16-MAR-2001; 2001US-0276854P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus
Epitope; E7
                                                                 15-MAY-2003
                                                                                                  AA016630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAR-2002; 2002WO-US008033.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wild-type HPV-E7 protein sequence
                                                                                                                               AAO16630 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or viral antigens.
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                                                                                                                                                                                                                                                                                 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hung
                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                    Conservative
antigen; CD4-positive T cell activation;
                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y; cytostatic; virucide; protozoacide; antibacterial; CTL;
anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; HPV;
                                                                                                                                                                                                                                                                                                                                                                  99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93pp; English.
                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                  Score 512; DB 5;
Pred. No. 2.2e-57;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                 Length 98;
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RESULT 25
ADF09516
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises an epitope of the human papillomavirus E7 antige that is capable of activating CD4-positive T cells that are specific to uterine cancer lesions. The epitope the invention is useful for preventing and treating uterine cancer. The present amino acid sequence represents the human papillomavirus E7 antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel epitope of human papilloma virus E7 antigen capable of activating CD4-positive T cells specific to (pre-)uterine cancer lesion, applicable in drug compositions for preventing and treating uterine cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-156946/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUN-2001; 2001JP-00173803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       uterine cancer lesion
         Jackson
                               (CURA-)
                                                                                                                                                                                                                                 12-FEB-2004
                                                                                                                                                                                                                                                                          ADF09516 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 34; 40pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maeda H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-2002; 2002WO-JP005747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus
                                                                                                                              WO2003068940-A2
                                                                                                                                                                         human papilloma virus; HPV; cancer.
                                                                                                                                                                                                          Human papillomavirus 16 E7
                                                              14-FEB-2002; 2002US-0356911P
                                                                                     14-FEB-2003; 2003WO-US004594
                                                                                                           21-AUG-2003
                                                                                                                                                    Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (KIRI ) KIRIN BEER
                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                         61
                                                                                                                                                                                    protein-protein interaction;
                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                               CURAGEN CORP.
HOFFMANN LA ROCHE INC
         Þ
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Okubo M;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                 (first entry)
         œ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                   99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                type 16
        Lewin DA,
                                                                                                                                                                                                           SEQ ID NO:17
                                                                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 512; DB 6;
Pred. No. 2.2e-57;
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           Cuthill
                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                      virucide;
                                                                                                                                                                                      cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 98;
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                                                                                                                                                                                                                                                                                                                                                                                                                        0,
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RESULT 26
ADF18632
ID ADF18
XX ADF18
XX ADF18
XX ADF18
XX HUMAN
XX HPV;
XX HPV;
XX HO200
XX HUMAN
XX I 19-AE
XX HPT;
DR WPI;
DR WPI;
DR WPI;
DR WPI;
DR WPSI;
DR WPI;
DR WPSI;
DR WPI;
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Best Local Similarity
Matches 95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel purified complex comprising a first polypeptide and a second polypeptide, where the polypeptides comprise defined amino acid sequences listed in the specification, and where the first polypeptide binds to the second polypeptide. A complex of the invention has virucide and cytostatic activity, and may have a use as a vaccine. The complex is useful for identifying agents for treating or preventing a conditions involving altered level of the complex, e.g. human papilloma virus (HPV) infection, or cancer. The compositions, antibodies, vectors and methods are useful for treating such diseases. The sequences shown in ADF09500-ADF09583 represent proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New purified complex comprising a first polypeptide and a second polypeptide, useful for identifying agents for treating/preventing a condition involving altered level of the complex e.g. human papilloma virus infection, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                     Identifying a compound that inhibits E7 cellular proliferation activity by administering a compound to a system, where the system maintains Akt activity and selecting a compound that decreases the amount of Akt
                                                                                                                                                                                                                                                                                                                                                                                                                                                               19-APR-2002; 2002US-0374245P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPV; oncoprotein E7; cytostatic; gene therapy; kinase; enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-APR-2003; 2003WO-US012667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003088922-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADF18632 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example
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DB; ADF09608.
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                                                                                                                                                                                                                                                                                                                                                                                                      VIND
                                                                                                                                                                                                                                          ADF18633, ADF18634.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQXP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                          Westbrook TF;
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Pred. No. 2.2e
0; Mismatches
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.2e-57;
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Disclosure;

SEQ ID

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8

119pp; English

present

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ADL90076
ID ADL90
XX ADL900
XX ADL900
XX ITMAL
DT 17-JU
XX ITMAL
X
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                             The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in
                                                                                                                                                                                                                                                                                Generating an immune response to an antigen, useful desired T cell responses comprises administering an one peptide epitope of the antigen attached to the i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98
                                                                                                                                                                                                                     Disclosure;
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14-MAR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus 16-E7 protein, SEQ ID 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADL90076 standard; protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ASTR-) ASTRAL INC.
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95; Conserv
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                                                                                                                                                                                                                  Fig 1G; 154pp;
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2003WO-US007995
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pred. No. 2.2e-57;
pred. No. 3;
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                                                       Query Match
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                                                                                                                                                                  The specification describes a method for constructing a synthetic polynucleotide from which a polypeptide is producible at a different level in a Chinese Hamster Ovary (CHO) cell compared to when using a parent polynucleotide encoding the same polypeptide. The method comprises selecting a first codon of the parent polynucleotide for replacement with a synonymous codon, where the synonymous codon is selected on the basis that it exhibits a different translational efficiency in the CHO cell than the first codon in a comparison of translational efficiencies of codons in test CHO cells. The method is useful for constructing synthetic polynucleotides which are translated more efficiently, compared to the parent polynucleotide. The present sequence represents Human papillomavirus type 16 (HPV16) E7 protein. The E7 polynucleotide was codon-modified, to demonstrate the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Constructing a synthetic polynucleotide, useful for producing a polypeptide at a higher level in a Chinese Hamster Ovary cell, compriselecting a first codon of the parent polynucleotide for replacement
                                                                                                              Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a synonymous codon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; Fig 2; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYQU ) UNIV QUEENSLAND
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                           Score 512; DB 8; Length 98; Pred. No. 2.2e-57;
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Pred. No. 2.2e-57;
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Matches
                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a wild type E7 protein from human papillomavirus type 16 (HPVI6), which is used to produce fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV) -associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                 Sequence
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
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cancer; immune response; lower
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                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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Pred. No. 2.2e-57;
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to papilloma-virus specific (PVS) protein and fusion protein constructs. The invention also relates to vaccine formulations comprising viral capsomeres and methods for their production. The fusion protein is useful for treating or preventing a papilloma virus infection in an animal, particularly humans and is also useful in the production of vaccines. The present sequence is human papilloma virus (HPV) strain HPV16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion proteins comprising an amino acid sequence from a first and a second papilloma-virus specific protein, useful in vaccines for treating or preventing a papilloma virus infection in an animal, particularly
Human papillomavirus type 16
                                         10-FEB-2005
                                                                                                                   ADU66362 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 98
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06-APR-1999;
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                                                                               ADU66362
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                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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Pred. No. 2.2e-57;
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The invention comprises a nucleic acid molecule (DNA vaccine) that encodes a fusion polypeptide which is useful as a vaccine composition. The nucleic acid of the invention contains: a first nucleic acid encoding a polypeptide that promotes processing via the MHC class I pathway; a second sequence encoding a signal peptide; and a third sequence encoding a natigenic polypeptide. The DNA vaccine of the invention is useful for inducing or enhancing an antigen specific immune response, or to inhibit growth or prevent re-growth of a tumor expressing Human papillomavirus (HPV) E7 or E6 protein. The present amino acid sequence represents a processing that the present amino acid sequence represents a process to the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence represents a process that the present amino acid sequence presents and the present amino acid sequence presents are present amino acid sequence present amino acid sequence presents and the present amino acid sequence present amino acid 
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                                                                                                                                                                                                                                                    Human papillomavirus
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E7 protein; E6 protein.
08-SEP-2003; 2003US-00657399
                                                                                                                                                                                                                                                                                                                                                High throughput screening; pharmaceutical; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>..</u>
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for the (immuno-) histological detection of high risk HPV E7 protein.

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RESULT 33
AD769083
ID AD769083
AZ AD769083
AC AD769
AC AD
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a method of ameliorating human papillor virus (HPV) proliferation. The method involves administring an inhibit of E7-induced cyclin-dependent kinases (CDK2) phosphorylation or an inhibitor of E7-binding CDK2 kinase complex that reduces HPV E7-induced CDK2 kinase activity. The present sequence is the human papillomavirus I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cytostatic; immunohistol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ameliorating human papillomavirus proliferation involves administering inhibitor of E7-induced cyclin-dependent kinases 2 phosphorylation or inhibitor of E7-binding cyclin-dependent kinases 2 kinase complex that reduces kinase activity.
New combination of antibodies comprises an anti-HPV-16 E7 antibody and anti-HPV-18 E7 antibody, useful for preparing a diagnostic composition
                                                                                                                                                                                                                                                                                                                                                                                                               WO2005026731-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anogenital;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPV 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 1; 20pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fisher C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-AUG-1999; 99US-00382616.
01-DEC-2000; 2000US-00728466.
                                                                                                                                                     Zwerschke WP,
                                                                                                                                                                                                                                                          17-SEP-2003;
                                                                                                                                                                                                                                                                                                          17-SEP-2004; 2004WO-EP010484.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADY69083;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADY69083 standard;
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                                                                                                                                                                                                          (AMYN-) AMYNON
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(HEWW/) HE W.
                                                                             2005-242459/25
DB; ADY69082.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           He W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Therapy; human papillomavirus; E7 protein; logical detection; Pap-smear; cervical; carcinoma; mamma; head; neck; prostate; sexually transmitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         æ
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                                                                                                                                                                                                                                                          2003EP-00020564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
                                                                                                                                                     Jansen-Duerr
                                                                                                                                                                                                          BIOTECH GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein;
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Pred. No. 2.
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                                                                                                                                                     Fiedler M,
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ing an inhibitor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  probay;
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Best

Local

99.0**%**;

Length 98;

Query Match

Sequence

98

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CC fragment in a goat, and affinity-purifying antibodies as obtained in the CC eliciting step, and an anti-HPV-18 E7 antibody. The combination of CC antibodies is useful for the preparation of a diagnostic composition for CC (immuno-) histological detection is darried out on Pap-smears, cervical CC (carcinoma) biopsies, anogenital biopsies, mamma biopsies, bead- or neck CC biopsies, or prostate biopsies. The diagnostic composition is used for CC cancer, for measuring the status of an existing sexually transmitted disease or cancer, or for screening therapy efficiency in the treatment CC disease or cancer, or for screening therapy efficiency in the treatment CC disease is a high risk HPV infection or where the cancer is cervical CC cancer, breast cancer/mamma cancer, prostate cancer/neoplasia (AIN). The CC cancer, breast cancer, and/or anogenital cancer/neoplasia (AIN). The CC combination of antibodies or the diagnostic composition are useful in an CC in vitro method for the detection of high risk HPV-31, HPV-33, HPV-35, HPV-39, HPV-45, HPV-52, HPV-58, and/or HPV-59, HPV-58, and/or HPV-59, HPV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody raised against this protein may be used in a combination cantibodies which comprises an anti-HPV-16 E7 antibody obtainable by eliciting an in vivo humoral response against HPV-16 E7 protein or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents human papillomavirus-16 (HI antibody raised against this protein may be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 2; 146pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HPV-16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein.
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61
                       61
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                                                                                                l Similarity
95; Conser
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                               Conservative
                                                                                                 0;
                                                                                               Score 512; DB 9;
Pred. No. 2.2e-57;
0; Mismatches 3
98
                                                                                                 Indels
                                                                                                 0
                                                                                                 Gaps
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RESULT 34
ARA40816
ID ARA40816
AC ARA40
XX ARA40
DT 28-JI
XX ARA11
XX Immuz
KW Vacci
XX Vacci
XX Vacci
XX Vacci
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18-JUL-2003; 2003US-0488527P.
31-DEC-2003; 2003US-0533792P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunogenicity;
vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-apoptotic vector HPV E7
                                                                                                                                                                                                                                                                                                                                                                    24-FEB-2004; 2004WO-US005292
                                                                                          (UYJO ) UNIV JOHNS HOPKINS
'n
Hung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard; protein;
    ć,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immunogenicity-potentiating polypeptide;
    K:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic
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IPP;

T-cell;

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AEBILT 35
AEBIL1999
ID AEBIL
XX AEBIL
XX AEBIL
XX AEBIL
XX TUMOX
XX TUMOX
XX TUMOX
XX CANCE
XX HUMAN
XX WO200
XX 07-JU
XX 24-DE
XX 24-DE
XX 17-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CC acid vector comprising a first sequence encoding an antigenic polypeptide cor peptide, and optionally, a second sequence linked to the first compensation of the much period cor peptide, and optionally, a second sequence linked to the first compensation mucleic acid vector encoding an anti-spotcotic polypeptide. CC and a second nucleic acid vector encoding an anti-spotcotic polypeptide. CC when the second vector is administered with the first vector to a compensation of the second vector is administered with the first vector to a compensation of the invention than composition for the invention than composition for the response to the antigenic polypeptide. The invention further includes a particle comprising a material that is suitable for introduction into a cell or an animal by particle composition; a pharmaceutical composition capable of inducing or composition; a pharmaceutical composition capable of inducing or composition; a pharmaceutical composition capable of inducing or capable of inducing or enhancing an antigen specific composition antigen specific composition in a subject; increasing the numbers of CDB+ CTLs and inducing the growth of a tumor in a subject; The nucleic acid composition is useful as compositic acitivity. This sequence represents ananti-apoptotic vector HPV composition of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid composition comprising a first nucleic acid vector encoding an antigenic polypeptide and a second nucleic acid vector encoding an anti-apoptotic polypeptide, useful as an immunogen for inhibiting the growth of a tumor.
                                                                                                                                                                                              Human papillomavirus type 16
                                                                                                                                                                                                                                    Tumor-associated antigen; vaccine; papilloma; cytostatic; neoplasm;
cancer; HPV16 E7.
                                                                                                                                                                                                                                                                                              HPV16 E7 protein
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GENBANK; NC_001526.
                                                                           24-DEC-2003; 2003WO-NL000929
                                                                                                                                                           WO2005060993-A1
                                                                                                                                                                                                                                                                                                                                    08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                           AEB11989
                                                                                                                                                                                                                                                                                                                                                                                                              AEB11989 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a novel nucleic acid composition useful as an immunogen. The composition comprises a combination of: a first nucleic
    (UYLE-)
                                      24-DEC-2003; 2003WO-NL000929.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 6; 158pp; English
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    VIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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    LEIDEN
                                                                                                                                                                                                                                                                                                                                    (first
    MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                  entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                  98
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Pred. No. 2.2e-57;
0; Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 98;
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Best Local
13
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                                                                                                             Similarity
               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                 Conservative
                                                                                                             99.0%;
96.9%;
                                                                                                 <u>.</u>
                                                                                                              Score 512; DB 9;
Pred. No. 2.2e-57;
                                                                                                 Mismatches
                                                                                                                        Length 98
98
                                                                                                 Indels
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                                                                                                 Gaps
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RESULT 36
ABC96392
ID ABC96392;
XX
AC ABC96392;
XX

AC D1-DEC-2005 (first entry)
XX

XX

HUMAN papilloma virus infection; virucide; cancer; cytostatic; vaccine; XX

KW epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
XX

YX

PM W02005089164-A2.
XX

PM W02005089164-A2.
XX

PM 03-JAN-2005; 2005WO-US000077.
XX

PR 31-DEC-2003; 2003US-0533211P.
PR 02-JUL-2004; 2004US-0584652P.
XX

(EPIM-) EPIMMUNE INC.
PA (EPIM-) EPIMMUNE INC.
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AEC98871
ID AEC98
XX AEC98
AC AEC98
XX 01-DE
XX 01-DE
XX 02-DE
XX 04-DE
XX 04-DE
XX HPV_1
XX Humar
XX Humar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the CC polynucleotide, vector and/or polypeptide and a carrier), a cell CC (comprising the polynucleotide, vector or polypeptide), inducing an CC immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the cepitopes in the vaccine protein are disclosed in the tables referred to comprising the useful in preparing a composition for inducing an immune CC in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune CC defense against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a composition in an HPV protein used to derive epitopes for the vaccine of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CHES/)
(NEWM/)
(MOTH/)
(BAKE/)
(SOUT/)
(BABE/)
               Human papillomavirus type 16
                                              Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                              HPV_16 Envelope protein E7.
                                                                                                                                01-DEC-2005
                                                                                                                                                                 AEC98871
                                                                                                                                                                                                AEC98871 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CHEN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUAN/
                                                                                                                                                                                                                                                                                61
                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                               95;
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BAKE D.
SOUTHWOOD S.
BABE L M.
CHEN Y.
DEYOUNG L M.
HUANG M T F.
POWER S D.
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                                   MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 512; DB 9; Length 98
Pred. No. 2.2e-57;
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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Power SD;
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AED13078 ID AED: XX

AED13078 standard; protein; 98

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RESULT 38

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                                                                                                                                                                                                                                                                                       CC construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigane. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence CC encoded by the polymucleotide, a composition (comprising the polymucleotide, vector and/or polypeptide and a carrier), a cell CC (comprising the polymucleotide, vector or polypeptide), inducing an CC immune response against human papillomavirus virus (HPV) and making the CC polymucleotide, vector or polypeptide. The epitopes are derived from CC different strains of HPV and are from the El, E2, E6 and E7 proteins. The CC epitopes may be linked via a GP-anchor/spacer peptide. The order of the CC epitopes in the vaccine protein are disclosed in the tables referred to CC in the claims of the specification. The polymucleotide, vector or composition for inducing an immune CC response against human papillomavirus virus (HPV) and thus providing a CC defense against human papillomavirus virus (HPV) and thus providing a CC defense against human papillomavirus virus (HPV) and thus providing a CC defense against human papillomavirus virus (HPV) and thus providing a consense of the consens
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Best Local :
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                                                                                                                                                                                                                                  Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte
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02-JUL-2004; 2004US-0584652P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 10; Page 350; 518pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a new polynucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CTL) epitopes, useful in preparing a
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BABE L M.
CHEN Y.
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HUANG M T
POWER S D.
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                                                                                                           MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK 60
                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                           MIGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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Huang MTF,
                                                                                                                                                       Score 512; DB 9;
Pred. No. 2.2e-57;
0; Mismatches 3;
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Power
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    comprising a multi-epitope
                                                                                                                                                                                            Length 98;
  98
                                     98
                                                                                                                                                           Indels
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RESULT 39
AED64360
ID AED64
XX AED64
XX AED64
XX AED64
XX AED64
XX Vacci
KW Yacci
KW fusio
XX Yunan
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Best Local Similarity
Matches 95; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a novel vaccine composed of an antigen protein and a second protein as an s-(methyl mercury)-1-cysteine (CMH class II) ligand. The second protein is taken from a group including human Lymphocyte Activation Gene (hLAG)-3. The first protein is a viral or bacterial antigen, a tumor antigen, parasitic antigen, or their mixtures. The viral antigens can be for hepatitis B (HBV), human papillomavirus (HPV), hepatitis C (HCV), human immunodeficiency virus (HIV), Epstein-Barr virus (BBV), cytomegalovirus (CMV), and their combinations. The bacterial antigens can be intracellular bacteria of tuberculosis, leprosy and listeria. A vaccine of the invention has virucide, and antibacterial activity. The present sequence represents the HPV16 wild-type E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Therapeutic vaccine, for viral and bacterial conditions, comprises antigen protein and a viral or bacterial protein, coupled together stable hydrogen or covalence bonds in biological media.
                           Vaccine; therapeutic; fusion protein; E7.
 Human
                                                                                                   12-JAN-2006
                                                                                                                                AED64360
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 98
                                                                     Human papillomavirus type 16 E7 protein.
                                                                                                                                                          AED64360 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 1; 51pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-APR-2004; 2004FR-00003848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPV16 E7 wild-type protein sequence
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DB; AED13076.
papillomavirus
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                                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                   (first entry)
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 type 16
                                                                                                                                                                                                                                                                                                                                                                99.0%;
                                          papillomavirus infection; virucide; infection;
                                                                                                                                                           98
                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                Score 512; DB 9;
Pred. No. 2.2e-57;
0; Mismatches 3
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RESULT 40
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Best Local :
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03-APR-2001;
04-SEP-2003;
                                                                                                                                                                             Gene expression; therapeutic; immune acquired immune deficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to fusion protein comprising papilloma virus-specific (PVS) protein and their encoding polynucleotides. The invention is useful in preparing a composition for treating and preventing papilloma virus infection in humans. The present sequence the Human papillomavirus type 16 E7 protein.
         Smith LR,
                                                                                                                                                                                                               HPV16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New fusion protein comprising an amino acid sequence from a first second papilloma virus-specific (PVS) protein, useful in preparing composition for treating or preventing papilloma virus infection.
                                                                           06-JUN-2005; 2005WO-US019592
                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                                     23-FEB-2006
                                                                                                                                                                                                                                                                                  AEE94089
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                                                     04-JUN-2004; 2004US-0576819P
                                                                                                 15-DEC-2005
                                                                                                                        WO2005118874-A1
                                                                                                                                                                   infection; immune disorder.
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                               (AMHP ) WYETH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 95;
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                                                                                                                                                                                                                                                                                standard; protein; 98
                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVOSTHVDIRTLEDLLMGTLGIVCPICSOKP
         Shahabi V,
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2001US-00824017.
2003US-00654129.
                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                          99.0%;
                                                                                                                                            type 16.
          Sidhu MK;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 512; DB 9;
Pred. No. 2.2e-57;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                             stimulation; HIV infection;
E7 protein; anti-HIV; virucide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         useful in preparing ma virus infection.
                                                                                                                                                                                                                                                                                                                                          98
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WPI; 2006-047579/05

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RESULT 41
ADQ88451
ID ADQ88
XX ADQ88
XX ADQ88
XX ADQ88
XX ADQ88
XX APV16
XX HPV16
XX HPV16
XX HPV17
XX HUMAI
XX RU221
XX Z2-O0
XX Z2-O0
XX Z2-O0
XX AD16
PT Palti
XX PI
DR N-PS;
XX PI
PT Recoi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the same protein or polypeptide as a wild-type polynucleotide. The invention also relates to a method for enhancing expression of a gene, a method of preventing or treating a disease in a mammal, a composition comprising a modified polynucleotide describe above and a pharmaceutical vector. The method additionally comprises adding an immunoglobulin leader sequence, such as an IgE leader sequence, to the modified polynucleotide. The composition is useful for preparing a medicament for inducing an immune response in a mammal or for treating an infection or condition, e.g. HIV or AIDS in a mammal. The polynucleotide and methods are useful for enhancing gene expression. This sequence represents the HPV16 E7 protein used in the scope of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Preparing a polynucleotide, useful for enhancing comprises assembling oligonucleotides comprising a modified polynucleotide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method of preparing a polynucleotide that provides enhanced expression of a gene, comprising assembling oligonucleotides comprising surrogate codons to form a modified
                                                                                                                                                                                                             22-OCT-2002; 2002RU-00128131
                                                                                                                                                                                                                                                                                                    Human papillomavirus; HPV16
                                                                                                                                                                                                                                                                                                                                                                HPV16 E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ88451 standard; protein; 99 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 98
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                                                                                                                                                                                22-OCT-2002; 2002RU-00128131.
                                                                                                                                                                                                                                                                                                                                HPV 16; E7 gene; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                              23-SEP-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polynucleotide, comprising a predetermined nucleic acid sequence encoding
                               vaccination
                                                                                                                       Paltsev
                                                                                                                                                   (BIOM=)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                         2004-446846/42
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                                                                           ADQ88450
                                                                                                                                                   BIOMEDINVEST
                                                                                                                                                                                                                                                                                                                                                                protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                               protein composition, of tumor diseases in
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                                                                                                                       Severin
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                                                                                                                                                                                                                                                                                                                                                                                              entry)
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                                                                                                                       ES,
                                                                                                                                                   STOCK CO
                                                                                                                       Kiselev OI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>,</u>
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Pred. No. 2.2e-57;
0; Mismatches 3
                               'n
                               anus-genital sphere
                                             useful in immunotherapy
                                                                                                                                                                                                                                                                                                                                   tumour
                                                                                                                       Kiselev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Disclosure;

Page

7;

specific

antigen

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ADY92615
ID ADY92625
XX ADY9262
XX ADY92
XX ADY92
XX ANTID
XX ANTID
XX E7 on
XX IMMUN
XX HUMAN
XX HUMAN
XX HUMAN
XX HUMAN
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XX IMMUN
XX HUMAN
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Best Local (
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The new invention relates to methods and compositions that allow production of antigen specific antibodies to antigens that have traditionally been unable to elicit an adequate and specific immune response. The method comprises producing monoclonal antibodies specito an antigen of low immunogenicity by chemically conjugating the ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; monoclonal antibody; antibody production; hybridoma; screening; E7 oncoprotein; immuno-diagnosis; diagnosit; immunoconjugate; immunoassay; radioimmunoassay; enzyme-linked immunosorbent assay; transmissible spongiform encephalopathy; cerebroprotective; cervical intraepithelial neoplasia; cytostatic; immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 99 AA;
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                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                            Producing monoclonal antibodies specific to an antigen of low immunogenicity by immunizing an animal with the chemically conjugated antigen, useful for detecting cervical intraepithelial neoplasia.
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (KISE/)
(SVES/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kiselev VI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2003; 2003RU-00128660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-SEP-2004; 2004WO-RU000373
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                                                                                                                                                                                                                                                                                                                                                                           2005-273121/28.
DB; ADY92614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KISELEV V I.
SVESHNIKOV P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; protein; 99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                        SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sveshnikov
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96.9%;
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                                                                                                                                                                                     72pp; English.
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Pred. No. 2.2e-57;
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RESULT 43
AAB31608
ID AAB31
XX AAB31608
AC AAB31
XX Heat
XX Heat
XX Hympi
XX E7 pi
XX WO200
XX WO200
XX Human
PN WO200
XX WO300
XX WO300
XX WP1
PN Sieg
XX WP1
DR WP1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC and a nucleotide sequence encoding HSP70 and transfecting a host cell control with the plasmid. The nucleotide sequence encoding E7 oncoprotein CC comprises ADY92614. The nucleotide sequence encoding HSP70 CC comprises ADY92618. Alternatively, the conjugating is performed CC chemically using glucaraldehyde. Screening for specificity is done by CC various assays such as radioimmunoassay, enzyme-linked immunosorbent CC assay, or sandwich immunoassay. The antibodies are useful for determining CC if a subject is at risk of developing spongiform encephalopathy CC comprising an antibody that specifically detects Prion protein. The Prion CC protein peptide comprises ADY92619, ADY92620 or ADY92622. Antibodies specific to E7 oncoprotein are useful for detecting cervical cells and screening the specimen for the presence of E7 oncoprotein. The monoclonal antibodies comprise at least two immunoglobulin isotype is IgG2a or IgG2b. The immunoglobulin isotype has specificity for a different antigenic determinant than the second immunoglobulin isotype. The present sequence HPV16 E7 oncoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                 lymphocyte; E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to a carrier molecule, immunizing an animal with the conjugated antigen, harvesting B cells from the animal, creating a hybridoma from the harvested B cells, and screening the hybridoma for specificity to the native antigen. The antigens can be B7 oncoprotein, Prion protein peptide, hyaluronic acid or matrix metalloprotease 3. The carrier molecule is HSP70. The chemical conjugation comprises creating a plasmid with a nucleotide sequence encoding the antigen, such as B7 oncoprotein
                     N-PSDB; AAF25008
                                                                                  Siegel M,
                                                                                                                                                                  08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                   Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; Lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB31608 standard; protein; 121
                                           WPI; 2001-138361/14
                                                                                                                                                                                                         10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                       18-JAN-2001.
                                                                                                                                                                                                                                                                                            WO200104344-A2
                                                                                                                                                                                                                                                                                                                                   Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of a His-tagged HPV16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-APR-2001
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                                                                                                                           STRESSGEN BIOTECHNOLOGIES CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                    Chu NR,
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                                                                                                                                                                    99US-0143757P
                                                                                    Mizzen LA
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96.9%;
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Pred. No. 2.2e-57;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 99
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RESULT 44
AAB31616
ID AAB31
XX Heat
XX Iymph
XX Iymph
XX Iymph
XX Iymph
XX Hoolo
OS Mycob
OS Human
XX Iymph
XX IO-JU
XX 
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                                                                                                                                                                                 Screening for compounds that stimulate Th1-like responses in CD4+lymphocyte cells.
                                                                                                                                                                                                                                                                                 N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                        Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; Lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                    Example 13; Fig 12; 88pp; English.
                                                                                                                                                                                                                                                                              WPI; 2001-138361/14.
N-PSDB; AAF25023.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200104344-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid sequence of Hsp10-E7 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB31616 standard; protein; 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 121 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 4; Fig 3; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                                                                                                                                                         (STRE-) STRESSGEN BIOTECHNOLOGIES
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95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                            Chu NR,
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Pred. No. 2.8e-57;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 121;
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The present sequence represents a fusion protein comprising Mycobacterium tuberculosis heat shock protein (Hsp) 10 fused at its 3' end to HPV16 E7 protein. The fusion protein is used in the method of the invention. The

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostalic; respiratory-Gen, antiasthmatic; vaccine; immunomodulator; immune response; atopic disease; altergy; seasonal respiratory allergy; perennial respiratory allergy; allergic rhinitis, hayfever; nonallergic rhinitis; vasomotor rhinitis; irritant rhinitis; grass pollen allergy; weed pollen; tree pollen; animal danders; allergic asthma; food allergy; house dust mite allergy; fungal spore; cancer; tumour progression; T cell lymphoma; melanoma; lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flammulina velutipes.
Human papillomavirus.
   This invention relates to a novel Fve (Flammulina velutipes) polypeptide comprising at least one biological activity of native Fve protein, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-OCT-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel Fve fusion protein mutant sequence #48.
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                                                                                               Claim 6;
                                                                                                                                                                                                              New Fve
                                                                                                                                                                                                                                                                                                                                                              Chua KY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-APR-2003; 2003GB-00008988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-APR-2004; 2004WO-SG000098
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                                                                                                                                                                                                                                                                                                                                                                                                                      (SCTE-)
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DB; ADT75832.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer; breast cancer; prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                e polypeptide that is a fragment, homologue, variant or derivative protein and that comprises a biological activity of native Fve n, useful for preventing and treating allergy or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV NAT SINGAPORE
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                                                                                         286pp;
                                                                                                                                                                                                                                                                                                                                                                                                                      TECHNOLOGY & RES
                                                                                                                                                                                                                                                                                                                                                              Kolatkar PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%;
                                                                                         English
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Pred. No. 5.3e-57;
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Fve protein,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HPV fusion protein D1/3-E7-His(HPV16).
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                                                                                                                                                                                                                                                                                                                          24-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                               18-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein;
                                                                                                                                                                                               Dalemans WLJ,
                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .mmunological fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen; prevention; treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry
                                                                                                                                                                                               Gerard
                                                                                                                                                                                                                                                                                                                                 97GB-00027262
                                                                                                                                                                                                                                                                                                                                                                                               98WO-EP008563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          B6 protein; E7 protein; E6/E7; immunomodulator; tumour;
usion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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96.9%;
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Pred. No. 5.8e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
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Composition comprising induce immune response

t an E6,

E7

မ္ E6/E7

fusion protein

from

MPV

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N-PSDB;

1999-405485/34 DB; AAX78791.

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RESULT 47
AAY02631
ID AAY0263
AC AAY02
AC CAIme
KW Chime

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Best Local :
This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAX25375-X25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce ar immune response in a patient to an HPV antigen. They can also be used i preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                Disclosure; Fig 1; 95pp; English.
                                                                                                                                                                                                                                                                                                       treatment
                                                                                                                                                                                                                                                                                                                           Human Papilloma Virus (HPV)
                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY02631 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9910375-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chimeric; E6; E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProtDthr126-E7-His tail protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                                      AAX29780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          I; Page 46-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHGDTFTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                               or prophylaxis of HPV induced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cabezon Silva T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          benign; malignant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion protein; protein D; vaccine; immunotherapy;
enign; malignant; virus; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.0%;
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                                                                                                                                                                                                                                                                                                                              fusion proteins - useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delisse AEF,
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Pred. No. 6.1e-57;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                       lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerard CMG;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                   in vaccines
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be used for
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114

MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 173 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60 Matches

Local

Similarity 95; Conserv

Conservative

Indels

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Gaps

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RESULT 48
AED52631
ID SEP 52631
AC AED52
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Best Local S
Matches 95
                                                          Query Match
                                                                                                                                                                                    The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an B6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (cLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion protein; vaccine; papilloma;
virucide; uterine cervix tumor; E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-2005
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                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 1; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tyrrell
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2005-557648/57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein D1/3-E7-His(HPV16).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                               220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             220 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            influenzae; strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                               $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98IN-CH001903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%;
                           99.0%;
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Score 512; UB .,
Pred. No. 6.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 512; DB 2; Pred. No. 6.1e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; papillomavirus infection; D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein.
                                                    Length 220;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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RESULT 50
AAY02636
ID AAY02
XX
AC AAY02
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AC AAY02
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AC AAY02
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                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                              AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonuclectide. The products of the invention can be used to induce arimmune response in a patient to an HPV antigen. They can also be used if preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response; HPV antigen; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                        Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-405485/34.
N-PSDB; AAX78796.
17-OCT-2003
                                                                                                                                                                                                                                                         Sequence 239
                                                                                                                                                                                                                                                                                                                                                                                   Example VII; Page 53; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dalemans WLJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPV fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY25380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY25380 standard; protein;
                        AAY02636;
                                              AAY02636 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9933868-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                           193
                                                                                                                                                           133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                papillomavirus.
                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                          95;
                                                                                                                                                                                                                      Similarity
                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 192
                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein CLYTA-E7-His/HPV16
                                                                                                                                                                                                         99.0%;
ilarity 96.9%;
Conservative
                                                                                                                                                                                                                                                         Ą,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97GB-00027262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-EP008563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CMG;
                                                                                                                                                                                                                                                                                                                                                                                                          an E6,
to HPV
                                               239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239
                                                                                                                                                                                                         <u>,</u>
                                                                                                                                                                                                         Score 512; DB 2;
Pred. No. 6.8e-57;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                       Ε7
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                                                                                                                                                                                                                                                                                                                                                                                                                     or E6/E7
                                                                                                                                                                                                                                                                                                                                                                                                                       fusion protein
                                                                                                                                                                                                         ω
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                                                                                                                                                                                                                                Length 239;
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                                                                                                                                  98
                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                       from HPV
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be used for
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                                                                                                                                                                                                      RESULT 51
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Matches
                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             This sequence represents a chimeric 86 or 87 protein or 86/87 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Streptococcus pneunoniae CLYTA protein of the encoded protein. The protein can be used in a vaccine, for immuno-therapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 12; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-190587/16.
N-PSDB; AAX29785.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptococcus
Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLYTA-E7-His protein
                     Human papillomavirus Synthetic.
                                                                                                                                                       AED52644;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-JUN-1999 (first entry)
                                                                    Fusion protein; vaccine; papillo virucide; uterine cervix tumor;
                                                                                                       Fusion protein cLytA-E7-His/HPV16.
                                                                                                                                                                               AED52644 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric; E6; E7; fusion protein; CLYTA; vaccine; lesion; benign; malignant; virus; infection.
                                              Streptococcus
                                                                                                                               29-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK)
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                          133
                                                                                                                                                                                                                                           193
                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                          1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                          95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 192
                                                                                                                                                                                                                                                                                                                                                                                          239 AA;
                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cabezon Silva T,
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae.
                                              pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97GB-00017953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-EP005285
                                                                                                                                                                                                                                                                                                                                                    99.0%;
                                  type 16
                                                                    ; papilloma; « x tumor; E7;
                                                                                                                                                                               239
                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Delisse AEF,
                                                                                                                                                                                                                                                                                                                                          Score 512; DB 2; 1
Pred. No. 6.8e-57;
0; Mismatches 3;
                                                                        LytA.
                                                                                 cytostatic; papillomavirus infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gerard CMG;
                                                                                                                                                                                                                                            230
                                                                                                                                                                                                                                                                                                                                                                 Length 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunotherapy;
                                                                                                                                                                                                                                                                                                                                           Indels
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Chimeric

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RESULT 52
AD044066
ID AD044
XX AD044
XX AD044
XX AMino
XX E6 px
KW E6 px
KW cervi
KW anal
XX Annan
OS Synth
XX MO200
XX 15-AF
XX 15-AF
XX 15-AF
XX 13-OC
XX X XX
PA (AMHI
XX XX
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Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-Lyth, fusion protein of the invention.
                                                                                                                                                                                                                                                 E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AED52643.
               Smith L,
                                                                       03-OCT-2002; 2002US-0415929P
                                                                                                   02-OCT-2003; 2003WO-US031726
                                                                                                                                  15-APR-2004.
                                                                                                                                                            WO2004030636-A2
                                                                                                                                                                                                        Human papillomavirus type 16.
                                                                                                                                                                                                                                                                                            Amino acid sequence of an E7E6 fusion protein.
                                                                                                                                                                                                                                                                                                                         15-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                        ADO44066;
                                                                                                                                                                                                                                                                                                                                                                                  ADO44066 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 239 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to human Papilloma virus (HPV) fusion proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 11; Fig 12; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-557648/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tyrrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-MAR-2005.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-1997;
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                                            (AMHP ) WYETH HOLDINGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                Cassetti MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                  reproductive system cancer; penile cancer; vulvar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97EP-00179535
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%;
                                             CORP
                                                                                                                                                                                                                                                                                                                                                                                   248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 512; DB 9;
Pred. No. 6.8e-57;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                   ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 239;
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RESULT 53
AAY43480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2003
27-AUG-2003
26-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The specification describes human papillomavirus type 16 (HPV16). The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTIA4; E7; fusion protein; B7 receptor positive B cell; CTIA4 receptor positive T cell interaction; immune systautoimmune disease; lupus erythematosus; host-graft; transplant rejection; chimera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                          19-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY43480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB; ADO44067.
                                                                                                                  US5968510-A
                                                                                                                                                                                                        Protein
                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
Papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of a CTLA4-E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY43480 standard; protein; 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 72-73; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2004-316328/29.
                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(revised)
(first entry)
                                                                                                                                                                                                                                                             /note= "leader sequence"
27. .155
                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                       note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.0%;
                                                                                                                                                                                                                                 "CTLA4 sequence"
                                                                                                                                                                             "E7 sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 512; DB 8; 1
Pred. No. 7.1e-57;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interaction; immune system; nematosus; host-graft;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E7 polypeptides, (HPV) -associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising wild
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           suppression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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04-OCT-1996;

96US-00725776

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RESULT 54
AAYO1502
ID AAYO1
XX AAYO1
AC AAYO1
XX 26-MA
DT 26-MA
DE Aminc
XX CTLA4
KW CTLA4
KW solub
KW solub
KW solub
KW autoi
KW Jamur
KW
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Best Local S
Matches 95
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22-JAN-1993;
15-APR-1994;
18-JAN-1995;
05-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a soluble CTLA4 fusion protein, for use in the method of the invention. The specification describes a method for regulating CTLA4 receptor positive T cell interactions with B7 receptor positive B cells. The method comprises contacting the CTLA4-positive T cells with monoclonal antibody fragments reactive with CTLA4. This inhibits (and therefore regulates) interactions between CTLA4-positive T cells and B7 positive B cells. The method may be used for regulating CTLA4 receptor positive T cell interactions with B7 receptor positive B cells. In this way the immune system of an individual can be manipulated (especially lupus erythematosus) and to prevent host-graft and transplant rejection. (Updated on 27-AUG-2003 to correct OS field.) (Updated on 17-CT-2003 to standardise OS field)
                                                                                                                                                                                                                                                              immune system disease; graft versus host disease; psoriasis; graft transplant rejection; T cell lymphoma; benign lymphocytic autoimmune disease; lupus erythemsus; Grave's disease; Addison's disease; Crohn's disease; multiple sclerosis; ulcerative colitis; Sjogren's syndrome; mixed connective tissue viral proliferation; T cell activation; AIDS; HTLV1.
                                                                                                                                                                                                                                                                                                                                                                                                                                      CTLA4 receptor; immunoglobulin; Ig; fusion protein; B7 antigen; soluble CTLA4; T cell interaction; B7 positive cell; immune disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 253
   08-JUL-1997;
                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino terminal CTLA4-carboxy terminal E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-MAY-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY01502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY01502 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 37; 75pp;
                                                          23-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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93US-00008898.
94US-00228208.
95US-00375390.
95US-00465078.
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   97US-008B9666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 512; DB 2;
Pred. No. 7.3e-57;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ξ
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                                                                                                                                                                                                                                                                                                                                                                               lymphocytic angiitis;
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AAW97612
ID AAW97
XX AAW97
AC AAW97
AC AAW97
AC AAW97
XX 26-MA
DT 26-MA
XX CTLA4
XW CTLA4
XW SOlub
KW Solub
KW Solub
KW Solub
KW JUTOI
KW JUTOI
KW Addis
KW Ulcer
XX VITAI
XX Synth
OS Homo
XX US588
PD 23-M2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes a CTLA4 receptor/immunoglobulin (Ig) fusion CC protein which is reactive with the B7 antigen. DNA encoding the CTLA4 CC protein can be used in a vector in a host vector system for producing CC soluble CTLA4. The CTLA4 fusion protein can be used for regulating T cell interactions with B7 positive cells. The CTLA4Ig fusion protein can be used for regulating T cell cused for treating immune system diseases mediated by T cell interactions CC with B7 positive cells. The immune diseases mediated by T cell interactions CC with B7 positive cells. The immune diseases include graft versus host disease, psoriasis, immune disorders associated with graft cransplant rejection, T cell lymphoma, benign lymphocytic angiitis, and CC transplant rejection, T cell lymphoma, benign lymphocytic angiitis, and CC autoimmune diseases such as lupus crythematosus, Grave's disease. The CC colitis, Sjogren's syndrome, and mixed connective tissue disease. The CC colitis, Sjogren's syndrome, and mixed connective tissue disease. The CC colitis, The present sequence was created in the course of the invention KC HTLVI. The present sequence was created in the course of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                            soluble CTLA4; T cell interaction; B7 positive cell; immune disorder; immune system disease; graft versus host disease, psoriasis; graft transplant rejection; T cell lymphoma; benign lymphocytic angiit autoimmune disease; lupus erythematosus; Grave's disease; Addison's disease; Crohn's disease; multiple sclerosis; ulcerative colitis; Sjogren's syndrome; mixed connective tissue disease viral proliferation; T cell activation; AIDS: HTT.17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-JUN-1991;
22-JAN-1993;
15-APR-1994;
18-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                  Amino terminal CTLA4-carboxy terminal E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                  AAW97612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 37; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Damle NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 253
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93US-00008898.
94US-00228208.
95US-00375390.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 512; DB 2; 1
Pred. No. 7.3e-57;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulate T-cell interactions with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Linsley
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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23-MAR-1999 US5885796-A.

sapiens.

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AAY41132
ID AAY41132
ID AAY41132
ID AAY411
AC AAY41
AC AAY41
AC CTLA4
XX CTLA4
XX MONOC
KW MONOC
KW T Cell
KW Ineopl
KW inmun
KW inmun
KW diabe
OX Synth
OS Homo
PN US597
XX US597
XX 07-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The specification describes a CTLA4 receptor/immunoglobulin (Ig) fusion composed by the composition of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JAN-1993;
15-APR-1994;
18-JAN-1995;
                                                                                                                                                                                                                                 Monoclonal antibody; MAb; extracellular domain; CTLA4; B7 antigen; T cell interaction; inflammation; autoimmunity; transplantation; GCH neoplasia; infectious disease; graft versus host disease; psoriasis; immune disorder; lymphoma; leukemia; autoimmune disease; arthritis;
  07-JUN-1995;
                                                                                                                                                                                                               diabetes mellitis;
                                                                                                                                                                                                                                                                                                                                                        CTLA4/E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY41132 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-1991;
                                               02-NOV-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTLA4 receptor protein for use in treatment of immune system diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1995;
                                                                                           US5977318-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-228535/19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (BRIM ) BRISTOL-MYERS SQUIBB CO
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                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brady W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91US-00723617.
93US-00008898.
94US-00228208.
95US-00375390.
  95US-00488062
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                                                                                                                                                                                                               oncostatin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 512; DB Pred. No. 7.3e 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         e 512; DB 2; Le
. No. 7.3e-57;
ismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Linsley PS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                     CCHD
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AAW81586
ID AAW81
XX AAW81
XX AAW81
XX AAW81
XX O5-FE
XX CTLA4
XX CTLA4
XX CTLA4
XX CTLA4
XX CTLA4
XX CTLA6
XX Homo
OS Human
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                                                                                                                                                                                                                                                                                                                                                                                                                Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention provides new monoclonal antibodies (MAbs) which bind the certracellular domain of CTLA4 and prevent the binding of CTLA4 to B7 CC antigen. The MAbs can be used for regulating T cell interactions with B7 CC positive cells. They can also be used for preventing or reversing CC diseases and neoplasia. They can be used for treating diseases e.g. graft versus host disease (GCHD), psoriasis, immune disorders associated with CC lymphoblastic leukemia, resticular angiocentric R cell lymphoma, benign CC lymphocytic angitts, autoimmune diseases such as lugus erythematosus, CC anshimoto's thryoiditis, primary myxedema, Graves disease, pernicious CC anemia, autoimmune atrophic gastritis, Addison's disease, pernicious continue such esticular angioty myxedema, Graves disease, insulin CC dependent diabetes mellitis, Goodpasture's syndrome, myasthenia gravis, CC pemphigus, Crohn's disease, sympathetic ophthalmia, autoimmune uveitis, CC ulcerative colitis, Sjogren's syndrome, rheumatoid arthritis, CC ulcerative colitis, Sjogren's syndrome, rheumatoid arthritis, CC diseases. The present sequence represents the CTLA4/E7 fusion protein CC domain an amino terminal CTLA4 domain and a E7 carboxy-terminal CC domain of the cerminal CTLA4 domain and a E7 carboxy-terminal CC domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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22-JAN-1993;
15-APR-1994;
18-JAN-1995;
                                                                                                                                                                                                                                    AAW81586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example; Fig 37; 74pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New anti-CTLA4 monoclonal antibodies, used for treating e.g. inflammation, autoimmunity, transplant rejection, infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PA,
                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                         MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     253 AA;
                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brady W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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93US-00008898.
94US-00228208.
95US-00375390.
                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Damle NK,
                                                                                                                                                                                                                                    253
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 512; DB 2;
Pred. No. 7.3e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Linsley PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ledbetter JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                        215
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CTLA4 receptor; CTLA4-Ig; fusion protein; B7 extracellular domain; human; immunoglobulin; autoimmune disease; cancer; viral infection;

antigen; hinge; CH2; CH3;
T cell; immune system;
E7.

Human papillomavirus Homo sapiens 05-FEB-1999

(first entry)

CTLA4/E7 fusion protein sequence

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RESULT 58
AAW87562
ID AAW87
XX AAW87
XX AAW87
XX O1-MP
CT O1-MP
CT CTLA4
XX CD28;
KW CD28;
KW CTLA4
XX CTLA4
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                                                                                                                                                                                                                                                                            5
                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 95
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22-JAN-1993;
28-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                    This represents a CTLA4/E7 fusion protein. The invention provides a CTLA4 - Ig fusion protein that binds the B7 antigen and has a first amino acid sequence consisting of the extracellular domain of CTLA4 and a second amino acid sequence consisting of the hinge, CH2 and CH3 regions of a human immunoglobulin molecule. The fusion protein inhibits interaction of T cells with B7-positive cells and may be useful for treating immune system diseases, earcer or viral infections. The present sequence is an example of such a fusion protein and contains an amino-terminal CTLA4 domain and aN E7 carboxy- terminal domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fusion
system
                     CD28; B7; fusion protein; hinge CH2; CH3; human IgC-gamma1; CTLA4; CTLA4 receptor; ligand; regulation; T-cell interaction; B7-positive cell;
                                                                                        01-MAR-1999
                                                                                                                AAW87562;
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 8; Fig 37; 75pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-044666/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-JAN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
             ımmune
                                                               CTLA4-E7 fusion protein.
                                                                                                                                       AAW87562 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US5844095-A.
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                                                                                                                                                                                                        216
                                                                                                                                                                                                                                                          156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ξ
                                                                                                                                                                                                                                 61
             system disease.
                                                                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein of CTLA4 and immunoglobulin fragment -disorders.
                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                253
                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 253
                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                              MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Linsley PS,
                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                              æ
                                                                                       (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91US-00723617.
93US-00008898.
93US-00069693.
94US-00228208.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "CTLA4 partial sequence"
27. .154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "leader sequence"
27. .154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                155. .253
/note= "E7 partial sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note= "E7 carboxy terminal domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . 253
                                                                                                                                                                                                                                                                                                                       99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQUIBB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Damle NK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "CTLA4 amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                         253
                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                          Score 512; DB 2;
Pred. No. 7.3e-57;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminal domain"
                                                                                                                                                                                                                                                                                                           ω
••
                                                                                                                                                                                                                                                                                                                                    Length 253;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for treating
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune
                                                                                                                                                                                                                                                          215
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ADR47005
ID ADR4
XX
AC ADR4
AC ADR4
DT 18-N
XX
US Huma
XX
KW Cytc
KW prel
KW prel
KW buma
XX
KW huma
XX
KW huma
XX
KW huma
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                                                                                                                                                                                            RESULT 59
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                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                  Query Match
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22-JAN-1993;
15-APR-1994;
18-JAN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a CTLA4-E7 fusion protein. CTLA4 is a receptor protein having a high degree of homology with CD28. The CTLA4 receptor is identified as a ligand for the B7 antigen. The CTLA4 protein can also be used to construct a fusion protein of CTLA4 and human immunoglobulin (IG)-gammal. The CTLA4 protein was fused to the hinge CH2 and CH3 regions of human IgC-gammal. Soluble CTLA4-Ig fusion proteins can be used to regulate T-cell interactions with B7-positive cells and to
                                                   cytostatic; virucide; dengue virus; recombinant replicon; preM protein; C protein; NS1 protein signal; vaccine; cerv
                                                                                                                                                                                                                                                                                                                                                                                           Sequence 253 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Soluble CTLA4 protein that binds B7 antigen of activated B cells fusion proteins useful for regulating T-cell interactions with B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                       preM protein; C protein;
viral disease; antigen; 
                                                                                        Human papillomavirus type 16
                                                                                                                   18-NOV-2004
                                                                                                                                           ADR47005;
                                                                                                                                                                                                                                                                                                                                                                                                                  treat immune system diseases mediated by such interactions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 18; Fig 37; 75pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                     ADR47005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BRIM ) BRISTOL-MYERS SQUIBB CO
                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                       156
                           papillomavirus
                                                                                                                                                                                                                                                             13
                                                                                                                                                                                                                                                                                                                                         95;
                                                                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDBIDGPAGQABPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQABPDRAHYNIVTFCCK
                                                                                                                                                                                                                                    CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                 (first entry)
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94US-00228208.
95US-00375390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brady W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91US-00723617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95US-00459818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "signal peptide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     l6. .155
                                                                                                                                                                   protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .253
e= "E7 protein"
                                                                                                                                                                                                                                                                                                                                                     99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CTLA4 protein"
                                       ; NS1 protein signal; vaccine; dendritic cell; immune respon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Damle NK,
                                                                                                                                                                     256
                                                                                                                                                                                                                                                                                                                                         0
                                                                                          E7
                                                                                                                                                                                                                                                                                                                                         Score 512; DB 2;
Pred. No. 7.3e-57;
0; Mismatches 3
                                                                                         protein for Dengue virus vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kiener PA,
                                                                                                                                                                                                                                                                                                                                                                Length 253;
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                                                                                                                                                                                                                                                                                                                                          Indels
                                                    cervical
                                                                 deletion;
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                                                                                                                                                                                                                                                                                                                                          Gaps
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Human papillomavirus type 16.

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AEF40157
ID AEF4
XX
AC AEF4
AC AEF4
XX
DT 23-M
XX
DE Huma
XX
XX
Vacc
KW neop
XX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           obtained vaccines are useful in producing preventives or/and remedies for cancer like cervical cancer and viral diseases. Such vaccines can efficiently express antigen in infected cells, which is because dengue virus can infect dendritic cells, and can effectively present antigen to provide immunity effect. Different types of dengue virus can be used to repeatedly produce efficient immune response thereby strengthening the body's immune system against the pathogen that contains such antigen. Human papillomavirus (HPV) vaccines were prepared by using a gene-expressing system using of the full-length dengue virus cDNA clone (pRS/FLD2). The recombinant virus vectors were transfected into baby hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell lines. This sequence corresponds to the HPV type 16 E7 protein whose encoding gene is used as the gene of interest in the recombinant replicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A dengue virus recombinant replicon has a deletion of the complete coding sequence for preM protein of dengue virus and also includes elements of e.g. the non-coding region in the whole of the 5'-end, the coding region of the front 20 amino acids in the C protein, and the coding region of NS1 protein signal; coding regions of all non-structural proteins. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Virus-like particle vaccines containing dengue virus recombinant replicon as core for carrier, applicable in preventives or/and remedies for tumors like cervical cancer and viral diseases.
                Vaccine; virus-like particle; replicon; therapeutic; cancer; cytostatic; neoplasm; viral infection; virucide; infection; oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-JAN-2003; 2003CN-00115272.
30-JAN-2003; 2003CN-00115273.
                                                                    Human papillomavirus 16 (HPV-16) E7-E6 oncoprotein.
                                                                                                                                          AEF40157
                                                                                                                                                                            AEF40157 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; SEQ ID NO 2; 38pp; Chinese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-2004; 2004WO-CN000088
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DB; ADR47004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                         MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                       (first entry)
                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%;
                                                                                                                                                                              256
                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                        Score 512; DB 8; Length 256; Pred. No. 7.4e-57; O; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
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RESULT 61
AAR97561
ID AAR97
XX AAR97
XX 27-AU
DT 27-AU
DT 11-JP
XX Human
XW Human
XW Human
XW Human
XX WO961
XX WO961
XX Z7-JU
XX
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a virus-like particle (VLP) vaccine which contains dengue virus (DEN) recombinant replicon as its core. The DEN replicon contains exogenous nucleotide sequences such as human papillomavirus (HPV) antigen proteins, immune regulators or combination of HPV antigen and immune regulators. The invention is useful for producing a drug for the prophylaxis and treatment of cancer or viral infection. The present sequence is a human papillomavirus oncoprotein.
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30-JAN-2003; 2003CN-00115273
30-JAN-2004; 2004WO-00072274
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-AUG-2003
11-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR97561;
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N-PSDB; AEF40156.
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                                                     20-DEC-1994;
                                                                                                                                                                27-JUN-1996.
                                                                                                                                                                                                                                                                     Human papillomavirus
                                                                                                                                                                                                                                                                                                                             humoral
                                                                                                                                                                                                                                                                                                                                                 Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                         Human papilloma virus E6/E7 protein variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 2; SEQ ID NO 2; 24pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producing a drug for the prophylaxis and treatment of cancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-JUL-2005; 2005US-00192923
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                                                                                                          20-DEC-1995;
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     CSL
                                                                                                                                                                                                                                                                                                                           immune response; cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                           94AU-00000157
                                                                                                          95WO-AU000868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; 266
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Pred. No. 7.4e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                             immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 256;
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                                                                                                                                                                                                                                                                                                                             vaccine.
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ARBSULF 62
AAU02129
ID AAU02229
AC AAU02
AC AAU0
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse; granulocyte-macrophage-colony stimulating factor; GM-CSF; chimeric; heat shock protein; HSP; Flt-3 ligand; FL; exotoxin A; ET antigenic; immunogenic; cytotoxic T cell response; tumour; vaccine;
New chimeric polypeptide, useful as anti-tumor vaccines, comprises carboxy terminal fragment of heat shock protein, Flt-3 ligand or
                                                                                                                                                                                                                                                                    20-OCT-1999; 99US-00421608.
09-FEB-2000; 2000US-00501097.
                                                                                                                                                                                                                                                                                                                                                                                                                   26-APR-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200129233-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flt-3 ligand
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU02129 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 266 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 15-16; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine variants of human papilloma virus antigens - contain variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Edwards SJ,
                                                                                           WPI; 2001-290921/30
                                                                                                                                                                                                                                                                                                                                                      20-OCT-2000; 2000WO-US041422.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
                                                                                                                                                                                                         (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            immunotherapy.
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DB; AAT31833.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fusion protein. (Updated on 27-AUG-2003 to correct OS field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 258
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infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 512; DB 2;
Pred. No. 7.8e-57;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of a Pseudomonas exotoxin A (ETA dII), or a granulocyte-macrophage colony stimulating factor (GM-CSF); and (b) a second polypeptide domain containing an antigenic polypeptide. A composition comprising the chimeric polypeptide is useful for inducing an immune response such as a cytotoxic T cell response. The nucleic acid or vector encoding the chimeric polypeptide present in the composition is administered as naked that he composition is administered as naked that he composition is administered as naked that the composition is a composition of the composition is administration in the composition is administration in the composition of the composition is administration in the composit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      in construction of a chimeric polypeptide comprising: (a) a first polypeptide domain containing a carboxy terminal fragment of a heat sho protein (HSP), an Flt-3 ligand (FL), a cytoplasmic translocation domain of a Pseudomonas exotoxin A (ETA dII), or a granulocyte-macrophage color
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 9; Fig 19; 110pp;
                                              Siegel M,
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                                                                                                                                                                                                                             08-JUL-1999;
                                                                                                                                                                                                                                                                                                                10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                                                                                                                            18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of Hsp65-E7 fusion
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                                                                                                                                     (STRE-) STRESSGEN BIOTECHNOLOGIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 287
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                                              Chu NR,
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                                                                                                                                                                                                                             99US-0143757P
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                                                  Mizzen LA
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Pred. No. 8.7e-57;
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RESULT 64
AAB31613
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a fusion protein comprising Mycobacterium bovis heat shock protein (Hap) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen; glutathion-S-transferase; GST; E7 protein.
                                                                                                                                                                                                                   Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB;
                                                                           Screening
                                                                                                                                                                                                                                                                                                                           08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
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  Example 10;
                                                  lymphocyte
                                                                                                                                                                                                                                                                                                                                                                             10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                                                                                                                                                  18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200104344-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus.
Unidentified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of glutathion-S-transferase
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                                                                                                                                                                                                                                                                        (STRE-)
                                                                                                                                     2001-138361/14.
DB; AAF25016.
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DB; AAF25022.
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                                                    for compounds that stimulate eclls.
                                                                                                                                                                                                                 Chu NR,
Fig 9; 88pp;
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Pred. No. 8.9e-57;
0; Mismatches 3
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RESULT 65
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents a glutathion-S-transferase (GST) linked to HPV16 E7 protein, for purification purposes. The E7 protein was used to construct a fusion protein with Mycobacterium bovis heat shock proteins (Hsp). The fusion proteins are used in the method of the compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               fusion partner; immunogenicity; chimeric.
                                                                                                                                                                                                                     A new DNA sequence encoding a fusion protein comprising a mutagenized H (human papillomavirus) E6 or E7 coding sequence and a sequence encoding highly immunogenic fusion partner is useful to vaccinate against HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virucide; cytostatic; E6; E7 fusion fusion partner; immunogenicity; HPV
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                                                                                                                                            Disclosure;
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                                                                                                                                         Fig 5;
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                                                                                                                                         34pp; English
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infection; neoplasm; HbsAg-EE7T;
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The invention relates to a new DNA sequence encodes an E6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced codons which lead to enhanced translation in a mammalian cell, containi a mutation which results in production of a truncated non-functional

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RESULT 66
RESULT 68
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                                                                                                                                                                                                                                                                                                                                                                                                                          encoding encoding
The invention relates to a novel nucleic acid composition useful as an immunogen. The composition comprises a combination of: a first nucleic acid vector comprising a first sequence encoding an antigenic polypeptid or peptide, and optionally, a second sequence linked to the first sequence and encoding an immunogenicity-potentiating polypeptide (IPP); and a second nucleic acid vector encoding an anti-apoptotic polypeptide. When the second vector is administered with the first vector to a subject, a T cell mediated immune response to the antigenic polypeptide or peptide is induced that is greater in magnitude and/or duration than an immune response induced by administration of the first vector alone.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein, and encoding a highly immunogenic polypeptide fusion partner capable of enhancing immunogenicity of the E6 or E7 protein in the mammalian host. The invention is used as a vaccine for the prevention treatment of an HPV infection or a neoplasm associated with HPV infection. This sequence represents the HbsAg-EE7T fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-FEB-2003; 2003US-0449429P.
18-JUL-2003; 2003US-0488527P.
31-DEC-2003; 2003US-0533792P.
                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 18; 158pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic
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                                                                                                                                                                                                                                                                                                                                                                                          eic acid composition comprising a first nucleic acid vector
an anti-genic polypsptide and a second nucleic acid vector
an anti-spoptotic polypsptide, useful as an immunogen for
ng the growth of a tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nicity; immunogenicity-potentiating polypeptide; IPP; T-cell;
immune stimulation; tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÇĘ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vector E7-BCL-xL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.0%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349
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Pred. No. 1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 1e-9
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>س</u>
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                                                                                                                                                                                                           polypeptide
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention further includes: a particle comprising a material that is suitable for introduction into a cell or an animal by particle bombardment, bound to which is the first and second vectors or composition; a pharmaceutical composition capable of inducing or enhancing an antigen specific immune response, comprising the particle and a carrier or an excipient; inducing or enhancing an antigen specific immune response in a subject; increasing the numbers of CD8+ CTLs specific for a selected desired antigen in a subject; and inhibiting the growth of a tumor in a subject. The nucleic acid composition is useful as an immunogen for inhibiting the growth of a tumor, hence it has cyrostatic activity. This sequence represents ananti-apoptotic vector E7-DCI_XI. To the invention of the invention.
                                                                                                                                                                                                                                                              24-FEB-2003;
18-JUL-2003;
31-DEC-2003;
                                                                                                       New nucleic acid composition comprising a first nucleic acid vector encoding an antigenic polypsptide and a second nucleic acid vector encoding an anti-apoptotic polypsptide, useful as an immunogen for inhibiting the growth of a tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2005
                                                                                                                                                                              WPI; 2005-367009/37.
                                                                                                                                                                                                         Wu T,
                                                                                                                                                                                                                                                                                                                     24-FEB-2004; 2004WO-US005292
                                                                                                                                                                                                                                                                                                                                                 26-MAY-2005
                                                                                                                                                                                                                                                                                                                                                                            WO2005047501-A1
                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Anti-apoptotic vector E7-mtBCL-xL fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AEA40831
                                                                                                                                                                                                                                  (UYJO ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogenicity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               349 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                         CF,
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                                                                                                                                                                                                                                    JOHNS HOPKINS
                                                                                                                                                                                                                                                                           2003US-0449429P.
2003US-0488527P.
                                                                                                                                                                                                                                                               2003US-0533792P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              stimulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunogenicity-potentiating polypeptide; IPP; T-cell;
                                                                                                                                                                                                         Kin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.0%;
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Pred. No. 1.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumor; cytostatic
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The invention relates to a novel nucleic acid composition useful as an immunogen. The composition comprises a combination of: a first nucleic acid vector comprising a first sequence encoding an antigenic polypeptide or peptide, and optionally, a second sequence linked to the first sequence and encoding an immunogenicity-potentiating polypeptide (IPP);

Disclosure;

SEQ ID NO

21; 158pp; English.

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RESULT 68
AX25377
ID AAY25
XX AAY25
XX O6-SE
XX Pusio
KW Fusio
KW immun
KW HPV a
XX IMMAN
XX 
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CC When the second vector is administered with the first vector to a

CC subject, a T cell mediated immune response to the antigenic polypeptide

CC or peptide is induced that is greater in magnitude and/or duration than

CC an immune response induced by administration of the first vector alone.

CC The invention further includes: a particle comprising a material that is

CC suitable for introduction into a cell or an animal by particle

CC bombardment, bound to which is the first and second vectors or

CC composition; a pharmaceutical composition capable of inducing or

CC composition; a pharmaceutical composition capable of inducing or

CC and a carrier or an excipient; inducing or enhancing an antigen specific

CC immune response in a subject; increasing the numbers of CDB+ CTLs

CC specific for a selected desired antigen in a subject; and inhibiting the

CC growth of a tumor in a subject. The nucleic acid composition is useful as

CC an immunogen for inhibiting the growth of a tumor, hence it has

CC cytostatic activity. This sequence represents ananti-apoptotic vector E7-

CC mtBCL-xL fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
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                                                                                                                                                                                                              Composition comprising induce immune response
AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein f HPV (represented in AAY25375-Y25386). These constructs are optional
                                                                                                                                                                                                                                                                                                                                                                                                                            Dalemans WLJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response; HPV antigen; prevention; treatment.
                                                                                                                                             Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9933868-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HPV fusion protein D1/3-E6E7-His/HPV16.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SMIK)
                                                                                                                                                                                                                                                                                                                      1999-405485/34.
DB; AAX78793.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
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                                                                                                                                         III; Page
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                                                                                                                                         50; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                            CMG;
                                                                                                                                                                                                              an E6, E7 or E6/E7 to HPV.
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Pred. No. 1.1e-56;
0; Mismatches 3
                                                                                                                                                                                                                                              fusion protein from HPV
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Query Match Best Local Matches

95,

Similarity

99.0%; ilarity 96.9%; Conservative

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Score 512; DB 2; 1 Pred. No. 1.2e-56; 0; Mismatches 3;

Length 371;

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Best Local S
Matches 95
                     This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (RPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophillus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce a immune response in a patient to an HPV antigen. They can also be used preventing or treating HPV induced tumours
Sequence 371 AA;
                                                                                                                                            Disclosure; Fig 6; 95pp; English.
                                                                                                                                                                      Human Papilloma Virus (HPV) treatment or prophylaxis of
                                                                                                                                                                                                                                                               Bruck C,
                                                                                                                                                                                                                                                                                                                                                                       04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus.
Haemophilus influenzae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prot.D1/3-E6-E7-His/HPV16 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY02633;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY02633 standard;
                                                                                                                                                                                                                                                    Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                                                     22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                             17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                WO9910375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour;
                                                                                                                                                                                                                                                                                          (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                          1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lesion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      371 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                Cabezon Silva T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E7;
                                                                                                                                                                                                                                                                                                                     97GB-00017953
                                                                                                                                                                                                                                                                                                                                             98WO-EP005285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            benign;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n protein; protein
malignant; virus;
                                                                                                                                                                                                                                                                  Delisse AEF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371
                                                                                                                                                                      fusion proteins - useful in vaccines \ensuremath{\mathsf{HPV}} induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 512; DB 2;
Pred. No. 1.2e-56;
0; Mismatches 3
                                                                                                                                                                                                                                                                Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D; vaccine;
infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used for
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RESULT 70

AED52638

ID AED52

XX AED52

XX AED52

XX AED52

XX Pusio

XX Pusio

XX Pusio

XX Fusio

XX Fu
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                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AED52638 standard; protein; 371
                                                                                                                                                                                                                                                                                                                                                       Sequence 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Fig 6; 96pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-MAR-2005.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; vaccine; virucide; uterine cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae; strain 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2005-557648/57.
DB; AED52637.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             265
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                                                                                                                                                                                                                                       95;
                                                                                                                                                                                                                                                                      Similarity
CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 362
                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97EP-00179535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98IN-CH001903.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           type 16.
                                                                                                                                                                                                                                                                99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  papilloma; cytostatic; papillomavirus infection;
tumor; E7; D protein.
                                                                                                                                                                                                                                 Score 512; DB 9;
Pred. No. 1.2e-56;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                            Length 371;
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                                                                                                                                                                                                                                       Indels
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RESULT 71
AAY25381
ID AAY25
XX AAY25
XX AAY25
XX AAY25
XX AAY25
XX DG HPV 1
XX Fusic
XX Fusic
XX Fusic
XX HPV 2
XX HUMAI
XX HOUS
PR WO993
XX OB-JI

AAYOZ637
ID AAYOZ637
ID AAYOZ637
XX AAYOZ
XX 17-OC
DT 17-OC
DT 22-JU
XX
DE CLYTA
XX
KW Chime
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce an immune response in a patient to an HPV antigen. They can also be used for preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pusion protein; E6 protein; E7 protein; E6/E7; immu immunological fusion partner; CpG oligonucleotide; HPV antigen; prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-SEP-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY25381 standard; protein; 390 AA
                                                                                                                                17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUL-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9933868-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPV fusion protein CLYTA-E6E7-His/HPV16
                                                                              CLYTA-E6E7-His protein
                                                                                                                                                                                                                                                                     AAY02637 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-405485/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dalemans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-DEC-1997;
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                                                                                                                                                                                                                   AAY02637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example VIII; Page 55-56; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                      344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WLJ,
                                                                                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-EP008563
                                                                                                                                                                                                                                                                   protein; 390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 512; DB 2; L
Pred. No. 1.3e-56;
Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E7 or E6/E7
                                                                                                                                                                                                                                                                        $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  from HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Chimeric; E6; E7; fusion protein; CLYTA; vaccine; lesion; benign; malignant; virus; infection.

immunotherapy; tumour;

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RESULT 73
ARD52646
ID ARD52
XX ARD52
XX ARD52
XX Pusio
XX Fusio
XX Fusio
XX Yiruc
XX Strep
OS Strep
OS Synthman
OS Synthman
OS Synthman
OS Synthman
OX Synthman
XX IN980
XX XX
PB 04-MP
XX XX
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Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Streptococcus pneunoniae CLYTA protein of the encoded protein. The protein can be used in a vaccine, for immuno-therapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                      Human papillomavirus type 16. Synthetic.
                                                                                                                                                      rusion protein;
virucide; uteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus.
Streptococcus pneumoniae.
Chimeric.
                                        04-MAR-2005.
                                                                                                                               Streptococcus pneumoniae.
              24-AUG-1998;
                                                                IN9801903-I4
                                                                                                                                                                   Fusion
                                                                                                                                                                                             Fusion protein cLytA-E6-E7-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 390
                                                                                                                                                                                                                      29-DEC-2005
                                                                                                                                                                                                                                               AED52646;
                                                                                                                                                                                                                                                                        AED52646 standard; protein; 390 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 14; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Papilloma Virus (HPV) fusion proteins - useful in vaccines treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bruck C, Cabezon Silva
Lombardo-Bencheikh A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bruck C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-MAR-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                                                                                                                                                                                                                                       344
                                                                                                                                                                                                                                                                                                                                                                                         284
                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                   μ
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95; Conserv
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                                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                         MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 343
                                                                                                                                                                                                                                                                                                                                                                                                      MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                         uterine
                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                                                                                                     (first entry)
                98IN-CH001903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97GB-00017953
                                                                                                                                                                     vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-EP005285
                                                                                                                                                         cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'n
                                                                                                                                                       papilloma; cytostatic; papillomavirus infection;
tumor; E7; LytA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 512; DB 2;
Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delisse AEF,
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gerard CMG;
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                                                                                                                                                                                                                                                                                                                                       381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 390;
                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 74
AAM50663
ID AAM50
XX AAM50
XX 29-AU
DT 29-AU
DT 08-AF
XX Thiox
XX Thiox
XX Thiox
XX Thiox
XX Chime
ABChe
CS Homo
OS Esche
CS Chime
XX Chime
YT Prote
FT Pro
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (cLyth) or thioredoxin. The present sequence represents an HPV-Lyth, fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 390 AA;
                                                           WO200200892-A1
                                                                                                                                                                                                                                                   Cleavage-site
                                                                                                                                                                                                                                                                                                      Protein
                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Escherichia (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thioredoxin; ubiquitin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thioredoxin-ubiquitin-ProteinD1/3 E7-His triple fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29-AUG-2003
08-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAM50663;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAM50663 standard; protein; 421 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 12;
                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2005-557648/57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 14; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97EP-00179535
                                                                                                                                                                                                                                                      201.
                                                                                                                                                                                                                                                                                                                                                                                   /label= Thioredoxin
                                                                                                           /label= Histidine_tail
                                                                                                                                                                    /label= ProteinD1/3-E7
                                                                                                                                                                                                                          label=
                                                                                                                                                                                                                                                                               /label=
                                                                                                                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers,
                                                                                                                                                                                                .412
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                                                                                                                                                                                                                                                      . 202
                                                                                                                                                                                                                                                                                                         . 199
                                                                                                                                                                                                                    UBP1_cleavage_site
                                                                                                                                                                                                                                                                          Ubiquitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 proteinD1/3 E7; tumour; antigen; cancer; vaccine;
                                                                                                                                                                                                                                                                                                                                  Linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 512; DB 9;
Pred. No. 1.3e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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03-JAN-2002.

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RESULT 75
AAB31610
ID AAB31
XX AAB31
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is that of a triple fusion protein comprising, from CC the N-terminal end, Escherichia coli thioredoxin, human ubiquitin and human papillomavirus Proteinly/3 E7, followed by a histidine affinity tail. The triple fusion protein was produced in E. coli G1724 host cells CC transformed by an expression vector comprising DNA (see ABA91285) encoding the fusion. This is an example of the production of triple considered method of protein of interest, in this case ProteinD1/3 E7. A CC chaimed method of producing a recombinant protein of interest involves: CC claimed method of producing a recombinant protein of interest involves: CC claimed method of producing a recombinant protein of interest involves: CC claimed method of producing a recombinant protein of interest involves: CC claimed method of producing a recombinant protein of the triple fusion and a ubiquitin-specific endoprotease (especially UBP1 from Saccharomyces cerevisiae); and recovering the recombinant protein directly from the bacterial cells after it has been subjected to the action of the ubiquitin-specific endoprotease in vivo. In the present case, expression is controlled by the addition of the tryptophan. The recombinant protein can used as a vaccine for cancer therapy. (Updated on 29-AUG-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel DNA sequence encoding triple fusion protein comprising ubiquitin fused between thioredoxin and polypeptide of interest, useful for producing recombinant polypeptide of interest suitable for medicinal use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-JUN-2000; 2000GB-00015619.
30-OCT-2000; 2000GB-00026484.
   18-JAN-2001
                                                                                                                             Mycobacterium tuberculosis.
Human papillomavirus.
                                                                                                                                                                                                                                                                                             Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; Lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of Hsp40-E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB31610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB31610 standard; protein; 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABA91285
                                                                  WO200104344-A2
                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cabezon Silva TEV,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-JUN-2001; 2001WO-EP006952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 374
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AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delisse AEF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 1.4e-56;
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RESULT 76
AAB03790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                            12-SEP-2003
06-AUG-2003
13-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents a fusion protein comprising a Mycobacterium tuberculosis heat shock protein (Hsp) 40 fused at its 3' end to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Thi cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                        Heat shock protein; tumour specific antigen; colibacillus; microzyme; plant; immune response; tumour; cancer; human papillomavirus;
                                                                                                                                                                                                                                                                                                                                              AAB03790 standard; protein; 638
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 493 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Screening for compounds that stimulate Th1-like responses in CD4+ T lymphocyte cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF25013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JUL-1999;
                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                  Heat shock
                                                                                                                                                                                                                                                                                                                   AAB03790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 6; Fig 5A-B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-138361/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-2000; 2000WO-US018828
            24-SEP-1998;
                                     24-SEP-1998;
                                                                                            CN1248631-A
                                                                                                                       Chimeric.
                                                                                                                                    Human
                                                                                                                                                                           pointed condyloma.
                                                                29-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                  456 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        396 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                 papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRESSGEN BIOTECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chu NR,
                                                                                                                                                                                                                                  protein and tumour specific antigen fusion protein sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                        (revised)
                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                   bovis.
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              98CN-00112264
                                      98CN-00112264.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 512; DB 4;
Pred. No. 1.7e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORP
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RESULT 77
AAB31609
ID AAB31
XX AB31
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XX Heat
XX Heat
XX Heat
XX E7 ppz
XX E7 ppz
XX E7 ppz
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific antigen of human papillomavirus (HPV). The fusion protein can be expressed in collbacillus, microzymes and plants. The fusion protein can be used to make immunostimulant injections, as it can produce specific cell immune and humoral immune responses. It possesses prophylaxis and therapeutic capacity for preventing human papillomavirus (HPV) infection, but also can be used for immunotherapy of pointed condyloma, tumours and cancer caused by HPV. (Updated on 06-AUG-2003 to correct OS field.)

(Updated on 12-SEP-2003 to standardise OS field)
                                                    Screening for compounds that stimulate Th1-like responses in CD4+
                                                                                                                              WPI; 2001-138361/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9; Fig 1; 5pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New fusion protein for immunotherapy of venereal disease a heat shock protein of Mycobacterium bovis.
                                                                                                                                                                                                                                                                                          08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                            10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200104344-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB31609 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-431995/38
                        lymphocyte cells
                                                                                                                                                                                                                                         (STRE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium bovis
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                                                                                                                                                                                                                                         STRESSGEN BIOTECHNOLOGIES CORP
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                                                                                                        AAF25012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
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                                                                                                                                                                                  NR,
                                                                                                                                                                                                                                                                                          99US-0143757P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of Hsp65-E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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Pred. No. 2.4e-56;
0; Mismatches 3;
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RESULT 78
AAB31619
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
The present sequence represents a fusion protein comprising a Streptococcus pneumoniae heat shock protein (Hsp) 65 fused to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T
                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
Streptococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB31619 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 639 AA;
                                                                                                                                                                  N-PSDB; AAF25036.
                                                                                                                                                                                                                                                                         08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB31619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pathogens
                                                                                          Example 15;
                                                                                                                                   Screening for compounds that stimulate Th1-like responses in CD4+
                                                                                                                                                                                  WPI; 2001-138361/14.
                                                                                                                                                                                                                                                                                                                                       18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a fusion
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                                                                                                                      lymphocyte cells.
                                                                                                                                                                                                                                             (STRE-) STRESSGEN BIOTECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQXP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence of Hsp65-E7 fusion
                                                                                                                                                                                                               Chu NR,
                                                                                        Fig 15A-B; 88pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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Pred. No. 2.4e-56;
Mismatches 3;
                                                                                          English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 639;
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Matches
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Best Local
               The present sequence represents a fusion protein comprising a Aspergillus fumigatus heat shock protein (Hsp) 60 fused to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fission protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like response to the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like response to the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                                                                                              Example 16; Fig 16A-B; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Screening for compounds that stimulate Th1-like responses in CD4+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-2000; 2000WO-US018828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat shock plymphocyte;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino acid sequence of Hsp60-E7 fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB31620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB31620 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aspergillus fumigatus
Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                          lymphocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (STRE-) STRESSGEN BIOTECHNOLOGIES CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-138361/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                                                                                                                                                             cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ğ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-0143757P
response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Th1 response; Th1 cell; CD4+ T lymphocyte cell; Hsp10; Hsp60; Hsp71; microbial pathogen;
   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       647
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Pred. No. 2.4e-56;
microbial pathogens
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XAXEXBXBXBX8888XEXEXEXEXEXEXEXEXEXEXEXXSSSSSSSSXXX

Query Match
Best Local Similarity
Matches 94; Conserv

Conservative

98.8**%**; 95.9**%**;

Score 511; DB 7; L Pred. No. 2.9e-57;

Length 98; Indels

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Gaps

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                                                                            The present sequence is the protein sequence of human papillomavirus E7 cc oncoprotein. E7 promotes oncogenesis through an inhibition of p21Cip21 cc transport into the nucleus. E7 abrogates Raf-associated arrest and cc prevents inhibition of cyclin E-CDK2 activity without disrupting Raf cc induction of p21Cip21. E7 neither interacts with p21Cip1 nor derepresses p21Cip1-associated CDK2 activity, but instead reduces the association cc state levels of Akt, a regulator of p21Cip1 localisation, leading to loss co f p21Cip1 phosphorylation and accumulation of p21Cip1. E7 disrupts the cffects of Raf on Akt activity and prevents p21Cip1 nuclear accumulation. CC Maintenance of Akt activity is necessary and sufficient to bypass Raf carrest. The invention provides methods for identifying and using compounds capable of promoting the nuclear localization of p21Cip1. The methods can be used to inhibit aberrant cellular proliferation for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papilloma virus E7 oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 647
                                                               treatment of cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; SEQ ID NO 11; 119pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           activity and selecting a compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; ADF18636, ADF18637.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a compound that inhibits E7 cellular proliferation activity by administering a compound to a system, where the system maintains Akt activity and selecting a compound that decreases the amount of Akt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYRP )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Westbrook
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Pred. No. 2.5e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT 81
ADO44064
                                                                                                                              CC The present sequence represents a fusion protein, comprising E6 and E7 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion CC protein is designated E6E7PentM, and comprises an E6 amino terminus CC (where residues 63 and 106 have been replaced with glycine) and an E7 CC carboxy terminus (where residues 24, 26 and 91 have been replaced with CC glycine). E6E7PentM is representative of fusion proteins of the CC invention. The specification describes human papillomavirus E6 and E7 CC polypeptides, where the E7 polypeptide has mutations at any one or more CC of the amino acids corresponding to amino acids 24, 26 or 91 of the CC sequence given in ADO44073 and the E6 polypeptide has no mutations or has CC mutations at any one or more of the amino acids corresponding to amino acids 3 or 106 of there sequence given in ADO44072. The polypeptides of CC the invention are useful for treating or preventing human papillomavirus CC immune responses against HPV. They are also useful for treating lower CC castroints at all cracer. Cancers of anal cancer and other treating lower contents and the corresponded to the contents against HPV. They are also useful for treating lower contents and the cancer cancers of
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Best Local Similarity Matches 94; Conserv
                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                    Sequence 248
                                                                                                                      gastrointestinal
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 22; Page 70-71; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-316328/29.
N-PSDB; ADO44065.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of a fusion protein designated E6E7PentM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADO44064 standard; protein; 248
                                                                                                      reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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 Conservative
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                                                                                                   system, including
                98.8%;
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Score 511; DB 8;
Pred. No. 9.6e-57;
1; Mismatches 3
                                                                                                   e.g. anal
ling penile
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                                                                                                   cancer, and other cancers of and vulvar cancer.
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                                Length 248;
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Indels
0,
Gaps
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MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60

Matches Query Match Best Local

94; Similarity

Conservative

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Score 510; DB 8; I Pred. No. 1.3e-56; 1; Mismatches 3;

Length 248 Indels

0,

Gaps

0,

98.6%;

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RESULT 82
AD044062
ID AD044
XX AD044
XX AD044
XX AMIno
XX E6 pr
KW E6 pr
KW Cervi
XX Synth
XX O3-OC
XX O3-OC
XX AMHE
XX O3-OC
XX AMHE
XX O3-OC
XX CAMHE
XX O3-OC
XX CAMHE
XX CAMC
XX CAM
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                                                           The present sequence represents a fusion protein, comprising E6 and E7 CC polypeptides from human papillomavirus type 16 (HPV16). The fusion CC protein is designated E6E7TetM, and comprises an E6 amino terminus (where residues 63 and 106 have been replaced with glycine) and an E7 carboxy CC terminus (where residues 24 and 26 have been replaced with glycine). CC E6E7TetM is representative of fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, cc where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
   Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus type 16. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 22; Page 68-69; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADO44063.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO2004030636-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence
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penile cancer; vulvar cancer.
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RESULT 83
AD044060
ID AD044
XX AD044
XX AD044
XX AD044
XX E6 p
XX E6 p
XX Amin
XX Amin
XX Amin
XX Amin
XX Amin
XX Ann
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                                                                                                                                                                                                                                                                                                                                                                                CC type B6 and B7 polypeptides from human papillomavirus type 16 (HPV16).

The specification describes human papillomavirus E7 and E7 polypeptides, where the B7 polypeptide has mutations at any one or more of the amino acids 24, 26 or 91 of the sequence given in AD044073 and the B6 polypeptide has no mutations or has mutations at any one or more of the amino acids 24, 26 or 91 of the sequence given in AD044072. The polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
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                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
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                                                                                                                                                                                                                                                                                                                                    Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002; 2002US-0415929P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-APR-2004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of an E6E7 fusion protein
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DB; ADO44061.
                                                                                              151
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                                                                                                                                                                                                                                               Similarity
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                              MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cassetti MC;
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                                                                                                                                                                                                                                         98.5%;
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                                                                                                                                                                                                            Score 509; DB 8;
Pred. No. 1.7e-56;
1; Mismatches 3
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                                  98
                                                                                                                                                                                                                                                                        Length 248;
                                                                                                                                                                                                                Indels
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:
                                                                                                                                                                                                            Gaps
                                                                                              210
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RESULT 84
AAXSO703
ID AAX50
ACC AAX50
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention describes the construction of a novel polypeptide with immunogenic and altered biological function of a protein, where the polypeptide has regions of the protein of about 10-40 amino acids in a different order. The polypeptide, or its DNA, is useful for active immunization without cross-reactivity and problems associated with the biological function of the protein. This sequence represents the human papillomavirus type 16 E7 protein which is used to illustrate the method of the invention
                                                                                                  06-AUG-2003
07-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E7 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPV16 E7 protein
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                                                  HPV 16E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 25; 33pp; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ24129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus
                                                                                                                                                                                    AAB49453;
                                                                                                                                                                                                                                       AAB49453 standard; protein; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-023362/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmunization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic protein with altered biological function, useful for active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  211 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEDEIDGPRGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                  (revised)
(first entry)
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95.9%;
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Immune response; gene therapy; antigen presentation; vaccine; cancer;

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RESULT 86
AAO22639
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC The present invention relates to an expression vector comprising a CC promoter, signal sequences, an antigen, a cell-binding element, and a CC polyadenylation sequence. The expression vector can be used directly or CC after transduction of antigen-presenting cells, in vaccines for treatment CC and prevention of cancer, infections and autoimmune diseases. Vectors CC similar to the expression vector of the present invention, but expressing CC that contain MHC-II restricted epitopes for activation of CD4+ cells or CC elicitation of an immune response in vivo. The identified polypeptides are CC (in APC) or vector containing DNA that expresses the polypeptides are CC (in APC) or vector containing DNA that expresses the polypeptides are CC which hamper the above conditions. The present sequence is HPV CC which hamper the secretion of the protein, which has a string of charged residues CC to result in the present protein, stablises the protein and facilitates CC secretion. The coding sequence for the present protein was used to CC construct the expression vector of the present invention. (Updated on 06-
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                             Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth; cancer; human papilloma virus; cervix; cell-mediated immune response;
                                                                                             HPV-16 protein
                                                                                                                              15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel vector expressing secreted antigen fused to cell binding element, useful in vaccines for treatment of e.g. cancer and infection, also
Human papilloma virus
                                                                                                                                                                                           AAO22639 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 98 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 17; 163pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-007312/01
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06-MAY-1999;
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                                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                           MHGDTFTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to correct
                                                                                                                                                                                                                                                                                                                                       MHGDTPTLHEYMLDLQPETTDLYCYEQLSDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                             (first entry)
                                                                                           sequence,
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99US-0132752P.
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                                                                                             SEQ ID No
                                                                                                                                                                                            86
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Pred. No. 9.5e-57;
1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 98;
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ARESULT 87
ARO22923
ID ARO22
XX ARO22
XX ID-DE
XX ID-DE
XX Virus
CKW Virus
KW fusic
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XX humar
XX EP124
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel method for determining the possibility of recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV) or suspected of being infected with HPV, and has or had a (pre-)cancerous growth on or around the cervix. The novel method comprises incubating an E6 or E7 peptide of HPV with a sample from the patient, and assaying the sample for a cell-mediated immune response against the peptide. The method is useful for determining the possibility and preventing the recurrence of a (pre-)cancerous growth in a patient infected with HPV or suspected of being infected with HPV. The HPV E6 or E7 peptides are useful in immunotherapy for the preventing or reducing the risk of development of (pre-)cancerous growths. This sequence
                                                                                                                                                                          Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine; fusion partner; immunogenicity; HPV infection; neoplasm; HPV16; human papillomavirus-16; EE7T-sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determining a possible recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV), comprises incubating the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
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23-MAR-2001; 2001EP-00107271
                                   23-MAR-2001; 2001EP-00107271.
                                                                                                                                        Human papillomavirus
                                                                                                                                                                                                                                                  Human papillomavirus-16 (HPV16)
                                                                                                                                                                                                                                                                                     12-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                          AA022923;
                                                                                                                                                                                                                                                                                                                                                           AAO22923 standard; protein; 111
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                                                                        25-SEP-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYCYEQLSDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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Pred. No. 9.
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                                                                                                                                                                                                                                                EE7T-protein sequence
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).5e-57;
nes 3;
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                                                                                                                                                                                                                                                                                                  24-OCT-2003
25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a new DNA sequence encodes an B6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced by codons which lead to enhanced translation in a mammalian cell, containing a mutation which results in production of a truncated non-functional protein, and encoding a highly immunogenic polypeptide fusion partner capable of enhancing immunogenicity of the E6 or E7 protein in the mammalian host. The invention is used as a vaccine for the prevention or treatment of an HPV infection or a neoplasm associated with HPV infection. This sequence represents the human papillomavirus-16 (HPV16) EE7T-protein sequence of the invention
                                                                                                                                                                   Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A new DNA sequence encoding a fusion protein comprising a mutagenized HPV (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a highly immunogenic fusion partner is useful to vaccinate against HPV
                                                                                                                                                                                                           Human papillomavirus type 16.
                                                                                                                                                                                                                                                Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 111 AA;
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 Boursnell MEG,
                                                                            10-MAR-1992;
                                                                                                      01-OCT-1992.
                                                                                                                                WO9216636-A1
                                                                                                                                                                                                                                                                        HPV 16 E7 protein fragment.
                                                                                                                                                                                                                                                                                                                                                       AAR27724;
                                                                                                                                                                                                                                                                                                                                                                               AAR27724 standard; protein;
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                           (IMMU) IMMUNOLOGY LTD
                                                  14-MAR-1991;
                                                                                                                                                                                                                                     immunotherapeutic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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(revised)
(first entry)
                                                   91GB-00005383
                                                                            92WO-GB000424
Inglis SC,
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                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98.1%;
96.9%;
                                                                                                                                                       "start of HPV-16 E7 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                 262
 Munro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 507; DB 5;
Pred. No. 1.1e-56;
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ARYOROZO
ID AAYOR
XX AYOR
XX 27-AU
DT 27-AU
DT 08-JU
XX L1 pr
XW L1 pr
XW cervi
XW cervi
XW antig
XX MO991
XX 15-AF
PD 15-AF
XX 06-OC
XX WPI;
DR WPI;
DR WPI;
DR WPI;
DR WPI;
DR WPI;
DR WHIRI
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Best Local Similarity
Matches 94; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The fragment of DNA contg. the HPV-16 E6/E7 coding region was prepd. by PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using oligonucleotides SO5 and SO6. The prod. of the second reading frame is the HPV-16 E7 protein whereas the third reading frame encodes HPV-16 E6. The E6 and E7 ORPs are fused together to form a single continuous ORP via site directed mutagenesis and the immortilising potential of E7 is removed by altering two key codons of the HPV E7 sequence. The single ORF of HPV-16 E6/E7 may be inserted into vaccinia virus DNA at neutral sites (pref. by inserting two sets of the DNA in opposite orientations to overcome the problem of intertypic recombination) to make a recombinant virus vector for use immunotherapeutically to activate cells of the immune system against HPV. See also ARR27723-43. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant virus vectors encoding human papillomavirus proteins - for treating and vaccinating against HPV infections and conditions caused them, such as cervical cancer.
                                                                                                                                                                                                                                                                                                                                      L1 protein; capsomer; virus; vaccine; infection; treatment;
cervical carcinoma; fusion protein; anti-capsid; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2003
08-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 262 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Human papilloma virus E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY08020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY08020 standard;
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                                             N-PSDB;
                                                                                            Gissmann L,
                                                                                                                                                          06-OCT-1997;
                                                                                                                                                                                         06-OCT-1998;
                                                                                                                                                                                                                                                                                       Human papillomavirus
                                                                                                                                                                                                                                                          WO9918220-A1
                                                                                                                          (LOYO ) UNIV LOYOLA CHICAGO
                                                                                                                                                                                                                          15-APR-1999
                                                              1999-264026/22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                               AAX37567.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTPRICYOSTHVDIRTLEDLIMGTLGIVCPICSOKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                            Mueller
                                                                                                                                                                                                                                                                                                                                                                                                                     (revised)
(first entry)
                                                                                                                                                                                         98WO-US020965
                                                                                                                                                            97US-00944368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein;
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95.98;
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Pred. No. 6.1e-56;
0; Mismatches 4,
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                                                                                                                                                                                                                                                                                                                                     ; prevention;
E7 protein;
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Human papilloma virus against HPV infection.

(MPV)

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fusion protein capsomers, used

in vaccines

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RESULT 90
ADJ32548
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Best Local
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                                                                                                                                                                                                             12-OCT-2000;
24-OCT-2000;
12-OCT-2001;
15-MAR-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention describes novel vaccines comprising a human papilloma virus (HPV) capsomer, composed of a HPV L1 fusion protein or a HPV L1 truncated protein. The vaccines can prevent or treat human papilloma virus infection. Such therapeutic vaccinations can be used for relief against, e.g. cervical carcinoma. Construction of chimeric proteins comprising amino acid residues from L1 protein, and e.g. E6 or E7 protein, which give rise to chimeric capsomers, combines prophylactic and therapeutic functions of a vaccine. Capsomers can promote elimination of persistently infected cells. Capsomers can also escape neutralization by pre-existing anti-capsid antibodies and hence possess longer circulating half-life as compared to chimeric virus-like particles. The fusion protein, which forms the capsomer, provides increased antigenicity. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                         Land
                                                    Reducing the proliferation of a cancer cell involves inhibiting ligand binding to an integrin receptor on the cancer cell, where the integrin
                                                                                               WPI; 2004-154528/15.
N-PSDB; ADJ32547.
                                                                                                                                                                                                                                                                                                                04-DEC-2003.
                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus.
                                                                                                                                                                                                                                                                                    17-MAR-2003;
                                                                                                                                                                                                                                                                                                                                           US2003224993-A1.
                                                                                                                                                                                                                                                                                                                                                                                                brain tumour; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                               myeloma; carcinoma; glioma; plasmocytoma; sarcoma; thyoma; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                             Integrin; cell proliferation; cancer; melanoma; adenoma; lymphoma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus (HPV) type 16 E7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADJ32548 standard; protein;
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                                                                                                                                                                     (DELE/)
                                                                                                                                                                                   (LAND/)
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                                                                                                                                                                    DELEU L.
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                                                                                                                                         Deleu L;
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                                        comprises
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                                                                                                                                                                                                            ; 2000US-0239705P.
; 2000US-0242812P.
; 2001WO-US032127.
; 2002US-0365078P.
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                                                                                                                                                                                                                                                                                    2003US-00392113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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Pred. No. 2.3e-56;
0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein.
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Disclosure;

SEQ ID NO

29; 161pp; English

stimulate

responses

response

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RESULT 91
AAB31607
ID AAB31
XX AAB31
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                      The present sequence represents the HPV16 E7 protein. HPV16 E7 was fused to a heat shock protein (Hsp), and used used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprises contacting naive lymphocytes in the detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp40, Hsp40, and Hsp71. The method may be used to identify
                                                                                                                                                                                                                                                                                                                                                                                                Screening for compounds that stimulate Th1-like responses lymphocyte cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus
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                                                                                                                                                                                                                                                                                                                                          Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Siegel M, Chu NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-ЛПТ-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-JUL-2000; 2000WO-US018828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200104344-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Amino acid sequence of the HPV16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB31607 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2001-138361/14.
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                                                                                                                                                                                                                                                                                                                                      3; Fig 2; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 504; DB 8; Pred. No. 2.3e-56;
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                         The invention relates to a novel composition comprising human papillomavirus (HPV) antigens or portions linked via hydrophobic bonds or mixed with very small size proteoliposomes (VSSP's). The invention further comprises a method for treating a tumor expressing an HPV antigen CC by administering an effective amount of this composition. The novel composition has cytostatic activity. The composition is useful for CC composition has cytostatic activity. The composition is useful for CC suitable for use in the pharmaceutical industry as vaccines in human CC therapeutics for cancer treatment. The cellular immune response against CC therapeutics for cancer treatment. The cellular immune response against CC cytotoxicity, ensuring that cells which exhibit the HPV antigen are CC destroyed more effectively. This sequence represents a Neisseria CC meningitials pl.7.16 delta 5 and HPV-16 E7 fusion protein, used in the CC expression of HPV antigens of the invention.
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Best Local :
                                                                                                                                                                                                                                                                                             Vaccine composition for boosting cellular immune response against human papilloma virus (HPV) antigens, contains HPV antigens linked via hydrophobic bonds or mixed with very small size proteoliposomes (VSSP's)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-OCT-2003; 2003CU-00000224.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2004; 2004WO-CU000010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N. meningitidis P1.7.16 delta
                                                                                                                                                                                                                                                                                                                                                                                                                          Torrens Madrazo IDC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Neisseria meningitidis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INGG-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENT ING GENETICA & BIOTECNOLOGIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MDGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                 SEQ ID NO 7; 62pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            infection;
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                                                                                                                                                                                                                                                                                                                                                                                                           Acosta 0;
                                                                                                                                                                                                                                                                                                                                                                                                                        Guillen Nieto GE, Fernandez Molina LE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 503; DB 4;
Pred. No. 3.1e-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 and HPV-16 E7 fusion protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            stimulation; vaccine;
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                                                                                                                                                                                                                                                                                                proteoliposomes (VSSP's)
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                                                                                                                                                                                    an HPV antigen
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Sequence 490

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MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK

Conservative

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Mismatches

Indels

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MDGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK

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RESULT 93
AAB31614
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Best Local Similarity
Matches 93; Conserv
Query Match
Best Local S
                                                                                                                                        The present sequence represents a fusion protein comprising Mycobacterium bovis heat shock protein (Hsp) 65 fused at its C terminal to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-138361/14.
N-PSDB; AAF25019.
                                                                       Sequence 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening for compounds that stimulate Th1-like responses in CD4+lymphocyte cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
Mycobacterium bovis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of Hsp65-E7 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB31614 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 11; Fig 10A-B; 88pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-JUL-2000; 2000WO-US018828
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (STRE-) STRESSGEN BIOTECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IHGDTPTLHEYMLDLQPETTDLYCYEQLSDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chu NR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                         AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mizzen LA
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97.3%;
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Score 503; DB 4;
Pred. No. 3.5e-55;
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Pred. No. 2.5e-55;
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                      Length 648,
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RESULT 95
AAB31618
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AAB31617
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                                                                                                                                                                     Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                                     The present sequence represents a fusion protein comprising Mycobacterium tuberculosis heat shock protein (Hsp) 71 fused to a HPV16 E7 protein. The fusion protein is used in the method of the invention. The specification describes a method of determining whether a compound stimulates a Thilike response. Thi cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1 like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Thilike responses in response to microbial pathogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                             Sequence 711
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                                                                                                                                                                                                                                                                                                                                                                                                                               Example 14; Fig 13A-B; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Screening for compounds that stimulate Th1-like responses lymphocyte cells.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus.
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                                                                                                                                                                       94;
                                                                                                                                                                                      Similarity
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                                                                                                                                      MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 98
                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                              MDGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chu NR,
                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mizzen LA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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95.9%;
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                                                                                                                                                                    Score 503; DB 4; Length 711; Pred. No. 4e-55; O; Mismatches 4; Indels
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RESULT 96
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Best Local S
Matches 94
                                                                                                                                                                                                                                                                                                                                        The present sequence represents a fusion protein comprising a HPV16 E7 protein fused to a Mycobacterium tuberculosis heat shock protein (Hsp) 71. The fusion protein is used in the method of the invention. The stimulates a Th1-like response. Th1 cells are a subset of CD4+ T lymphocyte cells. The method comprises contacting naive lymphocytes in vitro with a fusion protein comprising at least a fragment of Hsp, and then detecting the TH1-like response exhibited by the cell sample. The proteins which may be used in the method of the invention are Hsp65, Hsp40, Hsp10, Hsp60, and Hsp71. The method may be used to identify compounds that stimulate Th1-like responses in response to microbial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus.
Mycobacterium tuberculosis.
                                                                           ABB81111 standard; protein;
                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 14; Fig 14A-B; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening for compounds that stimulate \mbox{Th1-like} responses in lymphocyte cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Siegel M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Heat shock protein; Hsp; Th1 response; Th1 cell; CD4+ T lymphocyte cell; lymphocyte; Hsp65; Hsp40; Hsp10; Hsp60; Hsp71; microbial pathogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of E7-Hsp71 fusion protein.
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DB; AAF25031.
                                                                                                                                            61
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                                                                                                                                                                                                                                                    94;
                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                               MDGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                       724
                                                                                                                                            CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mizzen LA;
                                                                                                                                                                                                                                                             97.3%;
95.9%;
                                                                             99
                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                               Score 503; DB 4;
Pred. No. 4.1e-55;
                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                    4.
                                                                                                                                                                                                                                                                           Length 724;
                                                                                                                                              98
                                                                                                                                                                       86
                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                    0,
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                                                                                                                                                                                                                                                    Gaps
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HPV E7 antigenic protein

05-NOV-2002

(first entry)

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ABB82376
ID ABB82378
XX ABB82378
AC ABB82
XX
AC ABB82
XX
XX
DT 08-JJ
XX
XX
Immut
KW hepat
KW E7 pp
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                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a new nucleic acid molecule (I) encoding a fusion polypeptide useful as a vaccine composition. (I) comprises a first nucleic acid sequence encoding a first polypeptide or peptide that promotes processing via the Major Histocompatibility Complex (MHC) class I pathway (MHC-I-PP) and/or promotes development or activity of an antigen presenting cell (APC). The second nucleic acid sequence is linked in frame to the first nucleic acid sequence or to a linker nucleic acid sequence and encodes an antigenic polypeptide or peptide. The methods and compositions of the present invention are useful as therapeutic vaccine for cancer and for major viral infections, such as hepatoma and cervical cancer, that cause morbidity and mortality. They can also be used in treating animal diseases, such as equine herpesvirus, bovine viruses, Marek's disease, retroviral and lentiviral diseases and rabies, in the veterinary medicine context. The present sequence represents the human repetitions are represents the human partitions.
Immunogenicity; cytostatic; virucide; protozoacide; antibacterial; CTL;
hepatotropic; anti-HIV; vaccine. cytotoxic T lymphocyte; tumour; HPV;
E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid molecule encoding a fusion polypeptide that promotes processing via the Major Histocompatibility Complex class I pathway and/or promotes activity of an antigen presenting cell, useful as va for cancer and viral infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Major histocompatibility complex; MHC; antigen presenting cell; APC; antigen; cytostatic; virucide; gene therapy; CD8; vaccine; therapeutic; cancer; viral infection; HPV; E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ
                                                                                                  08-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2002; 2002WO-US002598.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus.
                                                                  Modified HPV-E7
                                                                                                                                      ABB82376
                                                                                                                                                                      ABB82376 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                papillomavirus (HPV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS.
                                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                             93;
                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
                                                                                                                                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                  (first entry)
                                                                amino acid sequence.
                                                                                                                                                                    protein;
                                                                                                                                                                                                                                                                                                                                                                                                          96.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E7 antigenic protein
                                                                                                                                                                        99
                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                            Score 500; DB 5;
Pred. No. 7.6e-56;
0; Mismatches 3
                                                                                                                                                                                                                                                         96
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                                                                                                                                                                                                                                                                                                                                                                                                                            Length 99
                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine
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RESULT 98
ADE21865
ID ADE21
XX
AC ADE21
XX
AC ADE21
XX
DT 29-JA
DT 29-JA
DX HPV-1
XX
Chime
KW Gene
XX
GS Humar
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid molecule that encodes a fusion CC polypeptide, comprising a first nucleic acid sequence encoding a comprise at least one immunogenicity-potentiating CC polypeptide, optionally, fused in frame with the nucleic acid, a linker nucleic acid encoding a linker peptide, and a nucleic acid that is linked in frame to them, and that encodes an antigenic peptide or polypeptide. CC rist encicled a cid molecule, polypeptides and vectors are useful as conceines for enhancing immune responses, primarily cytotoxic T CC vaccines for enhancing immune responses, primarily cytotoxic T CC antigens, and for inhibiting growth or preventing re-growth of a tumour. CC the packaging cell line is useful for generating alphavirus replicon comparticles without contamination from replicon-competent virus. The packaging cell line is useful for generating alphavirus replicon compatities b virus, hepatitis C virus, human immunodeficiency virus, hepatitis B virus, hepatitis C virus, human immunodeficiency virus, as malaria, and bacteria that grow intracellular parasites such as malaria, and bacteria that grow intracellularly such as mycobacteria conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-740856/80.
N-PSDB; ABV73162.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 20; 93pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid molecule encoding an antigenic fusion polypeptide useful as vaccines for enhancing or inducing immune responses, primarily cytotoxic T lymphocytes (CTL) responses to specific antigens such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus
                                                                  chimeric fusion; translocation;
                                                                                                    HPV-16 E7 protein SEQ ID NO:7.
                                                                                                                                                                                                       ADE21865 standard; protein; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2001; 2001US-0276854P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18-MAR-2002; 2002WO-US008033
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                                                                                                                                        29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                  therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or viral antigens.
                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                              CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ
                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                        (first entry
                                                    cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOPKINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     96.7%;
96.9%;
                                                       tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                   °;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 500; DB 5; Pred. No. 7.6e-56;
                                                    n; antigenic; cytostatic; HPV-16; E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 99
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                      immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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Human papillomavirus

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RESULT 99
ADO05276
ID ADO05
XX
AC ADO05
XX
AC ADO05
XX
DT 29-JU
DT 29-JU
XX
XX
MX
Trans
KW Trans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CC having at least one antigenic peptide. Also described: (1) an expression CC vector comprising (I) operatively linked to a promoter and optionally, to CC one or more regulatory elements that enhance expression of the nucleic CC acid in a cell; (2) a particle comprising (I) or the expression vector; (3) a cell that has been modified to comprise (I) or the expression vector; (2) a cincent polypeptide comprising a first domain with a CC translocation polypeptide; and a second domain comprising an antigen CC capable of inducing or enhancing an antigen specific immune response, CC comprising (I), expression vector, particle, cell, cell of the particle, CC or the chimeric polypeptide; and a carrier or excipient; (6) inducing or enhancing an antigen specific immune response, CC comprising an antigen specific immune response, CC or the chimeric polypeptide; and a carrier or excipient; (6) inducing or CC enhancing an antigen specific immune response by administering the CC composition described above; (7) increasing the number of CDS + CTLs composition described above; and (8) inhibiting the growth of a tumour in CC a subject by administering the composition described above; and subject by administering the CC cytostatic activity, and can be used in immunotherapy, and gene therapy. The present sequence represents HPV-16 E7, which is used in the CC exemplification of the present sequence represents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
major histocompatibility complex; MHC class I; vaccine; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes a nucleic acid (I) encoding a chimer: fusion or fusion polypeptide comprising a first domain with a translocation polypeptide, and a second domain comprising an antigen having at least one antigenic peptide. Also described: (1) an express
                   Translocation domain;
                                                         Human papillomavirus type 16 E7 protein.
                                                                                                     29-JUL-2004
                                                                                                                                                                               ADO05276 standard; protein; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid encoding a chimeric fusion or fusion polypeptide comprising a first domain with a translocation polypeptide, and a second domain with an antigen having at least one antigenic peptide, useful for treating cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-APR-2003; 2003WO-US010235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
                                                                                                                                                                                                                                                                                                                                                                                            WHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                   (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96.7%;
96.9%;
                bacterial toxin; exotoxin A domain II; ETA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 500; DB 7;
Pred. No. 7.6e-56;
0; Mismatches 3
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RESULT 100
ADU66377
ID ADU663
AC ADU663
AC ADU663
XX
DT 10-FEB
XX
DE Human
XX
Vaccin
KW vaccin
KW vaccin
KW vaccin
KW E7 pro
XX
PN WO2004
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                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to nucleic acid encoding a chimeric polypeptide comprising a translocation domain of a bacterial toxin and at least one antigenic peptide. The preferred translocation domain is domain II of Pseudomonas aeruginosa exotoxin A (ETA(dII)) and the preferred antigen is human papilloma virus type 16 (HPV-16) E7 which is a model tumour antigen. The antigenic peptide comprises an epitope that binds to and is presented on the cell surface by major histocompatibility complex (MHC) class I proteins. The nucleic acid of the invention is useful as vaccine composition for enhancing antigen specific immune response, increasing the number of CD8+ cytotoxic T lymphocytes (CTLs) and for inhibiting the growth of a tumour. The present sequence is HPV-16 E7 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-OCT-1999;
09-FEB-2000;
20-OCT-2000;
04-APR-2001;
                                                                                                                              10-FEB-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (WUTT/)
                             Human papillomavirus type 16
                                                         vaccine; MHC class I pathway;
E7 protein; E6 protein.
                                                                                                                                                          ADU66377;
                                                                                                                                                                                     ADU66377 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; SEQ ID NO 7; 48pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel chimeric polypeptide e.g., Pseudomonas aeruginosa exotoxin A domain II/human papilloma virus-16 E7 peptide useful for inducing or enhancing antigen specific immune response, or for inhibiting growth of tumor in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-356187/33.
N-PSDB; ADO05275.
                                                                                                Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-APR-2002; 2002US-00115440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD8+ cytotoxic T lymphocyte; CTL;
                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                         61
                                                                                                                                                                                                                                                                                   61
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                                                                                                                                                                                                                                                                                                                                                                      Similarity
93; Conserv
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                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ
                                                                                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ 96
                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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2000WO-US041422.
2001US-0281003P.
                                                                                                                              (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99US-00421608
                                                                                                                                                                                    protein; 99
                                                                                                                                                                                                                                                                                                                                                                                   96.7%;
96.9%;
                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                   Score 500;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                   (HPV16)
                                                                      antigen
                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tumour;
                                                                                                E7 protein - SEQ
                                                                       specific
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••
                                                                       immune response; tumor;
                                                                                                                                                                                                                                                                                                                                                                                                Length 99;
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Best Local S
Matches 93
                                                                                                                                                                                                                                                                                                                         The invention comprises a nucleic acid molecule (DNA vaccine) that encodes a fusion polypeptide which is useful as a vaccine composition. The nucleic acid of the invention contains: a first nucleic acid encoding a polypeptide that promotes processing via the MHC class I pathway; a second sequence encoding a signal peptide; and a third sequence encoding an antigenic polypeptide. The DNA vaccine of the invention is useful for inducing or enhancing an antigen specific immune response, or to inhibit growth or prevent re-growth of a tumor expressing Human papillomavirus (HPV) E7 or E6 protein. The present amino acid sequence represents a human papillomavirus type 16 (HPV16) E7 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid molecules encoding a fusion polypeptide comprising an antigen, a signal peptide, and a heat shock protein, useful as a vaccine for inducing or enhancing immune response or for inhibiting or preventing tumor growth.
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                                                                                                                                                                                                                                                                                             Sequence 99 AA;
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N-PSDB; ADU66361.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; SEQ ID NO 2; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-2003; 2003US-0467602P.
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                                                                        61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ 96
                                                                                                                                                                    1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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93; Conservat
                                                                                                                                                   MHGDTPTLHBYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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ilarity 96.9%;
Conservative
                        2006, 05:10:00
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Maximum Match 100%
Listing first 100
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 GenCore version (c) 1993 - 2006
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| S-08-860-165-10
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| S-09-485-885-10
| S-09-485-885-10
| S-09-485-885-14
| S-09-485-885-14
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3-980-523A-2
3-763-616-1
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US-10-980-523A-4
US-09-980-523A-1
US-09-913-204-1
US-09-913-204-1
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US-08-934-915-163
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US-08-934-915-163
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US-09-941-528B-46524
US-09-941-528B-46524
US-09-941-528B-46526
US-09-941-528B-4652
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244, Appl
466, Appl
17, Appl
167, Appl
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US-09-980-523A-2

Sequence 2. Application US/09980523A

: Patent No. 6783763

; GENERAL INFORMATION:
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                                                                    RESULT 2
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Patent No. 5679509
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                  Matches 149;
                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,239B
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: Jagtiani, Ajay A.
REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UNME-0001
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (703) 817-9453
TELEPAX: (703) 803-9387
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Wheeler, Cosette M. APPLICANT: Parmenter, Cheryl A. TITLE OF INVENTION: Methods and TITLE OF INVENTION: Distinguishi TITLE OF INVENTION: Cervical Can NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COPPRAFING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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CITY: Centreville
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: not relevant
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STREET: 6126 Rocky Way Court
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                                                                                                                                                  KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                         KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 158
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Distinguishing a Subset of HPV that is Associated with an
Increased Risk of Developing Cervical Dysplasia and
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Pred. No. 8.2e-86;
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RESULT 3
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                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/763,616
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: PCT/AU99/00724
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: AU PQ1645/99
PRIOR FILING DATE: 1999-07-15
PRIOR APPLICATION NUMBER: AU PP5733/98
PRIOR PILING DATE: 1998-09-04
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                    SEQ ID NO 1
LENGTH: 158
TYPE: PRT
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APPLICANT:
APPLICANT:
                                                              Query Match
Best Local Similarity
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TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE IR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
                                             Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BERNARD, HANS-ULRICH APPLICANT: TAN, YEE JOO APPLICANT: TING, ANTHONY EUGENI
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: TING, ANTHONY EUGENE
APPLICANT: SIM, MUI MUI
TITLE OF INVENTION: THERAPBUTIC COMPOUNDS AND METHODS
FILE REFERENCE: BERN3001/JDB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver.
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                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 158
TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/09763616
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Pred. No. 1.7e-85;
1; Mismatches 2
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                                           Score 823; DB 3;
Pred. No. 1.7e-85;
1; Mismatches 2;
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                                                                                    Length 158;
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US-08-316-239B-3
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                                                                                                                                                                                                                        Matches 148;
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Best Local Similarity
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Patent No. 5679509
                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPAX: (703) 803-9387 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20120-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RANGE JOSTANIA AJAY A.

REGISTRATION NUMBER: 35,205
REFERENCE/DOCKET NUMBER: UN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 817-9453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wheeler, Cosette M.
APPLICANT: Parmenter, Cheryl A.
APPLICANT: Parmenter, Cheryl A.
TITLE OF INVENTION: Methods and a Diagnostic Aid for
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and
TITLE OF INVENTION: Cervical Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/316,239B FILLNG DATE: 30-SEP-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 162 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
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128
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                                 KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                     MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                        AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                                                                                                                             MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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6126 Rocky Way Court
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98.0%;
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CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOPTWARE: PATENTIN NOS: 27
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US-09-359-382-10
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US-08-860-165-10
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SEQ ID NO 10
LENGTH: 266
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/09359382 Patent No. 6306397
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APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: REAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
                                           LENGTH: 26
TYPE: PRT
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EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
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CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
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                   ORGANISM: Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
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mes 148; Conserv
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Pred. No. 3.2e-85;
1; Mismatches 2;
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APPLICANT: MALLIAROS, JIM
APPLICATION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 01727/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
PRIOR APPLICATION NUMBER: PCT/AU98/00080
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Pacentin Ver. 2.1
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US-09-367-309A-1
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US-09-485-885-4
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                                                                                                                                                                                                                   Sequence 4, Application US/09485885
Patent No. 6342224
                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -09-367-309A-1
            CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
                                                                                                                               AppLICANT: Bruck, Claudine
AppLICANT: Cabezon Silva, T
AppLICANT: Delisse, Anne-Ma
AppLICANT: Gerard, Catherin
                                                                                               APPLICANT: Lombardo
                                                                                 FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 266
TYPE: PRT
ORGANISM: Human papillomavirus type 16
PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                           KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                         AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKFLCDLLIRCINCQKFLCFEEKQRHLD 127
                                                                                                                                                                                                                                                                                                                                                                                                               AVXDKCLKPYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 158
                                                                                                               Lombardo-Bencheikh, Angela
                                                                                                                               Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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Conservative
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                                                                                   B45107
                                                                                              Vaccine
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 GB 9717953.5
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1; Mismatches
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Pred. No. 3.2e-85;
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2;
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SOFTWARE: FASTSE
SEQ ID NO 10
LENGTH: 292
TYPE: PRT
ORGANISM: Homo 8
US-09-485-885-10
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows V
SEQ ID NO 4
ENGTH: 273
TYPE: PRT
ORGANISM: Homo sapien
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US-09-485-885-10
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                                                                                                                                                                                           Matches 148;
                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE:
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                                                                                                                          KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                             AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                                           AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
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Pred. No. 3.3e-85;
                                                                                                                                                                                           Score 823; DB 2; Length 29; Pred. No. 3.6e-85; Indels 1; Mismatches 2; Indels
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   283
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US-09-485-885-6 ; Sequence 6, Application US/09485885 ; Patent No. 6342224

GENERAL INFORMATION:

Bruck, Claudine

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; ORGANISM: Homo sapien
US-09-485-885-6
                                                                                                                                                        US-09-485-885-14
                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: GB 9717953.:
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOPTWARE: FastSEQ for Windows Version
SEQ ID NO 14
                                                                                                Query Match
Best Local
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Patent No. 6342224
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
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APPLICANT:
APPLICANT:
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Best Local Similarity
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CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
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CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT EILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
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APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 19
NUMBER OF SEQ ID NOS:
                                                                                                                                                                    LENGTH: 390
TYPE: PRT
ORGANISM: Homo sapien
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                                                                                              Similarity
MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                                                                                              99.2%;
98.0%;
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Pred. No. 4.8e-85;
1; Mismatches 2
                                                                           Score 823; DB 2;
Pred. No. 5.1e-85;
1; Mismatches 2
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                                                                                                              Length 390,
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APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
TITLE OF INVENTION: POLYPEPTIDES FROM CEBS BINDING PRO
TITLE OF INVENTION: PRANSCRIPTIONAL REGULATION
FILE REFERENCE: N73477C GCW
CURRENT APPLICATION NUMBER: US/09/701,080C
CURRENT APPLICATION NUMBER: GB 9811303.8
PRIOR APPLICATION NUMBER: GB 9811303.8
PRIOR FILING DATE: 1998-05-26
PRIOR PPLICATION NUMBER: GB 9900157.0
PRIOR PPLICATION NUMBER: GB 9900157.0
PRIOR PILING DATE: 1999-01-05
PRIOR PILING DATE: 1999-01-05
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US-09-462-993-1
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US-09-701-080C-18
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; LENGTH: 151
; TYPE: PRT
                                                                SOFTWARE:
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1,
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                                                                                                                                                                                                                                                                                                                                                                                                            Patent No. 6884786
                                                                                                                                                                TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNO
TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
FILE REFERENCE: 017753-122
CURRENT APPLICATION NUMBER: US/09/462,993
CURRENT FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR FILING DATE: 1998-07-17
                                                                                                        PRIOR APPLICATION NUMBER: FR 97/09152
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 23
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ORGANISM: Artificial Sequence
                      TYPE: PRT
                                              LENGTH:
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147; Conser
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                                                                                    PatentIn Ver. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/09462993
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                                                                                                                                                                                                                                                                                                                                            BALLOUL,
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                                                                                                                                                                                                                                                                                                                        BIZOUARNE, Nadine
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ilarity 97.4%;
Conservative
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Pred. No. 6.1e-85;
1; Mismatches 3
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
ITILE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
INUMBER OF SEG ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEG ID NO 12
LENGTH: 172
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US-09-359-382-12
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Sequence 12, Application US/09359382
Patent No. 6306397
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
APPLICANT: FR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 172
TYPE: PRT
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96.8%;
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Pred. No. 2.5e-80;
1; Mismatches 2;
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Pred. No. 5.7e-51;
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
ITITE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
INUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 14
LENGTH: 172
TYPE: DET
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CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                        , OTHER INFORMATION: Description of Artificial Sequence: Gene Pusion US-08-860-165-14
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US-08-860-165-14
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LENGTH: 172
TYPE: PRT
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Patent No. 6004557
GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                  TYPE: PRT
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nes 92; Conserv
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61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYN 93
|| |||||||||||||||||||||
137 AVCDKCLKFYSKISEYRHYCYSLYGTTLRSHHH 169
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                                                                                                                                                                     Similarity
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                                                                                                                                                                  57.6%;
92.5%;
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96.8%;
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Pred. No. 5.7e-51;
L; Mismatches 2
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Pred. No. 2.6e-46;
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RESULT 17 US-09-359-382-14

Sequence 14, Applion Patent No. 6306397

Application US/09359382

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US-08-117-083-10
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                                                                                                                                                                      COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT ****
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/08117083 Patent No. 5719054
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SEQ ID NO 14
LENGTH: 172
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-09-359-382-14
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CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION UMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
            TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-58
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1994-12-20 NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 017227/0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: EDWARDS, Stirlin APPLICANT: COX, John Cooper
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                      TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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                                                      415-398-3249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Boursnell, Michael
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92.5%;
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Pred. No. 2.6e-46;
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; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-247-904B-10
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Query Match 54.9%; Sometime 56.1%; Pure Matches 87; Conservative 21;
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                                                                                                                                                                              TELEFAX: (617) 832-7000 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
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                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: DEM PC COMPATIBLE
COMPUTER: ASCII(text)
CURRENT APPLICATION DATA:
                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
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TOPOLOGY: lin
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TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
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                                                                                                                         LENGTH: 158 amino acids
TYPE: amino acid
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OTHER INFORMATION:
OTHER INFORMATION:
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the open reading frame."
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Pred. No. 3.6e-46;
5; Mismatches 8;
 Score 455.5; DB 1;
Pred. No. 8.2e-44;
11; Mismatches 42;
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RESULT 20
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; MOLECULE TYPE:
US-08-767-942A-19
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Best Local S
Matches 87
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                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Rolfe, Mark
APPLICANT: Chiu, M. Isabel
APPLICANT: Chiu, W. Isabel
APPLICANT: Berlin, Vivian
APPLICANT: Damagnez, Veronique
APPLICANT: Draetta, Giulio
APPLICANT: Guillaume, Cottarel
TITLE OF INVENTION: UBIQUITIN CONJUGATING ENZYMES
NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/767,942A
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-029.04
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 17-DEC-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 617-832-1000
TELEFAX: 617-832-7000
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                               122 KORFHNIRGRWTGRCMSCCRSSR-----TRRETQL 151
124
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87; Conserv
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KRRPHNIAGHYRGQCHSCCNRARQERLQRRRETOV 158
                                                                                                                                                                                                                                                                                                                                     158 amino acids
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                                                                                                                                                                                                                 54.9%; Score 455.5; DB 2
56.1%; Pred. No. 8.2e-44;
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                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                    DB 2;
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RESULT 21
US-08-117-083-14
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Patent No. 5
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                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 415-398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins NUMBER OF SEQUENCES: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Boursnell, Michael E. APPLICANT: Inglis, Stephen C. APPLICANT: Munro, Alan J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
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NAME: Dreger, Walter H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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LENGTH: 271 amino acids
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TELEPHONE: 415-398-3249
                                                                                                                                                                                                                                                                                          LOCATION: 1..271
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                              NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94111
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                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
   125
                          122 KORFHNIRGRWTGRCMSCCRSSR-----TRRETQL 151
                                                                    65 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKDLNPAEKLHLNE 124
                                                                                       62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLDK 121
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5719054
                                                                                                                                      5 FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                    2 FODPOERPRKLPOLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
KRRFHNIAGHYRGOCHSCCNRAROERLORRRETOV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Walter H. Dreger
4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .unbeR: US/08/117,083
10-SEP-1993
N: /77
                                                                                                                                                                                                                                                                                                                                                                               protein
                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                            54.9%; Score 455.5; DB : 56.1%; Pred. No. 1.6e-43;
                                                                                                                                                                                                                                                                                              /note= "Xaa refers to stop codon
the open reading frame."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14:
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                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                               DB 1;
                                                                                                                                                                                                                                               Length 271;
                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                 Gaps
                                                                                                                                               64
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US-09-485-885-21

Sequence 21, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine

Cabezon Silva, Teresa

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                                                                                                                                                                                                    ; SOPTWARE: FastSEQ for FastSEQ ID NO 23; LENGTH: 383; TYPE: PRT; ORGANISM: Homo Bapien US-09-485-885-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-485-885-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 278
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Fas
SOFTWARE: Fas
; SEQ ID NO 21
FONCTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, App. No. 634227
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cabezon APPLICANT: Delisse, APPLICANT: Gerard, APPLICANT: Gerard, APPLICANT: Lombardo TITLE OF INVENTION: FILE REFERENCE: B45:
                                                                                                                               Matches
                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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CURRENT FILING DATE: 2000-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lombardo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                  Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
ANT: Bruck, Claudine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            175 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                       115 FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87;
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                                                                                                                             87; Conservative
                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                               FastSEQ for Windows Version 3.0
VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                            FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FastSEQ for Windows Version 3.0
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lombardo-Bencheikh, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09485885
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Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
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1998-08-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vaccine
                                                                                                                           54.9%; Score 455.5; DB 2; 56.1%; Pred. No. 2.4e-43; tive 21; Mismatches 42;
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                                                                                                                                                                Length 383;
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US-09-000-094-20
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                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                  Best Local
                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 672
TELEPAX: (202) 672-5
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: WEBB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     175 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE 234
132 WTGRCMSC 139
                                     73 KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                             72
                                                                                                                  13 IDOLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG 72
                                                                                                                                                      12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                                                                                                                                                               Similarity
51; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: WO PCT/AU96/00473 
*FILING DATE: 26-JUL-1996
                                                            KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BENT, Stephen A REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 20007-5109
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WILLIAMS, Mark Philip
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                                                                                                                                                                                           36.6%; Score 304; DB 2;
39.8%; Pred. No. 3.4e-26;
tive 29; Mismatches 48
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                                                                                                                                                                                                 48;
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133 WKGRCLHC 140

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US-10-011-749-20
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                                                                                                                                                                                                   Query Match
Best Local Similarity
Thes 51; Conser
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Patent No. 6726912
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIA Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
OFFICE OF THE PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: WEBB, Elizabeth Ann
132 WTGRCMSC 139
                                                       73
                                                                                72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                     13 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                        12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                           KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202)
                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 368 amino acids
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                                                                                                                                                                                                                   Conservative
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COX, John Cooper
                                                                                                                                                                                                                 36.6%; Score 304; DB 2;
39.8%; Pred. No. 3.4e-26;
ative 29; Mismatches 48
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TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-000-094-22
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US-09-000-094-22
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Patent No. 6365160
GENERAL INFORMATION:
                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 375 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
APPLICATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 017227/0137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133
133 WKGRCLHC 140
                                  132 WIGRCMSC 139
                                                                         73 KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                     13 IDQLCKTPNLSMHTLQINCVFCKNALTTABIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                          12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                                                                                                                                                                                                   51;
                                                                                                              72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (20
TELEFAX: (202)
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                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MARGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
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                                                                                                                                                                                                                                                      36.6%;
                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                      Score 304; DB 2; Length 375; Pred. No. 3.5e-26;
                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Version #1.30
                                                                                                                                                                                                                                       48;
                                                                                                                                                                                                                                       Indels
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US-09-000-094-24

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RESULT 27
US-10-011-749-22
; Sequence 22, Applicatio
; Patent No. 6726912
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 22: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: ADDATE: 27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
133
                                         132 WTGRCMSC 139
                                                                                                                                                                                    13 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                           73
                                                                                                                                72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS 71
WKGRCLHC 140
                                                                                        KINQYRHFDYAGYATTVEEETKODILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 375 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/10011749
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WILLIAMS, Mark Philip
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RESULT 28

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US-10-011-749-24

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; Sequence 24, Application US/10011749

; Patent No. 6726912
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEPHONE: (202) 672-5399
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 24, Application US/09000094
Patent No. 6365160
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 51; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 465 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                                                                        133
                                                                                                                                                                                   132 WIGRCMSC 139
                                                                                                                                                                                                                              73
                                                                                                                                                                                                                                                                      72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                                    13 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                                                                                                                                                                                                 12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                                                                                                        WKGRCLHC 140
                                                                                                                                                                                                                              KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/000,094 FILING DATE: 21-Apr-1998 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: WO PCT/AU96/00473 FILING DATE: 26-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                              36.6%; Score 304; DB 2;
39.8%; Pred. No. 4.5e-26;
ative 29; Mismatches 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Elizabeth Ann
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                                                                                                                                                                                                                                                                                                                                                                                                                   48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 465;
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RESULT 30

US-09-000-094-46

; Sequence 46, Application US/09000094

; Patent No. 6365160

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 672-53
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PETENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: WEBB
                                                                                                                                          133
                                                                                                                                                                                132 WTGRCMSC 139
                                                                                                                                                                                                                      73 KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                                                                                                                                                                      13 IDÓLCKTFNLSMHTLQINCVFCKNALTTAEIÝSYAYKHLKVLFRGGYPÝAACACCLEFHG
                                                                                                                                                                                                                                                                                                                                           12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS
                                                                                                                                                                                                                                                            72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR
                                                                                                                                                                                                                                                                                                                                                                                   51;
                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                          WKGRCLHC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 465 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 20007-5109
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TELEFAX: (202) 672-5399
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MARGETTS, Mary Brigid
COX, John Cooper
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                                                                                                                                                                                                                                                                                                                                                                                   36.6%; Score 304; DB 2;
39.8%; Pred. No. 4.5e-26;
tive 29; Mismatches 48
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TOPOLOGY: Innear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-000-094-46
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                                                                                                                             RESULT 31
US-10-011-749-46
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Sequence 46, Application US/10011749
Patent No. 6726912
GENERAL INFORMATION:
APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 39.89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (202) 672-5300
TELEPAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
NUMBER: AUTORNATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PRECENTIN Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 29,7
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EDWARDS, Stirling John TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: WEBB, Elizabeth Ann
MARGETTS, Mary Brigid
COX, John Cooper
FRAZER, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
                                                                                                                                                                                                                                                                                                                                                                                699 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                                                819 WKGRCLHC 826
                                                                                                                                                                                                                                                       132 WTGRCMSC 139
                                                                                                                                                                                                                                                                                                759 KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 818
                                                                                                                                                                                                                                                                                                                            72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                       12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MCMILLAN, Nigel Alan John WILLIAMS, Mark Philip
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLONEY, Margaret Bridget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    36.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 304; DB 2; Length 1587;
Pred. No. 2e-25;
19; Mismatches 48; Indels
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TOPOLOGY: linear

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
US-10-011-749-46
                                                                                                                                                           RESULT 32
US-08-363-586-4
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                                                                                                              Sequence 4, Application US/08363586 Patent No. 5629161
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Best Local Similarity
                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202) 672-5:
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
APPLICANT: Mueller, Martin APPLICANT: Gissmann, Lutz TITLE OF INVENTION: Use of TITLE OF INVENTION: Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORWATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/10/011,749
PILING DATE: 11-Dec-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                 132 WTGRCMSC 139
                                                                                                                                                                                                                                                                                                                                              759
                                                                                                                                                                                                                                                                                                                                                                                                                                       699 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG
                                                                                                                                                                                                                                                                                                                                                                                       72 KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Conservative
                                                                                                                                                                                                                                                                                                                                              KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                      WKGRCLHC 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAZER, Ian
, Lutz
Use of HPV-16 E6 and E7-Gene Derived
Peptides for the Diagnostic Purpose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36.6%; Score 304; DB 2; Length 1587; 39.8%; Pred. No. 2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48; Indels
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US-09-980-523A-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 19.6%; Score 163; DB 1; Best Local Similarity 100.0%; Pred. No. 1.7e-11; Matches 30; Conservative 0; Mismatches 0;
                                                                                                                NUMBER OF SEQ ID NOS: 2. SOFTWARE: PatentIn Ver. SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 4, Application US/09980523A
Patent No. 6783763
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,586
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 07/909,296

FILING DATE: 09-JUL-1992

APPLICATION NUMBER: EP 91111720.8

FILING DATE: 13-JUL-1991

ATTORNEY/AGENT INFORMATION:

NAME: Wadler, Linda A.

REGISTRATION NUMBER: 33,218

REGISTRATION NUMBER: 33,218
                                                                                                                                                                                                                                 TITLE OF INVENTION: POLYEDITOPIC PROTEIN FRAGMENTS OF THE E6 AND TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR TITLE OF INVENTION: PARTICULARLY IN VACCINATION

FILE REFERENCE: WOB1 A0 INS

CURRENT APPLICATION NUMBER: US/09/980,523A

CURRENT FILING DATE: 2002-04-29

PRIOR APPLICATION NUMBER: PRIOR OF THE CATE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: CHOPPIN, APPLICANT: BOURGAU
LENGTH: 30
TYPE: PRT
ORGANISM: Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MEODEGERERKLEOLCTELOTTIHDILLEC 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : CHOPPIN, JEANNINE
: BOURGAULT VILLADA, ISI
: GUILLET, JEAN-GERARD
CONNAN, FRANCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FERRIES,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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APPLICANT: GISSMAN. Lutz
APPLICANT: MULLER, Martin
APPLICANT: MULLER, Herman
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR
TITLE OF INVENTION: CHIMERIC CAPSOMERS FROM BPV
FILE REFERENCE: 035280134PCUS00
CURRENT APPLICATION NUMBER: US/09/913,204
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: DET/DE00/00426
PRIOR FILING DATE: 2000-02-10
PRIOR FILING DATE: 2000-02-11
PRIOR PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR FILING DATE: 2000-05-31
PRIOR FILING DATE: 2000-05-97
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEO ID NOS: 24
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
SEQ ID NO 8
SEQ ID NO 8
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US-09-913-204-17
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US-09-913-204-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Appli
Patent No. 6953579
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                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-CERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: WOB1 AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
CURRENT FILING DATE: 2002-04-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Human Papillomavirus
                   ORGANISM: Bovine papilloma virus
                                        TYPE: PRT
                                                             LENGTH: 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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    Application US/09980523A
    6783763

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 19.2%; Score 159; DB 2;
Similarity 96.6%; Pred. No. 4.6e-11;
28; Conservative 1; Mismatches 0
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100.0%; Pred. No. 1.7e-11;
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GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: CONNAN, FRANCINE

FITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

TITLE OF INVENTION: PARTICULARLY IN VACCINATION

FILE REFERENCE: WOB1 AO INS

CURRENT APPLICATION NUMBER: US/09/980,523A

CURRENT FILING DATE: 2002-04-29

PRIOR APPLICATION NUMBER: CT/FR00/01513

PRIOR APPLICATION NUMBER: FCT/FR00/01513

PRIOR APPLICATION NUMBER: FCT/FR00/01513

PRIOR APPLICATION NUMBER: FCT/FR00/01513

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin Ver: 2.1
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US-09-980-523A-10
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Best Local Similarity
Matches 22; Conserva
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SEQ ID NO 10
LENGTH: 22
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 276
                                                                 APPLICANT: LOING, ESTÉLLE
APPLICANT: VERWAERDE, CLAUDIE
APPLICANT: GUILLET, JEAN GERARD
TITLE OF INVENTION: LIFOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
FILTE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: USB-97-AU-IN
CURRENT APPLICATION NUMBER: US/09/601,729
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PS/08/259
PRIOR APPLICATION NUMBER: 98 01439
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-06
                                                                                                                                                                                                                                                                                                                                                               APPLICANT: THIAM, KADER APPLICANT: AURIAULT, C. APPLICANT: GRAS-MASSE,
                                             NUMBER OF SEQ ID NOS: 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Human Papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CPEEKQRHLDKKQRFHNIRGRW 22
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                                                                                                                                                                                                                                                                                                                                                                 AURIAULT, CLAUDE
GRAS-MASSE, HELENE
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GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

APPLICANT: BOURGAULT VILLADA, ISABELLE

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: GUILLET, JEAN-GERARD

APPLICANT: FERRIES, ESTELLE

ITILE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

ITILE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

ITILE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

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ITILE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

ITILE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE

           GENERAL INFORMATION:

APPLICANT: DILLMER, LENA
APPLICANT: DILLMER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOWAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESSEE: MASON & ASSOCIATES, P.A.
STREET: 177577 U.S. HWY. 19 NORTH, SUITE 500
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US-08-934-915-167
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Local Similarity 100.0%; Pred. No. 3.1e-07;
108 22; Conservative 0; Mismatchea o.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67, Application US/08934915
5932412
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Similarity 100.0%; Pred. No. 1.1e-07;
23; Conservative 0; Mismatches 0;
CLEARWATER
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US-09-913-204-3
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                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: PCT/DE00/00426
PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
                                                                                                                                                 Query Match 14.3%; Score 119; DB 2
Best Local Similarity 28.9%; Pred. No. 1e-05;
Matches 35; Conservative 16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application Patent No. 6953579
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: GISSMAN. Lutz
APPLICANT: MULLER, Herman
APPLICANT: MULLER, Herman
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR
TITLE OF INVENTION: CHIMERIC CAPSOMERS FROM BPV
FILE REFERENCE: 035280134PCUS00
CURRENT APPLICATION NUMBER: US/09/913,204
CURRENT FILING DATE: 2001-08-10
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                                                                                                                                                                                                                                                      LENGTH: 137
TYPE: PRT
ORGANISM: Bovine papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
TYPE: amino acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          / Match 14.5%; Score 120; DB 1; Local Similarity 100.0%; Pred. No. 8.2e-07; Nes 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             131 RWTGRCMSCCRSSRTRRETQL 151
88 LEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR-WTGRCMSCCR-SSRT 145
                                                                   15 LDCLWCREPLTEVDAFRCMVKDFHVVIREGCRYGACTICLENCLATERRLWQGVPVTGEE 74
                                                                                                           28 LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RWTGRCMSCCRSSRTRRETQL 21
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US-09-913-204-7
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; ORGANISM: Bovine papilloma virus US-09-913-204-13
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PRIOR FILING DATE: 2000-02-10
PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
                                      PRIOR APPLICATION NUMBER: DE 199 05 883.0
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 13
LENCTH: 137
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6953579
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APPLICANT: MULLER, MERTHA
APPLICANT: MULLER, HERMAN
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES
TITLE OF INVENTION: CHIMERIC CAPSOMERS FROM BPV
FILE REFERENCE: 035280134PCUS00
CURRENT APPLICATION NUMBER: US/09/913,204
CURRENT FILING DATE: 2001-08-10
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                                                                                                                                                                               APPLICANT: MULLER, MARTIN
APPLICANT: MULLER, Herman
TITLE OF INVENTION: CHIMERIC VIRUS-LIKE PARTICLES OR
TITLE OF INVENTION: CHIMERIC CAPSONERS FROM BPV
FILE REFERENCE: 035280134PCUS00
CURRENT APPLICATION NUMBER: US/09/913,204
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/DE00/00426
PRIOR FILING DATE: 2000-02-10
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o. 6953579
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                                                                                                            US-08-934-915-166
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Best Local Similarity
Matches 35; Conserva
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                                          Matches
                                                                         Query Match
                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHENG, HWE
TITLE OF INVENTION: S
TITLE OF INVENTION: 1
                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: Windows 3.0 SOFTWARE: Microsoft word 6.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
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APPLICANT:
                                                                                                                           MOLECULE TYPE:
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                                                                                                                                         LENGTH: 21 amino TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 22-SEP-1997
                                                          Local Similarity
                                                                                                                                                                                                                                           TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
115 KQRHLDKKQRFHNIRGRWTGR 135
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o. 5932412
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                                         20;
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                                            Conservative
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                                                        13.9%;
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28.9%; Pred. No. 1e-05;
tive 16; Mismatches
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                                                                                                                                                                                                                                                                                         1946.6
                                                          Score 115; DB 1
Pred. No. 3e-06;
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                                          Mismatches
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                                                                           DB 1; Length 21;
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RESULT 45
US-08-164-768-2
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GENERAL INFORMATION:
                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #10, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,285
FILING DATE: 06-UNU-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                            LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
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APPLICANT: Muller, Martin
TITLE OP INVENTION: Seroreactive Epitopes On Proteins
TITLE OP INVENTION: Human Papillomavirus (HPV)18
NUMBER OF SEQUENCES: 7
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APPLICATION NUMBER: US 0
FILING DATE: 08-MAY-1991
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MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (202)408-4000
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Manspeizer, David A.
REGISTRATION NUMBER: 37,540
REFERENCE/DOCKET NUMBER: 05552.1075-03000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: P 40 15 044.5 FILING DATE: 10-MAY-1990 CLASSIFICATION: 424
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                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                    4 DPQERPRKLPQLCTELQTTIHDIILECVYCK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20005-3315
                                                                                                                                                                             h 13.9%; Score 115; DB 1 Similarity 64.5%; Pred. No. 5e-06;
                                                                            DPTRRPYKLPDLCTELNTSLQDIEITCVYCK 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08466285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Dunner
1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                : (202) 308-4400
(202) 408-4400
Th NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US 07/947,992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 07/696,953
                                                                                                                                                        Mismatches
                                                                                                                                                                                                DB 1; Length 32;
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US-09-601-729-278
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: THIAM, KADER
APPLICANT: AURIAULT, CLAUDE
APPLICANT: GRAS-MASSE, HELENE
APPLICANT: LOING, ESTELLE
APPLICANT: VERWAERDE, CLAUDIE
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 278, App
Patent No. 668305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08164768 Patent No. 6322794
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                                                                               APPLICANT: GUILLET, JEAN GERARD
TITLE OF INVENTION: LIPOPEPTIDES CONTAINING AN INTERFERON FRAGMENT AND USES
TITLE OF INVENTION: THEREOF IN PHARMACEUTICAL COMPOSITIONS
FILE REFERENCE: USB-97-AU-IN
CURRENT APPLICATION NUMBER: US/9/601,729
CURRENT FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: PCT/FR99/00259
PRIOR FILING DATE: 1999-02-05
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 98 01439
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 281
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FORMAN, DAVID S.
REGISTRATION NUMBER: 33,694
REFERENCE/DOCKET NUMBER: 055
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: BLEUL, Conrad
APPLICANT: GISSMANN, Lutz
APPLICANT: MULLER, Martin
TITLE OF INVENTION: SEROREACTIVE EPITOPES
TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1300
CITY: Washington
CTATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT & ADDRESSEE: DUNNER, L.L.P.
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.9%;
l Similarity 64.5%;
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 DPQERPRKLPQLCTELQTTIHDIILECVYCK 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DPTRRPYKLPDLCTELNTSLQDIEITCVYCK 31
                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09601729
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Pred. No. 5e-06;
3; Mismatches
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CURRENT APPLICATION NUMBER: US/10/612,818
CURRENT FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: US 60/394,172
PRIOR FILING DATE: 2002-07-02
PRIOR PPLICATION NUMBER: US 09/828,645
PRIOR APPLICATION NUMBER: US 09/828,645
PRIOR FILING DATE: 2001-04-05
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PACENTIN VETSION 3.1
SEQ ID NO 4
LENGTH: 22
TYPE: DET
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OTHER INFORMATION: peptide
US-09-601-729-278
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US-08-934-915-44
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LENGTH: 20
TYPE: PRT
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Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Impact Diagnostics
APPLICANT: Impact Diagnostics
TITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruse
TITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi
TITLE OF INVENTION: Associated Cancers
FILE REFERENCE: 3352-2-2
                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Derived from the E6 early coding region of HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                            APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMA
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                    NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                STREET:
                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 EKORHLDKKORFHNIRGRWT 133
                                                                                                                                                                                                                                                                                                     44,
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CLEARWATER
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                                                                                                                                                                                                                                                                                                                                                                                                                                             RDGNPYAVXDKCLKFYSKISEY 76
                                                                                                                                                                                                                                                                                                   Application US/08934915
                E: MASON & ASSOCIATES, P.A.
17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13.7%; Score 114; I ilarity 100.0%; Pred. No. 3. Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13.7%; Score 114; DB 2; 95.5%; Pred. No. 4.2e-06;
                                                                                193
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                                                                                                                                                                               OF HUMAN
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RESULT 49
US-08-934-915-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
                                                                                                                                                                       STATE: FLORIDA
COUNTRY: U.S.A.
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOPTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHEFIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
                                                                                                                                    APPLICATION NUMBER: FILING DATE: 22-SEF
                                                                                                                                                                                                                                                                                                                                  STREET: 17757 U.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                     FILING DATE:
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
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                                                                                                                                    22-SEP-1997
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                                                                                                                                                           US/08/934,915
                                                                              07/949,836
37,133
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DB 1; Length 20; Pred. No. 1.4e-05;
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; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 50
US-08-934-915-163
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// MOLECULE TYPE: peptide
US-08-934-915-45
  Query Match 13.1%;
Best Local Similarity 95.0%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 163, Application US/08934915 Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 20 amino acids
                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: MICROSOFT WORD 6.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,
PILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: DILLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PRPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: USEFUL IN HUMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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TELEPAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 17757 U.S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 20 amino TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                   TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 1946.6
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 13.1%; Score 109; DB 1; Local Similarity 100.0%; Pred. No. 1.4e-05; es 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85 GTTLEQQYNKPLCDLLIRCI 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: MASON & ASSOCIATES, P.A.
17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILLNER, JOAKIM
                                                                                                                                                                                                                                                                                                                                                                                          07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US/08/934,915
                                                                                                                                                                                                                                                                                                         37, 133
  Score 109; DB 1; Length 20; Pred. No. 1.4e-05; Indels
                                                                                                                                                                                                                                                                                       1946.6
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Gaps
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RESULT 52
US-08-934-915-165
; Sequence 165, Application US/08934915
""" ant No. 5932412
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                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 164, Application US/08934915 Patent No. 5932412
                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION UNMER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DILLNER, LENA
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEB-MING
APPLICANT: CHENG, HWEB-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USBEUL IN IMMUNASSAY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC comparible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                           TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: FLORIDA
                                                                                                                               INFORMATION
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                   12.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    37, 133
                                                                                                                                                                                                 Score 104; DB 1;
Pred. No. 5.1e-05;
1; Mismatches 0
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                                                                                                                                                                                                                                    Length 20;
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                                                                                                                                                                                                       0
                                                                                                                                                                                                       Gaps
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APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC DEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

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RESULT 53
US-08-934-915-159
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Best Local Similarity
Matches 19; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 159, Application US/08934915 Patent No. 5932412
                                                                                                                                                                       APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARMATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,9:
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: MICCOSOFT WORD 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: DILLNER, JOAKIM APPLICANT: DILLNER, LENA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: CLEARWATER STATE: FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 813-538-3820
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                                                                                                                                                         FLORIDA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.5%; Score 104; DB 1; 95.0%; Pred. No. 5.1e-05; tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07/949,836
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                                                                                                                                                                                                                                                                                                                                                                                 OF HUMAN
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RESULT 54
US-08-934-915-160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                          COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,91

FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: DILLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: peptide
                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                       TELEFAX:
                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             160,
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17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/08934915
                                                         813-538-3820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.8%;
95.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAPILLOMAVIRUS 1, 5, 6, 8, 11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     193
                                                                                                                                                                                                                                                                                    US/08/934,915
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                                                                                                                                37,133
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                     160:
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                                                                                                                  1946.6
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Pred. No. 0.00024
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US-08-934-915-161
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                                                                                                                      ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-934-915-161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: DILLARE,
APPLICANT: DILLARE,
APPLICANT: CHENG, HW
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 161, Application US/08934915 Patent No. 5932412
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Best Local !
                                                                            Query Match
Best Local (
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                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                            NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,13:
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                          y Match 11.7%;
Local Similarity 85.0%;
nes 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 17757 U.S
CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                  TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 11.7%;
Local Similarity 90.0%;
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              REVYDFAFRDLCIVYRDGNP 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DILLNER, JOAKIM
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                                                                                                                                                                                                                                                                                                                                                                                                                       22-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PAPILLOMAVIRUS 1, 5, 6, 8, 11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNTHETIC PEPTIDES OF HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            193
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Pred. No. 0.00031
                                                          Score 97; DB 1; Le
Pred. No. 0.00031;
3; Mismatches 0;
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                                                                                       DB 1; Length 20;
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                                                         Gaps
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RESULT 56

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US-08-466-285-4
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APPLICANT: Grey, Howard
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT PILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 1999-12-10
RUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46524
LENGTH: 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 5753233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, VG
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,285
FILING DATE: 06-UN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
TO TOTATION WITMERED: US 08/164,768
PRIOR APPLICATION DATA:
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APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Bleul, Conrad
APPLICANT: Gissmann, Lutz
APPLICANT: Muller, Martin
TITLE OF INVENTION: Seroreactive Epitopes On Proteins
TITLE OF INVENTION: Human Papillomavirus (HPV)18
NUMBER OF SEQUENCES: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabo
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W., Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 11.3%; Score 94; DB 3; Land Land Land 10.0%; Pred. No. 0.00049; Pred. No. 0.00049; Nes 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1300 I St
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: D.C
FILING DATE: 21-SEP-1992
                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 FHNIRGRWIGRCMSC 139
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                                                                                                                      US 08/164,768
                           US 07/947,992
                                                                                                                                                                                                                  US/08/466,285
                                                                                                                                                                                                                                                                 Version #1.30
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US-08-164-768-4
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                           TELEPHONE: (202) 408-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/164,768
FILING DATE: 10-DEC-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: FORMAN, David S.
REGISTRATION UMBER: 33,694
REFERENCE/DOCKET NUMBER: 05552.1075-02000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: BLEUL, Conrad
APPLICANT: GISSMANN, Lutz
APPLICANT: MULLER, Martin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (202)408-400
TELEFAX: (202)408-4400
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANUEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Manspeizer, David A.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: 055
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE: 10-MAY-1
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SEROREACTIVE EPITOPES ON PROTEINS OF TITLE OF INVENTION: HUMAN PAPILLOMA VIRUS (HPV) 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 08-MAY CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: US
ZIP: 20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FINNEGAN, HENDERSON, FARABOW, GARRETT ADDRESSEE: DUNNER, L.L.P. STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQ 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
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single linear
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                                                                                                                                            (202) 408-4000
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Pred. No. 0.0016;
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US-09-641-528B-46535
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                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 60
US-08-934-915-162
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 162, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46535
LENGTH: 15
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Best Local
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celia, Esteban
APPLICANT: Celia, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REPERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
                                                                                                                                                                                                                APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN INMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                  NUMBER OF SEQUENCES: 193
CORRESPONDENCE ADDRESS:
ADDRESSE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 RGRWTGRCMSCCRSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQ 90
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                                                                                                  FLORIDA
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                                                                                                                                                                                                                                                                                                                                        DILLNER, JOAKIM
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Pred. No. 0.0016;
3; Mismatches
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5. 0.00082;
0;
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RESULT 61
US-08-363-586-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Mueller, N
APPLICANT: Gissmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. FOUTCH
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                              ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                              NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 024
TELECOMMUNICATION INFORMATION:
                                                                                                                 FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/909,296
PILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 91111720.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/363,586 FILING DATE: 23-DEC-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1300 I St
CITY: Washington
TELEPHONE: 202-408-4400
TO TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 813-538-3820
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Dunner
1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 amino acids
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                                 202-408-4000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lutz
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Pred. No. 0.0012;
2; Mismatches
                                                                   02481-1195-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1946.6
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Diagnostic Purpose
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FILE REFERENCE: 2060.0100001

CURRENT APPLICATION NUMBER: US/09/641,528B

CURRENT FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: US 60/172,705

PRIOR FILING DATE: 1999-12-10

NUMBER OF EQ ID NOS: 51505

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 46517

LENGTH: 15

TYPE: PRT
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US-07-909-122-2
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                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: SCHOOLNIK, GARY K.
APPLICANT: PALEFSKY, JOEL M.
TITLE OF INVENTION: DIAGNOSTIC
TITLE OF INVENTION: VIRUS
NUMBER OF SEQUENCES: 17
                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07909122
Patent No. 5415995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Gety, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 Page Mill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acids
                                                        COUNTRY: USA
ZIP: 94304-1018
                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match 10.8%; S. Local Similarity 100.0%; Conservative 0;
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                                                                                                              CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          66 CLKFYSKISEYRHYC 80
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                                                                                           California
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                                                                                                                                                                                                                       DIAGNOSTIC PEPTIDES OF HUMAN PAPILLOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.7%; Score 89; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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0.0018;
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0.0023;
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APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46523
LENGTH: 15
RESULT 65
US-09-641-528B-46525
; Sequence 46525, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
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TELEX: 706141
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 19920706
ATTORNEY/AGENT INFORMATION:
NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 25,952
REGISTRATION UMBER: 25,952
REGISTRATION UMBER: 28600-20105.01
TELEPHONE: (415) 813-5600
TELEPHONE: (415) 8494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 46523, Application US/09641528B Patent No. 7026443
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Best Local (
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear 09-122-2
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                                                                                                                                                                                                                                    10.2%; Score 85; 100.0%; Pred. No.
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                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                      DB 3;
0.0051;
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                                                                                                                                                                                                                     Indels
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APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
FURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46525
LENGTH: 15
TYPE: PRT
OPCONTAGE
                                                                                                                                                                                                                                                                           PATENT PILING DATE: 2000-08-15
PRIOR APPLICANT: Sette, Alessandro
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Sidney, John
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Gelis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: USING PEFTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46526
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; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46525
밁
                                                                                                                                                              ; FEATURE: ; OTHER INFORMATION: Peptide Derived from Human Papillomavirus US-09-641-528B-46526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-641-528B-46526
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Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                 Matches
                                                                                                  Query Match 10.2%;
Best Local Similarity 93.3%;
                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      134 GRCMSCCRSSRTRRE 148
                           78 HYCYSVYGTTLEQQY 92
                                                                                 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GRCMSCCRSSRTRRE 15
HYCYSLYGTTLEQQY
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                                                                                 Conservative
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100.0%; Pred. No. 0.0051;
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                                                                                 1.
                                                                                                  Score 85; DB 3; Length 15; Pred. No. 0.0051;
                                                                                 Mismatches
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RESULT 67 US-09-641-528B-51200 ; Sequence 51200, Application US/09641528B ; Patent No. 7026443

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RESULT 69
US-09-641-528B-46534
; Sequence 46534, Application US/09641528B
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                                                                                                                                                                                                                                                       ; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46519
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TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER: OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51200
LENGTH: 15
                                                                                                                                                                Query Match
Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 5155
SOFTWARE: PASTSEQ for Windows Version 4.0
SEQ ID NO 46519
                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
CURRENT FILING DATE: 2000-08-15
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FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                     44 DFAFRDLCIVYRDGN 58
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Celis, Esteban
Grey, Howard
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                                                                                                                                                                               Conservative
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                                                                                                                                                                                               Score 84; Pred. No.
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                                                                                                                                                                                               DB 3;
0.0067;
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0.0051;
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US-09-641-528B-46522
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
                                                                                                                                                                                                                                                                        APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 46522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: INDICING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46534
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Matches
                                                                              Matches
                                                                                                                     Query Match
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APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
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                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                             LENGTH: 15
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les 15; Conserv
                                                                                                    Local
                                                                                                                                                                                                                                              PRT
                                        29 ECVYCKQQLLRREVY 43
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                                                                                                  Similarity
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Southwood, Scott
Chesnut, Robert
Celis, Esteban
Grey, Howard
ECVYCKOQLLRREVY 15
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                                                                              Conservative
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                                                                                                  100.0%;
                                                                                                  10.0%; Score 83; DB 3; 100.0%; Pred. No. 0.0086;
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Mismatches
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RESULT 71 US-09-641-528B-46527

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; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528B-46527
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APPLICANT: Chesnut, Robert
APPLICANT: Corey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 1999-12-10
RUMBER OF SEQ ID NOS: 5195
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No. 7026443
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46527
                                                                                         Query Match
Best Local :
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                                                                       Matches
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CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS FILE REFERENCE: 2060.0100001
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                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                      FEATURE:
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                                42 VYDFAFRDLCIVYRD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
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                                                                                         Similarity
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Celis, Esteban
Grey, Howard
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                                                                       Conservative
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                                                                                         100.0%;
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                                                                                       Score 83;
Pred. No.
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Pred. No.
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                                                                       Mismatches
                                                                                         DB 3;
0.0086;
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0.0086;
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RESULT 73

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TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50556
LENGTH: 15
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Best Local Similarity 100.
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APPLICANT:
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                                              CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
ANACE ALANCE
ANACE ALANCE
                                                                                                                                                                                                       COUNTRY: USA
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, V
CURRENT APPLICATION UMBER: US/08/075,5411
APPLICATION UMBER: US/08/075,5411
FILING DATE: 10-JUN-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
STREET: 16
                NAME: NADEL, ALAN S REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
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Grey, Howard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08075541D
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1601 MARKET STREET, 36TH FLOOR
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                                    ALAN S
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APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Crey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT PELICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 51199
                                                                                                                                                                                            Sequence 51250, Application US/09641528B Patent No. 7026443
GENERAL INFORMATION:
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Matches
                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
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Best Local
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APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15
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LENGTH: 15 amino acids
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
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15; Conservative
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No.
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0.011;
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0.011;
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US-09-270-767-41452
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GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4152
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PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR, FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FRSESEQ for Windows Version 4.0
SEQ ID NO 51250
LENGTH: 15
                                                                                                                                                                                               Sequence 46518, Application US/09641528B Patent No. 7026443 GENERAL INFORMATION:
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APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Clis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
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Local Similarity 19.6%;
es 33; Conservativo
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                                                                                                                                                                                                                                                                                                                                                  486 GCNRAIMENYISALNSQWHPDCFVCRDCKKAVRGKSFYAMEGKPVCPQ 533
                                                                                                                                                                                                                                                                                                                                                                                                                                 426 AYCNGAILDKCVTALDKTWHTEHFFCAQCGQQFGEEGFHERDGKPYCRNDYFEMFAPKCN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 -----AVXDKCLKFYSKISEYRHY----CYSVYGTT-LEQQYNKPLC------
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Pred. No. 0
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US-09-641-528B-47291
; Sequence 47291, Application US/09641528B
; Patent No. 7026443
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Estaban
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Best Local Similarity 9...
14; Conservative
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Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46520
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APPLICANT:
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TITLE OF INVENTION: USING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060, 0100001
FILE REFERENCE: 2060, 0100001
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR PELING DATE: 1999-12-10
TRIMEDED OF SECULATION SECULATION OF SECULATION NUMBER: US 60/172,705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Peptide Derived from Human -09-641-528B-46518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Sette, Alessandro
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Peptide Derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                  Sidney, John
Southwood, Scott
Chesnut, Robert
Celis, Esteban
Grey, Howard
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Southwood, So
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100.0%; Pred. No. 0.019;
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1; Mismatches
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RESULT 82
US-09-641-528B-46532
; Sequence 46532, Application US/09641528B
n=tent No. 7026443
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Best Local Similarity
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US-09-641-528B-50558
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APPLICANT: Chiesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Crey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
TILE REFERENCE: 2060.0100001
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50558
LENGTH: 15
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LENGTH: 15
                                                                                    GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
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              APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sette, Alessandro APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                   Local
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NT: Chesnut, Robert
NT: Celis, Esteban
NT: Grey, Howard
F INVENTION: INDUCING (
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                                                               Southwood,
                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                   Scott
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Pred. No.
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CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS

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US-09-641-528B-46516
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                                                                                                   Sequence 46528, Application US/09641528B Patent No. 7026443 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46516
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46532
LENGTH: 15
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Best Local Similarity
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APPLICANT: Grey, Howard
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
TILE REFERENCE: 2060.0100001
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
CURRENT FILING DATE: 2000-08-15
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APPLICANT:
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                                                  APPLICANT: Sette, Alessandro APPLICANT: Sidney, John APPLICANT: Southwood, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sette, Alessandro APPLICANT: Sidney, John
                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/172,705 PRIOR FILING DATE: 1999-12-10
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                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from
   APPLICANT:
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10. 7026443
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Grey,
                Chesnut, Robert
Celis, Esteban
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Chesnut, Ro
                                                Southwood, Scott
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                                                                                                                                                                                                                                                                                                          9.4%;
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100.0%; Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                            Human Papillomavirus
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RESULT 86
US-09-270-767-46957
; Sequence 46957, A
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US-09-270-767-31740
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Best Local S
Matches 14
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CURRENT APPLICATION NUMBER: US/09/270,
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 31740
                                                                                                                                                Patent No. 6703491 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 46528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31740,
APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR PILING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH: 165
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                                                                                                                                                                                                                                                                                                                                                                          CTSFHYFPRLNENGKKLLLPCDFCDVNFEFAHDFLAHSEEKHLNKKKREKETRNTGAGRI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                        Application US/09270767
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6366
LENGTH: 572
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US-09-949-016-6366
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RESULT 88
US-09-641-528B-46521
; Sequence 46521, Application US/09641528B
; Patent No. 7026443
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Best Local Similarity
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ORGANISM: Drosophila melanogaster
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                                                                                                                      535 YKC
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                                                                                                                                                                                                                                                                             426 SLEGAPYCEGCYTDTLEKCNTCGEP--ITDRMLRATGK--AYHPHCFTCVVCARPLEGTS
                                                                                                                                                                                                                                      88 -LEQQYNKPLC-----DLLIRCINXQKPLCPE----EKQRHLDKKQRFHNIRGRWTGRC 136
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                                                                                                                                                                                                                                                                                                                    44 DFAFRDLCI-VYRD-----GNPYAVXDKCLKFYSKISEYRHYCYS-----VYGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                ch 9.3%; Score 77.5; l Similarity 22.4%; Pred. No. 2.41; Conservative 21; Mismatche
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                                                                                                                      537
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US-09-641-528B-50557; Sequence 50557, Application US/09641528B; Patent No. 7026443
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                                                                                                                                                     OTHER INFORMATION: Peptide Derived from US-09-641-528B-50557
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                                                                                                                                                                                                                                           TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51505
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 50557
LENGTH: 15
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CURRENT APPLICATION NUMBER: US/09/641,528B

CURRENT FILING DATE: 2000-08-15

PRIOR APPLICATION NUMBER: US 60/172,705

PRIOR PILING DATE: 1999-12-10

NUMBER OF SEO ID NOS: 51505

SOFTWARE: FastSEQ for Windows Version 4.0

SEO ID NO 46521
                                                        Query Match
Best Local Similarity 93.3
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APPLICANT: Sette, Alessandro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 9.3%;
Best Local Similarity 93.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sette, Alessandro APPLICANT: Sidney, John APPLICANT: Southwood, Scott
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Chesnut, Robert APPLICANT: Celis, Esteban APPLICANT: Grey, Howard
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Peptide Derived from Human Papillomavirus
                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                 TYPE: PRT
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                        50 LCIVYRDGNPYAVXD
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Chesnut, Robert
Celis, Esteban
Grey, Howard
LCIVYRDGNPYAVCD
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                                                                                              9.3%;
93.3%;
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Pred. No.
                                                                                              Score 77;
Pred. No.
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RESULT 90 US-09-641-528B-50559 ; Sequence 50559, Application US/09641528B

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TITLE OF INVENTION: No. 6989232el Proteins an
FILE REFERENCE: 21402-099
FILE REFERENCE: 21402-099
CURRENT APPLICATION NUMBER: US/09/939,853A
CURRENT FILING DATE: 2001-08-27
PRIOR APPLICATION NUMBER: 60/228,191
PRIOR APPLICATION NUMBER: 60/267,300
PRIOR PILING DATE: 2001-02-08
PRIOR FILING DATE: 2001-02-08
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US-09-641-528B-50559
                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 159
SOFTWARE: PatentIn Ver. 2
SEQ ID NO 15
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Best Local S
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SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 50559
LENGTH: 15
                                                                                                                                                                                                                       Matches
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Best Local :
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Patent No. 6989232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                         -09-939-853A-15
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APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
APPLICANT: Celis, Esteban
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.010001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/269,961
PRIOR FILING DATE: 2001-02-20
PRIOR APPLICATION NUMBER: 60/277,337
PRIOR FILING DATE: 2001-03-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/172,705 PRIOR FILING DATE: 1999-12-10
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APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                         Local Similarity
                                           366
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133
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                                                                                                                                                                       16 CTELO-TTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK-FYSKI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15;
                                                                                  SEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRW- 132
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-TGRCMSCC 140
                                                                                                                             CTEAEGRTWHMKHFACQECEHOLGGOR-----YIMREGKPY----CLACFDIMF 365
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                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                       9.2%; Score 76.5; D
24.0%; Pred. No. 5.3;
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                                                                                                                                                                                                                12;
                                                                                                                                                                                                                  Mismatches 33;
                                                                                                                                                                                                                                                           DB 2; Length 785;
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                                         ---VDQGQMSHDGQ-HWH 391
                                                                                                                                                                                                                53; Gaps
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RESULT 93
US-09-641-528B-46529
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US-07-909-122-4
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Patent No. 5415995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Patent No. 7026443
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILLING DATE: 2000-08-15
FRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILLING DATE: 1999-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/909,122
FILING DATE: 19920706
CLASSIFICATION: 19920706
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: BENZ, WILLIAM H.
REGISTRATION NUMBER: 25,952
REGISTRATION NUMBER: 2600-2010
TELEPAN: (415) 813-5600
TELEPAN: (415) 813-5600
                                                                                                                                                                                                        APPLICANT: Sette, Alessandro APPLICANT: Sidney, John
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: SCHOOL
APPLICANT: PALEFS
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
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LENGTH: 14 amino acids
TYPE: AMINO ACID
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ADDRESSEE: MORRISON & FOERSTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 9.2%; Score 76;
Local Similarity 100.0%; Pred. No.
nes 14; Conservative 0; Mismatc
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0.05;
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Sequence 16235, Application US/09248796A

Patent NO. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO (
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.132

CURRENT APPLICATION NUMBER: US/09/248,796A

CURRENT PILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/074,725

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

NUMBER OF SEQ ID NOS: 28208
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US-09-641-528B-46531
; Sequence 46531, Application US/09641528B
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                                                                                                                                                                                                                                                                                                   RESULT 95
US-09-248-796A-16235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Celis, Esteban
APPLICANT: Crey, Howard
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528B
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-11-10
NUMBER OF SEQ ID NOS: 51905
SOPTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 46531
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SOFTWARE: FRANCSEQ for Windows Version 4.0
SEQ ID NO 46529
LENGTH: 15
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GENERAL INFORMATION:
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Best Local Similarity
Matches 15; Conserv
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Best Local S
SEQ ID NO 16235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Peptide Derived from Human Papillomavirus
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Southwood, Scott
Chesnut, Robert
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100.0%; Pred. No.
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Pred. No. 0.054;
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0.054;
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US-09-949-016-8090
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Human
US-09-949-016-8090
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Celis, Esteban
APPLICANT: Gery, Howard
TITLE OF INVENTION: USING PEP
                                                                                                                                                                                                                                            RESULT 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8090
LENGTH: 250
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APPLICANT: VENTER, J.
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Best Local Similarity 22.9%;
Matches 33; Conservative
                                                                                                                                                                 GENERAL INFORMATION:
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Best Local
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 187
TYPE: PRT
ORGANISM: Candida albicans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           140 -----QKHWYNVYIWSKDRFHHI 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 RDGNPYAVXDKCLKFYS-KISEYRH----YCYSVYGTTLEQQYNKPLCDLLIRCINXQKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                         40 REVYDFAFRDLCIVYRDGNPYAVXD-----KCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                                                                                        66 GLCDLYPCCLCDYKLYCLRPSLRSLERKAIRAIEDEKRELAKLR-RTTNRILASSCCSSN
                                                                                                                                                                                                                                                                                                                                              26 RCIDEFSTRCLCDLYM--HPYCCCDLHPYPYCL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RLCNHRDTYHHHPYTCHHIFCLCICHGIYCHPCNDHVFACHHIFCHCIYHGTYRHPCICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9.1%;
  NG CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS PEPTIDE AND NUCLEIC ACID COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
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Pred. No. 1.2;
18; Mismatches
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Pred. No. 1.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 250;
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FILE REFERENCE: 2060.0100001

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US-09-186-723-7
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-377-309-7
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US-08-377-309-7
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GENERAL INFORMATION:
APPLICANT: MUIGILA, ROBERT A.
APPLICANT: MUIGILA, ROBERT A.
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN
TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005002
CURRENT APPLICATION NUMBER: US/09/186,723
CURRENT APPLICATION NUMBER: US/09/186,723
CURRENT FILING DATE: 1998-11-05
EARLIER APPLICATION NUMBER: 08/377,309
EARLIER PILING DATE: 1995-01-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 16
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: MUTGITA, ROBERT A.
APPLICANT: MUTGITA, ROBERT A.
TITLE OF INVENTION: RECOMBINANT HUMAN ALPHA-FETOPROTEIN
TITLE OF INVENTION: AN IMMUNOSUPPRESSIVE AGENT
FILE REFERENCE: 06727/005001
CURRENT APPLICATION UNMBER: US/08/377,309A
CURRENT FILING DATE: 1995-01-24
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LENGTH: 15
                                                                                                                                                                                              Sequence 7, Application US/09186723 Patent No. 6288034
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                           112 PNLNRFLGDRDFNQFSSGEKNIFLASFVHEYSRRHPQLAV---SVILRVAKGYQELLEKC
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                                                                                                                                                                                                                                                                                                                          FQTENPLECQDKGEEELQKYIQESQ 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----RDGNPYAVXDKCLKFYSKISEY--RHYCYSVYGTTLEQQYNKFLCDLLIRC 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDGEKIMSYICSQ-QDTLSNKITEC--CKLTTLE-----RGQCIIHAENDEKPEGLS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVY------
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; TYPE: PRT; ORGANISM: Homo sapiens US-09-186-723-7
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US-08-505-012-10
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 7
                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,012
FILING DATE: 21-UU-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/377,317
FILING DATE: 24-UAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06727/007001
TELECHAUS: (617) 542-5070
TELECHAUS: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: EXTITLE OF INVENTION: EXTITLE OF INVENTION: HUINUMBER OF SEQUENCES: 24CCORRESPONDENCE ADDRESS: ADDRESSE: Fish & picture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 9.0%;
Best Local Similarity 23.4%;
Matches 34; Conservative 2
Query Match 9.0%;
Best Local Similarity 23.4%;
Matches 34; Conservative 26
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APPLICANT: Murgit
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 393 amino acids
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MEDIUM TYPE: Floppy disk
                                                                                    MOLECULE TYPE: protein
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                                                                                                                    TYPE: amino acid
STRANDEDNESS: not
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                                                                                                      TOPOLOGY:
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225 Franklin Street, Suite 3100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                         (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 26; Mismatches
                                                                                                        linear
                                                                                                                 not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robert A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EXPRESSION AND PURIFICATION OF CLONED
 26;
 Score 74.5; DI
Pred. No. 3.9;
26; Mismatches
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Pred. No. 3.9;
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   44;
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                                  Length 393;
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   Indels
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Perfect score:
Sequence:
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Maximum
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Maximum
Listing
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  of,
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1: geneseqp198
2: geneseqp199
3: geneseqp200
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Match
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830
1 MFQDPQERPRKLPQLCT
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Gapop 10.0
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196.288 Million cell updates/sec
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   MFQDPQERPRKLPQLCTELQ......WTGRCMSCCRSSRTRRETQL
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  GenCore version 5.1.8 (c) 1993 - 2006 Biocceleration Ltd.
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 ADO44062
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ADO22636
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ADO44072
AAW35742
ADD44066
AAR22766
AAR22766
AAR22766
AAR26363
ABD199812
ABB11990
ABB11990
ABF88853
ABC98863
ABC98863
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ABC988520
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AAW35741
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Ado44062 Amino aci
Ado44064 Amino aci
Aao22636 HPV prote
Aao22636 HPV prote
Aao22636 HPV prote
Ado44072 Amino aci
Aaw35742 Human pap
Ado44060 Amino aci
Adu66364 Human pap
Aar22766 HPV B 6 pe
Aay82462 Human pap
Ado6363 Human pap
Ado6363 Human pap
Ado6363 Human pap
Ado6363 Hruman pap
Ado6363 HPV (onco
Aeb11990 HPV16 E 6
Aec96391 HPV prote
Aec96391 HPV prote
Aec96391 HVMan pap
Aaw35741 Human pap
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ADR47005
AEF40157
AAR27725
            AAR40919
ABD98533
ADF31985
ARB98434
ADO44075
AEA98537
AEA98635
AEC96405
AAB98447
ADO44081
AEC986462
AEA98534
AEC986462
AEA98534
AEC986424
AEC98656
AEA98538
AEC964264
AEA98538
AEC96426
AEA98538
AAR2725385
AAA725385
AAA725385
AAA725385
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AAY2539
AAY02635
AED52642
AAY02633
AED52642
AAY026337
AAD52638
AAY026381
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AAY25376
AAY02632
                                                                                                                                                                                                                                                                                               Aar97561 Human pap
Aay25376 HPV fusio
Aay02632 Prot. D1/3
Aed52634 Fusion pr
Aay25379 HPV fusio
Aay02635 CLVTA-E6-
Aed52642 Fusion pr
Aay25371 HPV fusio
Aay02637 CLVTA-E6E
Aed52646 Fusion pr
Aay25381 HPV fusio
Aay02637 CLVTA-E6E
Aed52646 Fusion pr
Ad044066 Amino aci
Aay9369 Papilloma
Aar40919 PPV E6 re
Ad044077 Amino aci
Aea99853 HPV (onco
Aec98865 HPV 31 En
Aec98865 HPV Jorote
Aab98434 Human pap
Ad044075 Amino aci
Aea98537 HPV [onco
Aec98868 HPV 3] En
Aec98868 HPV 3] En
Aea98536 HPV Jorote
Aec98868 HPV 38 En
Aea98536 HPV Jorote
Aec98868 HPV 38 En
Aea98536 HPV Jorote
Aec98868 HPV 39 En
Aea98536 HPV Jorote
Aec98868 HPV 30 En
Aea98536 HPV Jorote
Aec98868 HPV 30 En
Aea98536 HPV Jorote
Aec98868 HPV 30 En
Aea98536 HPV Jorote
Aec98868 HPV 52 En
Aec98879 HPV [onco
Aec98868 HPV 52 En
Aec98879 HPV [onco
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Adr47005 Human pa
Aef40157 Human pa
Aar27725 HPV 16
Aar277561 Human pa
                                  Aec98864
Aec96398
Aao22924
Aar27728
Aay25385
Aay02641
Aed52653
                                                                                                            Ado44074
Aea98547
Aeb11993
             Aay25386
Aay02642
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Aar79656
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Aec98867
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Ado44079
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Ado44085
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            Human pap
Amino aci
HPV (onco
Amino aci
HPV (onco
Amino aci
HPV 18 E6/
HPV-18 E6
HPV-1
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AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120

AVGDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINGQKPLCPEEKQRHLD 120

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121 61 13 ب

KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151

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CC protein is designated E6E7TetM, and comprises an E6 amino terminus (where residues 63 and 106 have been replaced with glycine) and an E7 carboxy CC terminus (where residues 24 and 26 have been replaced with glycine). CC E6E7TetM is representative of fusion proteins of the invention. The CC specification describes human papillomavirus E6 and E7 polypeptides, CC where the E7 polypeptide has mutations at any one or more of the amino caids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any cone or more of the amino acids corresponding to amino acids corresponding to amino acids corresponding to amino acids of the sequence given in AD044072. The polypeptides of the invention are CC there sequence given in AD044072. The polypeptides of the invention are cancers, such as cervical cancer. The fusion proteins and nucleic acids cancers, such as cervical cancer. The fusion proteins and nucleic acids cancers, the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
RESULT 1
AD044062
ID AD04
XX AD04
XX AD04
XX AD04
XX E6 p
XW E6 p
XW Cery
XW W020
XX Synt
XX W020
PR 03-0
PR 03-0
PR WPI;
PI Smit
XX WPI;
PR Usef
PR WPI;
CC The
CC
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98
99
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of a fusion protein designated E6E7TetM
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Ado44078
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3 Amino aci
6 Human pap
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1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60

Query Match Best Local Similarity Matches 149; Conserv

Conservative

0

Score 828; DB 8; L Pred. No. 4.6e-84; 0; Mismatches 2;

Length 248; Indels

0

Gaps

0

Best Local Similarity

99.8**%;** 98.7**%**;

Score Pred.

828; DB 8; No. 4.6e-84;

Length 248

Query Match

Sequence

248

8

99.8%;

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RESULT 2
AD044664
AID AD044
AX AD04
AD04
AX AD
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                                                             CC polypeptides from human papillomavirus type 16 (HPV16). The fusion CC protein is designated B6E7PentM, and comprises an E6 amino terminus CC (where residues 63 and 106 have been replaced with glycine) and an E7 CC (arboxy terminus (where residues 24, 26 and 91 have been replaced with CC glycine). E6E7PentM is representative of fusion proteins of the CC invention. The specification describes human papillomavirus E6 and E7 CC invention. The specification describes human papillomavirus E6 and E7 CC polypeptides, where the E7 polypeptide has mutations at any one or more CC of the amino acids corresponding to amino acids 24, 26 or 91 of the CC sequence given in AD044073 and the E6 polypeptide has no mutations or has CC mutations at any one or more of the amino acids corresponding to amino CC (HPV)-associated cancers, such as cervical cancer. The polypeptides of CC the invention are useful for treating or preventing human papillomavirus CC (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating commune responses against HPV. They are also useful for treating lower CC gastrointestinal tract cancers, e.g. anal cancer, and other cancers of CC the reproductive system, including penile and vulvar cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence represents a fusion protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                comprising E6 and PV16). The fusion
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Matches Qy Db Db Qy	
dd YO	121 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
RESULT 3	3 0 O22640 standard; protein; 151 AA.
AC AAC	AAO22640;
DT 15-	-2003 (first entry)
DE HPV	HPV-16 protein sequence, SBQ ID No 27.
KW Cytost KW cancer KW HPV; H	Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth; cancer; human papilloma virus; cervix; cell-mediated immune response; HPV-16.
OS Hum	Human papilloma virus.
PN WO2	WO2003008649-A1.
PD 30-	-JAN-2003.
PF 19-	9-JUL-2002; 2002WO-US023198.
PR 20-	20-JUL-2001; 2001US-0306809P.
YX Sas	KJ, Tortolero-
DR WPI	003-2
PT Det	Determining a possible recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV), comprises incubating
PT imm	mple with an HPV E6 of E/ peptide and detecting a cell-median e response.
XX Die	Disclosure; Page 129-130; 132pp; English.
	man papilloma virus (HPV) or suspected of being infected with HPV, and
CC has	s or had a (pre-)cancerous growth on or around the cervix. The novel thod comprises incubating an E6 or E7 peptide of HPV with a sample from
CC the	e patient, and assaying the sample for a cell-mediated immune response ainst the peptide. The method is useful for determining the possibility
CC and	d preventing the recurrence of a (pre-)cancerous growth in a patient ifected with HPV or suspected of being infected with HPV. The HPV E6 or
CC the	E7 peptides are useful in immunotherapy for the preventing or reducing the risk of development of (pre-)cancerous growths. This sequence represents an HPV-16 protein of the invention
SQ Sec	Sequence 151 AA;
Query Best I Matche	ery Match 99.5%; Score 826; DB 6; Length 151; st Local Similarity 98.7%; Pred. No. 4.2e-84; Local Similarity 98.7%; Pred. No. 4.2e-84; Conservative 0; Mismatches 2; Indels 0; Gaps 0
ঠ	1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60

á 멼 8

13 μ

AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD

120 60 60 0

MFQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY MPQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY

Indels

0

Gaps

Best Loca Matches Query Match

Local

al Similarity 149; Conserv

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RESULT 4
AA022636
ID AA022
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                                                                                                                                                                                     The invention relates to a novel method for determining the possibility of recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV) or suspected of being infected with HPV, and has or had a (pre-)cancerous growth on or around the cervix. The novel method comprises incubating an E6 or E7 peptide of HPV with a sample from the patient, and assaying the sample for a cell-mediated immune response against the peptide. The method is useful for determining the possibility and preventing the recurrence of a (pre-)cancerous growth in a patient infected with HPV or suspected of being infected with HPV. The HPV E6 or E7 peptides are useful in immunotherapy for the preventing or reducing the risk of development of (pre-)cancerous growths. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Determining a possible recurrence of a (pre-)cancerous growth in a patient infected with human papilloma virus (HPV), comprises incubating the sample with an HPV E6 or E7 peptide and detecting a cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; peptide therapy; immunotherapy; pre-; cancerous growth; cancer; human papilloma virus; cervix; cell-mediated immune response; HPV; HPV-16.
                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 125-126; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sastry KJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-JUL-2001; 2001US-0306809P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPV protein sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-MAY-2003
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                                                                                                                                  151 AA;
99.5%;
ilarity 98.7%;
Conservative
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Score 826; DB 6;
Pred. No. 4.2e-84;
0; Mismatches 2.
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RESULT 5
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                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 149
                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a wild type E6 protein from human papillomavirus type 16 (HPV16), which is used to produce fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating jamunume responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus type 16. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                             Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 76-77; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2002; 2002US-0415929P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-2004.
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61
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                                                                                                                         Н
                                                                                                                                                                                                                                                                                 Similarity
                                AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
AVCDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                   MFQDFQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                                                                                                                                                                                                                                                Conservative
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98.7%;
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                                                                                                                                                                                                                                            Score 826; DB 8;
Pred. No. 4.2e-84;
0; Mismatches 2
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                           Methods have been developed for distinguishing a subset of human CC papilloma virus (HPV) that is associated with an increased risk of C papilloma virus (HPV) that is associated with an increased risk of CC papilloma virus (HPV) that is associated with an increased risk of CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the CC sample and determining if the base at position 350 of the E6 gene (see CC AAT94723 and AAT94724 for comparison) is T or G, where the presence of GC at position 350 is associated with an increased risk of developing CC cervical dysplasia or cervical cancer; and (2) preparing a cervical sample to expose any HPV-16 E6 protein in the sample and determining if the amino acid at position 83 of the protein (see position 90 in AAW35741 and AAW35742 for comparison) is Val or Leu, where the presence of Val at CC position 83 that is associated with an increased risk of developing CC cervical dysplasia or cervical cancer. The present sequence represents the variant protein sequence for HPV-16 E6. The 350G variant correlates well with Pap scores: 350T:350G ratios among 45 HPV16 samples were 10:4 CC or negative Pap scores; 4:2 for CIN I, 1:6 for CIN II; 2:9 for CIN III; CC 0:3 for cancer. (Updated on 25-MAR-2003 to correct PF field.)
Sequence
                                                                                                                                                                                                                                                                                                                                                                                          Evaluating risk of cervical dysplasia or cervical cancer - variant form of human papilloma virus 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAT94742.
                                                                                                                                                                                                                                                                                                                                                        Claim 7; Col 23-26; 33pp; English.
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16-FEB-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wheeler CM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete genome; circular; human papillomavirus type 16; HPV16 E6; cervical dysplasia; cervical cancer; cervical smear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW35742;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW35742 standard; protein; 162
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162
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94US-00316239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "End of protein sequence even though 3 amino acid
residues are given following on"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Mutated from Leu in the reference (AAW35741)"
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Query Match Best Local Similarity

99.5%;

Score 826; DB Pred. No. 4.6e 0; Mismatches

DB 2;

Length 162; Indels

<u>0</u>

Gaps

0

Conservative

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RESULT 7
AD044060
ID 4060
ID 4060
AC AD04
XX AMIN
XX B6 F
XX AMIN
XX B6 F
KW Cerl
XX AMIN
XX WO2C
YN WPI
Y
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                                                         The present sequence represents an E6E7 fusion protein, comprising wild type E6 and E7 polypeptides from human papillomavirus type 16 (HPV16). The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 67-68; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2003; 2003WO-US031726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anal cancer; reproductive system cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of an E6E7 fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             penile cancer; vulvar cancer
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1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY

Query Match Best Local Similarity

99.5%;

Sequence 248

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Matches

149;

Conservative

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Score 826; DB 8; Pred. No. 7.7e-84; 0; Mismatches 2

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Best Local Similarity
                                                                                                                                                                                                   encodes a fusion polypeptide which is useful as a vaccine composition. The nucleic acid of the invention contains: a first nucleic acid encoding a polypeptide that promotes processing via the MHC class I pathway; a second sequence encoding a signal peptide; and a third sequence encoding an antigenic polypeptide. The DNA vaccine of the invention is useful for inducing or enhancing an antigen specific immune response, or to inhibit growth or prevent re-growth of a tumor expressing Human papillomavirus (HPV) B7 or E6 protein. The present amino acid sequence represents a human papillomavirus type 16 (HPV16) E6 protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                  antigen, a signal peptide, and a heat shoc for inducing or enhancing immune response tumor growth.
                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid molecules encoding a fusion polypeptide comprising an antigen, a signal peptide, and a heat shock protein, useful as a vacci for inducing or enhancing immune response or for inhibiting or prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  vaccine; MHC class I pathway; antigen specific E7 protein; E6 protein.
                                                                                                                                                                          Sequence 151 AA;
                                                                                                                                                                                                                                                                                                                                          The invention comprises a nucleic acid molecule (DNA vaccine) that
                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 5; 67pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-813972/80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-MAY-2003; 2003US-0467602P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus type 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYJO ) UNIV JOHNS HOPKINS
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                                                                                                                  148;
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                       61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
 61
                                                                            1 MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
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                                                         MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                               99.2%;
                                                                                                                 Score 823; DB 8; I Pred. No. 9.2e-84; 1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HPV16) E6 protein - SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response;
                                                                                                                                             Length 151;
                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                   or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                   as a vaccine
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Best Local Similarity
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22766
                                                                                                                                                                                                          The peptide is the sequence of the human papillomavirus HPV 16 E6 nucleoprotein. Peptides corresponding to regions (pref. epicopic regions) of HPV 16 E6 were synthesised by standard Merrifield synthesis. Examples of such peptides are E6 1-20, 8-20, 119-134 or 148-158. Compositions contg. these peptides, antibodies against the peptides, or recombinant cells contg. the gene encoding the immuno- genic peptides may be utilised in methods for inhibiting and treating HPV infection and tumour initiation and progression e.g. in the prevention or retardation of cervical warts and cervical carcinoma resulting from HPV infection. See also AAR2-2767. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 7; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                               cervical
                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic peptide(s) derived from E6 or E7 region of HPV16 -
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1992-132119/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
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21-SEP-1992
                                                                                                                                                                                      Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-SEP-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-APR-1992.
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                                                                                                                                         148;
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                     KKORFHNIRGRWTGRCMSCCRSSRTRRETOL 151
                                            MFQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                                                                                                                                                             warts or cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; peptide; 158
                                                                                          MFQDPQERPRKLPQLCTBLQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKORFHNIRGRWTGRCMSCCRSSRTRRETOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                        cells encoding them,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (revised)
(first entry)
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                                                                                                                                                   99.2%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blake J,
                                                                                                                                                                                                                                                                                                                                                                             resulting
                                                                                                                                       Score 823; DB 2;
Pred. No. 9.7e-84;
1; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hellstrom K,
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                                                                                                                                                                                                                                                                                                                                                                                          useful
                                                                                                                                                                                                                                                                                                                                                                               from
                                                                                                                                                                                                                                                                                                                                                                                          in
                                                                                                                                                                                                                                                                                                                                                                               HPV infection.
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                                                                                                                                                                                                                                                                                                                                                                                          treatment and
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hellstrom
                                                                                                                                         2
                                                                                                                                                              Length 158;
                                                                                                                                       Indels
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                                                                                                                                           Query Match
Best Local Similarity
Matches 148; Conserv
                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                cancers and/or warts. The present sequence represents a human papillomavirus E6 protein containing two zinc finger motifs, the exemplification of the present invention
                                                                                                                                                                                                                                                  The present invention describes an agent used in the treatment or prophylaxis of a disease caused or exacerbated by MPV (mammalian parphylaxis of comprising a compound capable of reducing, inhibiting or otherwise decreasing the activity of a protein encoded by an MPV gene by facilitating disruption of a chelated metal cation domain present in the protein. An agent of the present invention can be used to treat cervical cancer or its HPV associated precursor lesions or other HPV associated
                                                                                                                                                                                                                                                                                                                                                                                      Polysulfide and dithionodisulfide agents, useful for the treatment prophylaxis of diseases caused by mammalian papillomavirus, are disruptors of a chelated metal cation domain in an MPV gene encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY82462 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                   Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-256917/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bernard H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-1998;
15-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-MAR-2000
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            KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                           AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                           MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                             AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                            MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                            Conservative
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illomavirus; antiviral; cytostatic;
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99AU-00001645.
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                                                                                                                                                                                                                                                                                                                                                 78pp;
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                                                                                                                                            Mismatches
                                                                                                                                                      823; DB 3;
No. 9.7e-84;
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                                                                                                                                                                 Length 158
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                                                                                                                                                                                                                                                                    Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  An isolated human papilloma virus (HPV) epitope, useful in vaccines treating HPV infections.
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15-AUG-2000; 2000US-00641528.
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                                                                                                                                                                                                                                                                                                                                                           Sequence 158
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                                                                                                                                                                                                                                        Score 823; DB 4;
Pred. No. 9.7e-84;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a novel purified complex comprising a first polypeptide and a second polypeptide, where the polypeptides comprise defined amino acid sequences listed in the specification, and where the first polypeptide binds to the second polypeptide. A complex of the invention has virucide and cytostatic activity, and may have a use as a vaccine. The complex is useful for identifying agents for treating or preventing a conditions involving altered level of the complex, e.g. human papilloma virus (HPV) infection, or cancer. The compositions, antibodies, vectors and methods are useful for treating such diseases. The sequences shown in ADF09500-ADF09583 represent proteins of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New purified complex comprising a first polypeptide and a second polypeptide, useful for identifying agents for treating/preventing condition involving altered level of the complex e.g. human papillo virus infection, or cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 158 AA;
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HOFFMANN LA ROCHE INC.
                                                                                                         KKORFHNIRGRWTGRCMSCCRSSRTRRETOL 151
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Pred. No. 9.7e-84;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                   encodes a fusion polypeptide which is useful as a vaccine composition. The nucleic acid of the invention contains: a first nucleic acid encoding a polypeptide that promotes processing via the MHC class I pathway; a second sequence encoding a signal peptide; and a third sequence encoding an antigenic polypeptide. The DNA vaccine of the invention is useful for inducting or enhancing an antigen specific immune response, or to inhibit growth or prevent re-growth of a tumor expressing Human papillomavirus (HPV) E7 or E6 protein. The present amino acid sequence represents a human papillomavirus type 16 (HPV16) E6 protein of the invention.
AEA40817 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid molecules encoding a fusion polypeptide comprising an antigen, a signal peptide, and a heat shock protein, useful as a vaccine for inducing or enhancing immune response or for inhibiting or preventing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; SEQ ID NO 4; 67pp; English.
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E7 protein; E6 protein.
                                                                                                                                                                                                                                                                                                                         Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention comprises a nucleic acid molecule (DNA vaccine) that
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                                                                                          KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                   MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                    AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                   MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                          99.2%;
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                                                                                                                                                                                                                                                          Score 823; DB 8; I
Pred. No. 9.7e-84;
1; Mismatches 2;
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                                                                                                                                                                                                                                                                                          Length 158;
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The invention relates to a novel nucleic acid composition useful as an immunogen. The composition comprises a combination of; a first nucleic competition acid vector comprising a first sequence encoding an antigenic polypeptide or peptide, and optionally, a second sequence linked to the first combination of the second nucleic acid vector encoding an anti-apoptotic polypeptide. CC When the second vector is administered with the first vector to a combination polypeptide is induced that is greater in magnitude and/or duration than an immune response to the antigenic polypeptide cor peptide is induced by administration of the first vector alone. CC minume response induced by administration of the first vector alone. CC suitable for introduction into a cell or an animal by particle composition; a pharmaceutical composition capable of inducing or composition; a pharmaceutical composition capable of inducing or composition; a pharmaceutical composition capable of inducing or composition an antigen specific immune response, comprising the particle commune response in a subject; increasing the numbers of CD8+ CTLs specific for a selected desired antigen in a subject; and inhibiting the growth of a tumor, hence it has cytostatic activity. This sequence represents ananti-apoptotic vector HPV cc
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                                                                                                                                   Matches
                                                                                                                                                                Query Match
                                                                                                                                                                                                   Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid composition comprising a first nucleic acid vector encoding an anti-spoptotic polypeptide and a second nucleic acid vector encoding an anti-spoptotic polypeptide, useful as an immunogen for inhibiting the growth of a tumor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-FEB-2003; 2003US-0449429P.
18-JUL-2003; 2003US-0488527P.
31-DEC-2003; 2003US-0533792P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 7; 158pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunogenicity; vaccine; immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2004; 2004WO-US005292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Anti-apoptotic vector HPV
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                                                                                                                                                  Local Similarity
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                                                                                                                                 148;
 89
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                    AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                     MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunogenicity-potentiating polypeptide; IPP; stimulation; tumor; cytostatic.
                                                                                                                                                 99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E6
                                                                                                                             Score 823; DB Pred. No. 9.7e-
1; Mismatches
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                                                                                                                                                 823; DB 9;
No. 9.7e-84;
                                                                                                                                                                Length 158
                                                                                                                                   Indels
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128 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 158

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an antibody composition comprising a mixture of monoclonal antibodies that specifically bind to 86 proteins of human papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one of the monoclonal antibodies specifically binds to 86 proteins of at CC diagnostic kit (for detecting an HPV strains. Also included are a CC diagnostic kit (for detecting an HPV strains. Also included are a CC comprising the antibody composition above), a method of detecting an HPV CC comprising the protein in a sample, a method of detecting the presence of an oncogenic HPV 86 polypeptide in a sample (comprising a presence of an oncogenic HPV 86 polypeptide in a sample (comprising a first and a second binding partner is a PDZ domain protein and the second binding partner is a PDZ domain protein and the second binding partner is an antibody that specifically binds to the 86 proteins of at least three different oncogenic HPV strains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, particularly cervical cancer. The present sequence is an HPV 86 protein.
                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 13; 161pp; English
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                                                         KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                            MFQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
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                                                                                                                      AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 9.7e-84;
1; Mismatches 2
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158
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RESULT 16
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                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; SEQ ID NO 2; 53pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor-associated cancer; HPV16 E6.
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                                                                                                 AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drijfhout JW;
                                                                                                                                                                                                                                                                                                                                                                                    99.2%;
                                                                                                                                                                                                                                                                                                                                                                                       Score 823; DB 9; Pred. No. 9.7e-84;
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RESULT 17

ARC98863
ID ARC98
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XX AC99
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                                                                         The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the CC polynucleotide, vector and/or polypeptide and a carrier), a cell CC (comprising the polynucleotide, vector or polypeptide), inducing an CC immune response against human papillomavirus virus (HPV) and making the CC polynucleotide, vector or polypeptide. The epitopes are derived from CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The cpitopes may be linked via a GP-anchor/spacer peptide. The order of the cpitopes in the vaccine protein are disclosed in the tables referred to CC polypeptide is useful in preparing a composition for inducing an immune CC different squame papillomavirus virus (HPV) and thus providing a composition and thus providing a CC defense against human papillomavirus virus (HPV) and thus providing a composition is an HPV protein used to derive epitopes for the vaccine of the
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    The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16 EEL 214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the multi-epitope construct, a polypepitode comprising anino acid sequence encoded by the nolymplacities.
                                                                                                                   New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
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The present invention relates to novel fusion protein for inhibiting or preventing cancer induced by human papillomavirus type 16 (HPVI6). The fusion protein comprises an E7 peptide sequence of human papillomavirus type 16, a translocating peptide for translocation and a peptide fragmen
                                                                                                                                                                                                         New fusion protein comprising E7 peptide sequence of human papillomavirus type 16, useful for inhibiting or preventing cancer, e.g. cervical or lung cancer.
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Pred. No. 9.7e-84;
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obstetrics; neoplasm
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Methods have been developed for distinguishing a subset of hun papilloma virus (HPV) that is associated with an increased ris developing cervical dysplasia or cervical cancer. The methods (1) preparing a cervical sample to expose any HPV-16 E6 gene is sample and determining if the base at position 350 of the E6 c
                                                                                                                                                                                            Evaluating risk of cervical dysplasia or cervical cancer - variant form of human papilloma virus 16.
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-SEP-1993;
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                                                                                                                                                 Claim 7;
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(first entry)
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residues are given following on'
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No. 9.7e-84;
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The invention relates to a new DNA sequence encodes an E6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced by codons which lead to enhanced translation in a mammalian cell, containing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virucide; cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine; fusion partner; immunogenicity; HPV infection; neoplasm; HPV16; human papillomavirus-16; EE6T-sequence.
                                                                        Disclosure; Fig 2; 34pp; English.
                                                                                                                         A new DNA sequence encoding a fusion protein comprising a mutagenized HPV (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a (highly immunogenic fusion partner is useful to vaccinate against HPV
                                                                                                                                                                                                                                                       Cid-Arregui A,
                                                                                                                                                                                                                                                                                                                               23-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus.
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Pred. No. le-83;
1; Mismatches 2
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Best Local S
Matches 148
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25-MAR-2003
28-JUN-1995
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  The sequences of the E6 papillomavirus (HPV) 16 proteins in AAR63865-66,
                                                                                                                                            Human papilloma virus detection assay - by amplification using sustained sequence replication and hybridisation with a detecto
                                                                                                                                                                                                                       WPI; 1995-006821/01.
P-PSDB; AAQ75470.
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tes 148; Conserv
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                                                                                               Page 24-26;
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and E7 polypeptide-encoding regions of human and 18 are given in AAQ75470-71 and the enco, respectively. Probes and primers based on the continuation of the continuat
                                                                                               79pp; English.
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Pred. No. 1.1e-83;
1; Mismatches 2
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Best Local S
Matches 148
The present sequence represents a fusion protein, comprising E7 and E6 polypeptides from human papillomavirus type 16 (HPV16). The fusion protein is designated E7E6TetM, and comprises an E7 amino terminus (where residues 24 and 26 have been replaced with glycine) and an E6 carboxy terminus (where residues 63 and 106 have been replaced with glycine). B7E6TetM is representative of fusion proteins of the invention. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids corresponding to amino acids 63 or 106 of
                                                                                                                                                                                                                                 New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequences were used for HPV infection diagnosis; expression of E6 and diagnostic for cervical cancer or pre- malignant states. (Updated c 25-MAR-2003 to correct PN field.) (Updated on 16-OCT-2003 to standard) OS field)
                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                          Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                         03-OCT-2002; 2002US-0415929F
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                                                                                                                                                                                                    22; Page 73-74; 101pp; English.
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Pred. No. 1.2e-83;
1; Mismatches 2
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RESULT 24
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Matches 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      we procesn; E7 protein; fusion protein; cervical cancer; immune response.
                                                                                                                                                                                                                                                                    New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus
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                                                                                                                                                                                                                                                                                                                                                 2004-316328/29.
DB; ADO44071.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122
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                                                                                                                                                                                                                                               for
8, e.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINGQKPLCPEEKQRHLDK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FODPOERPRKLPOLCTELOTTIHDIILECVYCKOOLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                         Cassetti
                                                                                                                                                                                                                                            treating or .g. cervical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sequence of a fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ğ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         reproductive system cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                         N
N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.2%;
98.7%;
                                                                                                                                                                                                                                               preventing human cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein designated E7E6PentM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       823; DB 8;
No. 1.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gastrointestinal tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPV16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         penile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HPV-associated cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cancer; vulvar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                         E7 polypeptides, (HPV)-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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polypeptides from human papillomavirus type 16 (HPV16). The fusion protein is designated E7E6PentM, and comprises an E7 amino terminus (where residues 24, 26 and 91 have been replaced with glycine) and a carboxy terminus (where residues 63 and 106 have been replaced with glycine). E7E6PentM is representative of fusion proteins of the invention. The specification describes human papillomavirus E6 and E

The present sequence represents a fusion protein,

comprising

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E6

an

6

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Claim

Page 75-76; 101pp;

English

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RESULT 25
ADR47005
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypoptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypoptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gestrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                           Virus-like particle vaccines containing dengue as core for carrier, applicable in preventives like cervical cancer and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cytostatic; virucide; dengue virus; recombinant replicon; deletion; prem protein; C protein; NS1 protein signal; vaccine; cervical cancer; viral disease; antigen; dendritic cell; immune response;
                                                                                                                                                                        Pang
                                                                                                                                                                                                                                                                  30-JAN-2003; 2003CN-00115272.
30-JAN-2003; 2003CN-00115273.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR47005 standard; protein; 256 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the
                                                                                                                                        WPI; 2004-625870/60.
                                                                                                                                                                                                                    (SHAN-)
                                                                                                                                                                                                                                                                                                                30-JAN-2004; 2004WO-CN000088
                                                                                                                                                                                                                                                                                                                                                26-AUG-2004.
                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                               WO2004072274-A1
                                                                                                                                                                                                         (BEIJ-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                            papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62
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                                                                                                                                                                                                     SHANGHAI TENGEN BIOMEDICAL CO LTD.
TENGEN BIOMEDICAL CO.
BEIJING ORIENTAL TENGEN TECHNOLOGY DEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VGDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINGQKPLCPEEKQRHLDK 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KORFHNIRGRWTGRCMSCCRSSRTRRETQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.2%;
98.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 823; DB 8;
Pred. No. 1.7e-83;
0; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for Dengue virus vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ν
•-
                                                                          virus recombinant replicon or/and remedies for tumors
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A dengue virus recombinant replicon has a Example 2; SEQ ID NO 2; 38pp; Chinese.

deletion of the complete coding

producing a drug infection.

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RESULT 26
AEF40157
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               virus can infect dendritic cells, and can effectively present antigen to provide immunity effect. Different types of dengue virus can be used to repeatedly produce efficient immune response thereby strengthening the body's immune system against the pathogen that contains such antigen. Human papillomavirus (HPV) vaccines were prepared by using a gene-expressing system using of the full-length dengue virus cDNA clone (pRS/FLD2). The recombinant virus vectors were transfected into baby hamster kidney (BHK) cells to enable the screening of BHK-21 Tet-off cell lines. This sequence corresponds to the HPV type 16 E7 protein whose encoding gene is used as the gene of interest in the recombinant replicon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence for preM protein of dengue virus and also includes elements of e.g. the non-coding region in the whole of the 5'-end, the coding region of the front 20 amino acids in the C protein, and the coding region of NS1 protein signal, coding regions of all non-structural proteins. The obtained vaccines are useful in producing preventives or/and remedies for cancer like cervical cancer and viral diseases. Such vaccines can efficiently express antigen in infected cells, which is because dengue
                                                                                                                                                                              30-JAN-2003; 2003CN-00115272.
30-JAN-2003; 2003CN-00115273.
30-JAN-2004; 2004WO-00072274.
                                                                                                                                                                                                                                                                                                                                                                                     Vaccine; virus-like particle; replicon; therapeutic; cancer; neoplasm; viral infection; virucide; infection; oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus 16 (HPV-16) E7-E6 oncoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AEF40157 standard; protein; 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   encoding gene is
of the invention.
                                                               N-PSDB; AEF40156.
                                                                                 WPI; 2006-109169/11.
                                                                                                                                                                                                                                                                                                                        US2006018928-A1.
                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2006 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
            producing a drug for the prophylaxis and treatment of cancer or vi
                                                                                                                                                                                                                                                     29-JUL-2005; 2005US-00192923
                                                                                                                                                                                                                                                                                      26-JAN-2006.
                                                                                                                                                  (PANG/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                    PANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   256 AA;
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98.0%;
                                                                                                                                                                                                                                                                                                                                                      type 16.
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Pred. No. 1.7e-83;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   165
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RESULT 27
AAR27725
ID AAR27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 148;
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Best Local
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25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention provides a virus-like particle (VLP) vaccine which contains dengue virus (DEN) recombinant replicon as its core. The DEN replicon contains exogenous nucleotide sequences such as human papillomavirus (HPV) antigen proteins, immune regulators or combination of HPV antigen and immune regulators. The invention is useful for producing a drug for the prophylaxis and treatment of cancer or viral infection. The present sequence is a human papillomavirus oncoprotein.
                                           Recombinant virus vectors encoding human papillo treating and vaccinating against HPV infections them, such as cervical cancer.
                                                                                           WPI; 1992-349219/42.
N-PSDB; AAQ29389.
                                                                                                                                                                                                                                                                                    Key
Peptide
                                                                                                                                                                                                                                                                                                                                                           Virus vector; vaccinia virus; papillomavirus; HPV; human; amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR27725;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR27725 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 256 AA;
                                                                                                                             Boursnell MEG,
                                                                                                                                                                                                     10-MAR-1992;
                                                                                                                                                                                                                                                   WO9216636-A1
                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                    HPV 16
                     Disclosure; Fig la; 83pp; English.
                                                                                                                                                     (IMMU ) IMMUNOLOGY LTD
                                                                                                                                                                             14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example
                                                                                                                                                                                                                                                                                                                                               mmunotherapeutic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                   日6
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                                                                                                                                                                                                                                                                                                                                                                                  protein fragment.
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(revised)
(first en
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                                                                                                                                                                                                     92WO-GB000424
                                                                                                                             Inglis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein;
                                                                                                                                                                                                                                                                                                                                                                                                          entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; 24pp; English
                                                                                                                                                                                                                                                                        "HPV-16 E6 protein"
                                                                                                                             SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 263
                                                                                                                               Munro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 823; DB 10;
Pred. No. 1.7e-83;
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                                                      papillomavirus proteins -
ections and conditions caus
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The fragment of DNA contg. the HPV-16 E6/E7 coding region was prepd.

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RESULT 28
AAR97561
ID AAR97
XX AAR97
XX AAR97
XX 27-AU
DT 27-AU
DT 11-JA
XX Human
XX
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Best Local Similarity 98.0
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80: 3812 (1983)) using oligonuclectides SO5 and SO6. The prod. of the third reading frame is the HPV-16 E6 protein whereas the second reading frame encodes HPV-16 E7. The E6 and E7 ORFs are fused together to form a single continuous ORF via site directed mutagenesis and the immortilising potential of E7 is removed by altering two key codons of the HPV E7 sequence. The single ORF of HPV-16 E6/E7 may be inserted into vaccinia virus DNA at neutral sites (pref. by inserting two sets of the DNA in opposite orientations to overcome the problem of intertypic recombination) to make a recombinant virus vector for use immunotheraspeutically to activate cells of the immune system against HPV. See also ARR27723-43. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 24-OCT-2003 to standardise OS field)
A variant of the human papilloma virus (HPV) E6 or elicits a humoral and/or cellular immune response in vaccines against HPV or to treat HPV infection.
                                                                                                                                                                       Vaccine variants of human papilloma virus antigens - contain variants of E6 and/or E7 protein, pref. deletion mutants, and are used to treat or prevent HPV infection.
                                                                                                          Example 1; Page 15-16; 37pp; English.
                                                                                                                                                                                                                                                                                              N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                 Edwards SJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JUN-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papilloma virus; E6; E7; deletion mutant; HPV; immune humoral immune response; cellular immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papilloma virus E6/E7 protein variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-AUG-2003
11-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR97561 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 263 AA;
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DB; AAT31833.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                 Cox J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
(first entry)
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Pred. No. 1.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                    Frazer
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   E6 or E7 protein which ponse against HPV can be ction. The variant is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2
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RESULT 29
AAY25376
ID AAY25
XX AAY25
XX AAY25
XX AAY25
XX Pusio
KW Pusio
KW Immun
KW HPV a
XX Synth
OS Synth
OS Humar
XX U0993
XX 08-JI
XX 18-DI
XX
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Best Local Similarity
                                             AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAX25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce ar immune response in a patient to an HPV antigen. They can also be used f preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preferably a deletion mutant comprising at least half, and preferably two thirds of full length E6 or E7 protein starting from the N- or C- terminal, or is a full length E6 moiety fused to a full length E7 moiety. The variant optionally has a linkage moiety and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This sequence is a full length E6/E7 fusion protein. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                            Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                            Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dalemans WLJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-405485/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                      II; Page 48-49; 62pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevention;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerard
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98.0%;
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                                                                                                                                                                                                                                                                                                                            an E6,
to HPV
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                                                                                                                                                                                                                                                                                                                                                           E7
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                                                                                                                                                                                                                                                                                                                                                           or E6/E7
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. No. 1.8e-83;
ismatches 2;
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                                                                                                                                                                                                                                                                                                                                                           fusion
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Best Local Similarity
                                                                 This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                             Sequence
                                                                                                                                                                                                                                                                Bruck C, Cabezon S
Lombardo-Bencheikh
                                                                                                                                                                        Disclosure; Fig 3; 95pp; English.
                                                                                                                                                                                              Human Papilloma Virus (HPV) fusion proteins - us
treatment or prophylaxis of HPV induced lesions
                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus Haemophilus influenza
                                                                                                                                                                                                                                                                                                                          22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                               17-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Chimeric.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Prot.D1/3-E6-His/HPV16 protein.
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22-JUN-1999
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                                              273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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          99.2%;
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Score 823; DB 2;
Pred. No. 1.9e-83;
1; Mismatches 2;
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Pred. No. 1.9e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein D; vaccine
; virus; infection
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RESULT 31
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                                                                                                                                                                                                                     Query Match
Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) 86 and 87 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (cLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2005-557648/57.
N-PSDB; AED52633.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 16. Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein D1/3-E6-His/HPV16.
                                                                                                                                                                                                                                                                                                                               Sequence 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Fig 3; 96pp; English.
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                                                                                                                                                                                                                                                  Local Similarity
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                                                 61
                                                                                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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                                                                                                                                                                                                                  Pred. No. 1.9e
1; Mismatches
                                                                                                                                                                                                                                                Score 823; DB 9;
Pred. No. 1.9e-83;
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                                                                                                                                                                                                                                                                       Length 273;
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                                                                                                                                                                                                                  Gaps
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Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAX75375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce a immune response in a patient to an HPV antigen. They can also be used preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPV fusion protein CLYTA-E6-His/HPV16.
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                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example VI; Page 52-53; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition comprising an E6, induce immune response to HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPV antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                               121
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                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                     148;
                                                                                                                                                                                                                                            1 MFQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                           MFQDPQERPRKLPQLCTELQTTIHDIILECYYCKQQLLRREVYDFAFRDLCIYYRDGNPY 192
                                                                                                       AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                  AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                            292 AA;
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KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 283
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      prevention; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gerard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97GB-00027262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                        99.2%;
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                                                                                                                                                                                                                                                                                                                                           Score 823; DB 2;
Pred. No. 2e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E7 or E6/E7
                                                                                                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fusion
                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                       Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                     Indels
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RESULT 33
AAY02635
ID AAY02635 standard; protein; 292

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RESULT 34
AED52642
ID AED52
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AC AED52
XX
AC AED52
XX
DT 29-DE
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DE Fusic
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Best Local (
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                                                                                                                                                                                                                                                                                                                                  This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Streptococcus pneunoniae CLYTA protein of the encoded protein. The protein can be used in a vaccine, for limmuno-therapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bruck C, Cabezon S
Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus. Streptococcus pneumoniae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric; E6; E7; fusion professional profession benign; malignant;
          Fusion protein
                                 29-DEC-2005
                                                       AED52642;
                                                                           AED52642 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 10; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-AUG-1998;
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22-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLYTA-E6-His protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                  253
                                                                                                                                                        121
                                                                                                                                                                             193
                                                                                                                                                                                                                        133
                                                                                                                                                                                                                                                                                                                                                                                                                                               Papilloma Virus (HPV) fusion proteins - useful in vaccines ment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                    148;
                                                                                                                                                                                                                                              \vdash
                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                 KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                      292
                                                                                                                                                                            AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                           AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                  KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 283
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (revised)
(first en
                                                                                                                                                                                                                                                                                                              ₽
                                (first entry)
            cLytA-E6-His/HPV16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Silva T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        fusion protein; CLYTA; vaccine; immunotherapy; tumour;
alignant; virus; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                            99.2%;
                                                                             292
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                                                                                                                                                                                                                                                                 Score 823; DB 2
Pred. No. 2e-83;
1; Mismatches
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                                                                                                                                                                                                                                                                                        DB 2;
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                                                                                                                                                                                                                                                                                        Length 292;
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RESULT 35
AAY25377
ID AAY25
XX AAY25
AC AAY25
XX O6-SE
XX PO6-SE
XX FUSIO
KW FUSIO
KW Immun
KW HPV a
XX Synth
OS Synth
XX Synth
XX Human
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Best Local (
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Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-Lyth, fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                        Fusion
                                                                                                 HPV fusion protein D1/3-E6E7-His/HPV16
                                                                                                                         06-SEP-1999
                                                                                                                                                                         AAY25377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein; vaccine; papilloma; cytostatic; papillomavirus infection; virucide; uterine cervix tumor; E7; LytA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN9801903-I4
                                                            usion protein;
mmunological fi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SMIK)
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                               ancigen;
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DB; AED52641.
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                                                                                                                                                                                                                                                                                                                                                                                      148;
                                                                                                                                                                                                                                                                                                                                                  1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKFLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                     KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                           standard;
                                                                                                                                                                                                                                        KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                      AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                      292 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fig 10;
                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                               prevention; treatment.
                                                                                                                         (first
                                                            n; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; fusion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97EP-00179535
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                                                                                                                                                                        protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96pp; English
                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                  99.2%;
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                                                                                                                                                                           371
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                                                                                                                                                                                                                                                                                                                                                                                      Score 823; DB 9
Pred. No. 2e-83;
1; Mismatches
                                                                                                                                                                           ₿
                                                                                                                                                                                                                                                               151
                                                                                                                                                                                                                                                                                                                                                                                                               DB 9;
                                                                                                                                                                                                                                        283
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                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                292
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Synthetic.

Human papillomavirus

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RESULT 36
AAYO2633
ID AAYO2
XX AAYO2
XX AAYO2
XX 17-OC
DT 17-OC
DT 22-JU
XX Chime
KW Chime
KW tumou
XX Human
OS Human
OS Human
OS Human
OS Human
OS Human
YX WO991
XX YO4-MJ
XX 17-Al
XX 22-Al
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Best Local S
Matches 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce an immune response in a patient to an HPV antigen. They can also be used for
                                                                                                                                                                             Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy; tumour; lesion; benign; malignant; virus; infection.
                                                                                                                                                                                                                                                   17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Composition comprising induce immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dalemans WLJ, Gerard CMG;
                                          17-AUG-1998;
                                                                     04-MAR-1999.
                                                                                                                                      Human papillomavirus.
Haemophilus influenzae.
                                                                                                                                                                                                                         Prot.D1/3-E6-E7-His/HPV16 protein
                                                                                                                                                                                                                                                                                             AAY02633;
                                                                                                                                                                                                                                                                                                                      AAY02633 standard; protein; 371 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example III; Page 50; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-DEC-1998;
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               22-AUG-1997;
                                                                                               WO9910375-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1999-405485/34.
DB; AAX78793.
                                                                                                                                                                                                                                                                                                                                                                                                                     121
                                                                                                                                                                                                                                                                                                                                                                                                                                                 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                          KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
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                                                                                                                                                                                                                                                   (revised)
(first entry)
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               97GB-00017953
                                          98WO-EP005285.
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98.0%;
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to HPV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 823; DB 2;
Pred. No. 2.7e-83;
1; Mismatches 2
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AED52638

AED52638

AC AED5

XX AED5

XX Pusj

XX Pusj

XX Viri

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus Synthetic.
  WPI; 2005-557648/57.
N-PSDB; AED52637.
                                                                                                                                                                                  22-AUG-1997;
                                                                                                                                                                                                                                  24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; vaccine; papilloma; virucide; uterine cervix tumor; E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fusion protein D1/3-E6-E7-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AED52638
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 6; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Papilloma Virus (HPV) treatment or prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bruck C,
                                                                              Tyrrell AWR;
                                                                                                                                                                                                                                                                                      04-MAR-2005
                                                                                                                                                                                                                                                                                                                                      IN9801903-I4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AED52638 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lombardo-Bencheikh A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
                                                                                                                              (SMIK)
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                                                                                                                              SMITHKLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        influenzae; strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                  97EP-00179535
                                                                                                                                                                                                                                     98IN-CH001903
                                                                                                                                 BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           371
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 823; DB 2;
Pred. No. 2.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; papillomavirus infection; D protein.
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RESULT 38
AAY25381
ID AAY25
XX AAY25
XX AAY25
XX O6-SE
XX Pusic
XX Fusic
XX Immun
XX Immun
XX HPV a
XX Synth
OS Human
XX W0993
XX 08-JU
PF 18-DE
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PF 18-DE
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (20-127) the C-terminus of the equence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                             Composition comprising induce immune response
                                                  Example VIII; Page 55-56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-1999
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     AAX78791-X78801
                                                                                                                                                                                                                                            Dalemans WLJ,
                                                                                                                                                                                                                                                                                                                                                                                         18-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPV fusion protein CLYTA-E6E7-His/HPV16
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                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1999.
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                                                                                                                                                                     1999-405485/34.
DB; AAX78797.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l protein;
logical fu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prevention; treatment
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                                                                                                                                                                                                                                            Gerard
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                                                                                                                                                                                                                                                                                                                                                                                         98WO-EP008563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
usion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96pp; English
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98.0%;
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Pred. No. 2.7e-83;
                                                                                                                        E7
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                                                  English
                                                                                                                      or E6/E7
  acid
sequences which
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                                                                                                                        fusion
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                                                                                                                      protein
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RESULT 39
AAY02637
ID AAY02637
XX AAY02
XX AAY02
XX AAY02
DT 17-00
DT 22-UU
XX Chime
KW Chime
KW lesic
XX Lesic
XX Humar
OS Streg
OS Chime
XX Humar
OS Streg
IN W0991
XX 17-AU
XX 17-AU
XX MPI;
DR N-PSI
XX WPI;
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Matches
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Best Local
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                                                 This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of Etreptococcus pneunoniae CLYTA protein of the encoded protein. The protein can be used in a vaccine, for immuno-therapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to
                                                                                                                                                                                                                                                                                        Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruck C, Cabezon & Lombardo-Bencheikh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus Streptococcus pneumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric; E6; E7 lesion; benign;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17-OCT-2003
22-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                   treatment or prophylaxis of
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-190587/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-MAR-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLYTA-E6E7-His protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY02637;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY02637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9910375-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
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                                                                                                                                                                                                                                                                                                                                                                     AAX29786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard; protein; 390 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cabezon Silva T,
                                                                                                                                                                                                                                    Fig 14; 95pp; English.
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(first entry)
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                        preventing field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97GB-00017953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-EP005285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     malignant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     fusion protein;
alignant; virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.2%;
98.0%;
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Pred. No. 2.9e
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLYTA; vaccine; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
.9e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerard CMG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunotherapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                    in vaccines
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RESULT 40
AED52646
ID AED52
XX AED52
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XX Pusio
XX Pusio
XX Pusio
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XX Pusio
XX Chime
XX Synth
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OS Human
OS Synth
OS Human
OS Synth
OS Chime
XX Chime
XX IN980
XX AET
PF 22-AL
XX IN980
XX AET
PF 22-AL
XX Examg
XX WPI;
DR WPI;
CC Tink;
CC Tink;
CC Tink;
CC Tink;
CC Tink;
CC Haem
CC Stre;
CC Haem
CC Haem
CC Stre;
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CC Heem
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                                                Query Match
Best Local Similarity
                                 Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                              The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) B6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyca protein (CLyca) or thioredoxin. The present sequence represents an HPV-Lyta, fusion protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type 16. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fusion protein; vaccine; virucide; uterine cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AED52646 standard; protein; 390 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 390
                                                                                                                                                                                                                                                                                                       Example 12; Fig 14; 96pp; English.
                                                                                                                                                                                                                                                                                                                                          Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                            Tyrrell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion protein cLytA-E6-E7-His/HPV16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AED52646
                                                                                                 Sequence 390 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IN9801903-I4
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                          2005-557648/57.
DB; AED52645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
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                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98IN-CH001903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    accine; papilloma; cytostatic; papillomavirus infection; cervix tumor; E7; LytA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.2%;
                                                99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 823; DB 2;
Pred. No. 2.9e-83;
1; Mismatches 2
                                1;
                                                Score 823; DB 9;
Pred. No. 2.9e-83;
                                 Mismatches
                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 390
                                                                Length 390;
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                                 Indels
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                                Gaps
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FQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFYA

Matches Query Match Best Local (

148;

Conservative

0,

Local

Similarity

98.9**%**; 98.7**%**;

Score 821; DB Pred. No. 2.8e 0; Mismatches

e 821; DB 8; Le . No. 2.8e-83; ismatches 2;

Length 248; Indels

0

Gaps

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RESULT 41
AD044066
ID AD0444
XX AD044
XX AD044
XX AD044
XX B6 pr
KW E6 pr
KW anal
XX Human
OS Synth
XX D2-OC
XX 15-AF
XX D2-OC
XX IS-AF
XX New F
PT USEfil
PT CANCO
XX The |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                  The present sequence represents an E7B6 fusion protein, comprising wild cype E7 and E6 polypeptides from human papillomavirus type 16 (HPV16). C7 The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino C7 acids corresponding to amino acids 24, 26 or 91 of the sequence given in C8 ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of C8 there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated C9 cancers, such as cervical cancer. The fusion proteins and nucleic acids C9 cancers, such as cervical cancer. The fusion proteins and nucleic acids C9 cancers, the fusion proteins are useful for generating immune responses C9 against HPV. They are also useful for treating lower gastrointestinal C1 tract cancers, e.g. anal cancer, and other cancers of the reproductive C9 system, including penile and vulvar cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6 protein; E7 protein; fusion protein; HPV16; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
Sequence 248 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 72-73; 101pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ADO44067.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-OCT-2003; 2003WO-US031726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type 16. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Amino acid sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) WYETH HOLDINGS CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004-316328/29.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of an E7E6 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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AAX57808
ID AAY57
XX AA57
XX 20-MA
XX 20-MA
XX Trans
KW Creb
KW Creb
KW Cell
XX Viral
XX Unman
XX 10-DE
XX 26-MA
PR 26-MA
YX 26-M
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                                                                                                                                                                                                    The present invention describes a polypeptide comprising a Ctranscriptional adaptor motif (TRRM) or a TRRM-interaction motif (TRIM) CC (I). (I) can be used for identifying compounds (II) comprising a CC (I). (I) can be used for identifying compounds (II) comprising a CC polypeptide capable of disrupting an interaction between a TRRM sequence and/or a TRIM sequence. Polypeptides which bind to a TRRM sequence or a CC TRIM sequence are identified by incubating, the polypeptide with (I) and CC determining if the polypeptide interacts with (I). Compound (II) is CC useful for preparing a pharmaceutical composition and for disrupting an interaction between TRAM sequence and TRIM sequence in vitro, thereby CC inhibiting viral transcription or cell cycle progression in mammalian CC cells especially cancer cell. Compounds which disrupt interaction between CC TRIM/TRAM containing polypeptides can be used therapeutically to prevent CC or treat viral diseases and tumours. The polypeptides reduce conceptibility of cells to viral infection and regulate cell cycle concluding apoptosis and growth arrest and can be used to produce concluding apoptosis and growth arrest and can be used to produce continuous against the TRIM or TRAM sequences. HPV types associated with risk or low risk of cervical cancer can be distinguished based on the present sequence represents a HPV-16 E6 protein amino acid conceptible of the present sequence represents a HPV-16 E6 protein amino acid conceptible conception the present sequence represents a HPV-16 E6 protein amino acid conceptible con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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Query Match
Best Local Similarity
Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   creb binding protein; transcriptional regulation; cytostatic; antiviral; cell cycle inhibitor; viral transcription inhibitor; cancer; tumour; viral disease; viral infection; cell cycle; apoptosis; growth arrest.
                                                                                                                                                  Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel polypeptides cells useful for treating viral disease and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     O'connor MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAY-1998;
05-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPV-16 E6 protein amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transcriptional adapter motif; TRAM; TRAM interaction motif;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KORFHNIRGRWTGRCMSCCRSSRTRRETOL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fig 9; 73pp; English
   Conservative
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99GB-00000157.
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Score 818; DB 3; Length 151; Pred. No. 3.3e-83; Indels 1; Mismatches 3; Indels
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                                                                                                                                                                                                                                                                                                        Best Local Similarity
Matches 147; Conserv
                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                response to an antigen in a patient. The method comprises administe to the patient an immunoglobulin (Ig) or its portion where the Ig is least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. The present sequence is an antigen
                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 1G; 154pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Generating an immune response to an antigen, useful for generating desired T cell responses comprises administering an immunoglobulin one peptide epitope of the antigen attached to the immunoglobulin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bot A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-SEP-2002; 2002US-0412219P.
14-MAR-2003; 2003WO-US007995.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADL90078;
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                                                                                                                              AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                          MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                               KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            used to illustrate the invention.
Conservative
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                                                                                                                                                                                                                                                                                                     Score 815; DB 8;
Pred. No. 7.6e-83;
1; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                         Length 158
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RESULT 44
AAW99369
JD AAW99
AC AAW99
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AC AAW99
AX IT-OC
DT 21-MA
AX AITHL
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                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an antitumour composition containing a therapeutic or prophylactic agent or one or more immunogenic polypeptides, where at least one polypeptide is modified so that its intracellular localisation is different from that of the native polypeptide. This sequence represents an example of a modified immunogenic protein and corresponds to the E6 protein from human papillomavirus fused to the measles virus protein F signal peptide. The compositions, vectors and particles are used to treat or prevent cancers and tumours, specifically those associated with papillomavirus infection (e.g. cancer or low grade dysplasia of the cervix uteri). (Updated on 17-corr-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antitumour composition containing immunogenic polypeptide with altered localisation - or vector expressing this polypeptide, particularly for treating or preventing cervical cancer associated with human papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antitumour; immunogen; intracellular localisation; cancer; dysplasia; signal peptide; papillomavirus; infection; cervix uteri.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW99369 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kieny M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Papillomavirus
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21-MAY-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-JUL-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Measles virus.
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151
                                                     121
                                                                                                                                                                                                                                                                                                                                          143;
                                                                                                                                                                   19
                                                                                                                                                                                                                         36 MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                                          1 MFQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                                                                                                                                                  Similarity
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KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 181
                             KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                              AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPL-----QRHLD
                                                                                                                                                 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 54-55; 74pp; French.
                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                       Score 779.5; DB 2;
Pred. No. 1.2e-78;
1; Mismatches 2;
                                                                                                                                                                                                                                                                                                                              1.2e-78;
2;
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RESULT 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 108
                      E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Probes are designed to virus. The probes bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papilloma virus; HPV; benign; malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HPV E6 region product.
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                                                                                                                                        Amino acid
                                                                                                                                                                                              15-JUL-2004
                                                                                                                                                                                                                                                  ADO44077;
                                                                                                                                                                                                                                                                                                     ADO44077 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 16-17; 18pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting benign and/or malignant human papilloma virus - by detecting
DNA sequence of E6 and/or E7 region of human papilloma virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAQ48575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-AUG-1993
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Disulfide-bond
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                        121 EKKRFHNIGGRWTGRCMSCWKP--TRRETEV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MFQDPAERPYKLHDLCNEVEESIHEICLNCVYCKQELQRSEVYDFACYDLCIVYREGQPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                     sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                  protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69.9%; Score 580; DB 2; 71.5%; Pred. No. 1.5e-56; tive 13; Mismatches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detect benign and/or malignant human papilloma to the E6 and/or E7 region of human papilloma
                                                                                                                                     E6 polypeptide of HPV35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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RESULT 47
AEA98533
ID AEA98
XX AEA98
AC AEA98
XX O8-SE
XX O8-SE
XX Papil
KW Cance
XX Papil
KW Cance
XX Human
XX US200
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses. ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for representing immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
 US2005142541-A1
                                 Human papillomavirus;
                                                                    cancer; cervix
                                                                                  Papillomavirus
                                                                                                                                                      08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-OCT-2003; 2003WO-US031726
                                                                                                                   HPV (oncogenic
                                                                                                                                                                                      AEA98533;
                                                                                                                                                                                                                    AEA98533 standard; protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 80; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO2004030636-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AMHP ) WYETH HOLDINGS CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2004-316328/29.
DB; ADO44104.
                                                                                                                                                                                                                                                                                                        121
                                                                                                                                                                                                                                                                                                                                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tch 69.6%; al Similarity 71.5%; 108; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                        13
                                                                                                                                                                                                                                                                                                                                                                                                                                          H
                                                                                                                                                                                                                                                                                                        EKKRFHNIGGRWTGRCMSCWKP--TRRETEV 149
                                                                                                                                                                                                                                                                                                                                       KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                       GVCMKCLKFYSKISEYRWYRYSVYGETLEKQCNKQLCHLLIRCITCQKPLCPVEKQRHLE
                                                                                                                                                                                                                                                                                                                                                                                            AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                          MFQDPAERPYKLHDLCNEVEESIHEICLNCVYCKQELQRSEVYDFACYDLCIVYREGQPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFQDPQERPRKLPQLCTBLQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cassetti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ą,
                                                                                                                                                     (first entry)
                                                                  infection; virucide;
tumor; cytostatic.
                                                                                                                   strain) E6 amino acid sequence SEQ ID 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
N
                                 strain 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 578; DB 8; I
; Pred. No. 2.5e-56;
13; Mismatches 28;
                                                                                    E 6
                                                                                  protein; diagnosis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E7 polypeptides, (HPV) -associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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RESULT 48
ADF31985
ID ADF31
XX
AC ADF31
XX
T2-FE
DT 12-FE
DT 12-FE
DX
DE Human
XX
DX
Human
XX
FM human
XX
CN13E
XX
CN13E
XX
FM CN13E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC clast three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV by strains. Also included are a CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 polypeptide in a sample (comprising the presence of an oncogenic HPV E6 polypeptide in a sample (comprising a first and a second binding partner for an oncogenic HPV E6 polypeptide. CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins CC of at least three different oncogenic HPV strains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                      Human papillomavirus fusion gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                    Homo sapiens
                                                                                                                    human papillomavirus; cervix cancer
                                                                                                                                                                                          12-FEB-2004
                                                                                                                                                                                                                            ADF31985;
                                                                                                                                                                                                                                                             ADF31985 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 14; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-2003; 2003US-0532373P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2004; 2004US-00021949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (ARBO-) ARBOR VITA
                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                121 KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garman JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EKKRFHNIGGRWTGRCMSCWKP--TRRETEV
                                                                                                                                                                                                                                                                                                                                                                                                                  GVCMKCLKFYSKISEYRWYRYSVYGETLEKQCNKQLCHLLIRCITCQKPLCPVEKQRHLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MFQDPAERPYKLHDLCNEVEESIHEICLNCVYCKQELQRSEVYDPACYDLCIVYREGQPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Belmares MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69.6%;
71.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;; Score 578; DB
;; Pred. No. 2.5e
13; Mismatches
                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Somoza DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 9; I
2.5e-56;
1es 28;
                                                                                                                                                                                                                                                                                                                                                 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schweizer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                       120
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27-NOV-2002

CN1381583-A.

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ARBSULT 49
ARB98434
ID ARB98
XX ARB98
XX Z2-AU
XX Epito
XX Human
X
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Best Local Similarity
Matches 106; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to human papillomavirus E6/E7 fusion gene, its preparing process, the process for configuring the efficient expression carrier containing the gene and resultant expression carrier, the fusion protein prepared from the gene, and the application of the fusion gene and expression protein to medical science and medicine to treat cervix cancer are disclosed. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV, epitope; T cell; identification; vaccine; infection; genital wart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus E6/E7 fusion gene carrier and fusion protein vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-258260/26.
N-PSDB; ADF31984.
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                                An isolated human papilloma virus (HPV) epitope, useful in vaccines treating HPV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-2000; 2000WO-US033549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200141799-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neoplastic growth; antiviral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus protein HPV31 E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB98434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB98434 standard; protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 180 AA;
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                                                                                                                                   WPI; 2001-381497/40.
                                                                                                                                                                                                    Sette A,
                                                                                                                                                                                                                                                                                                                                           10-DEC-1999; 99US-0172705P
15-AUG-2000; 2000US-00641528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ONCO-)
                                                                                                                                                                                                                                                                       (EPIM-) EPIMMUNE INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MFQAPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVGAFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AVCDKCLKFYSKISEYRHYRYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPE
                                                                                                                                                                                                    Sidney J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fusion gene.
                                                                                                                                                                                                           Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 572; DB 7;
Pred. No. 1.5e-55;
1; Mismatches 6
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                                                                                                                                                                                                           Chesnut
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                                                                                                                                                                                                       Celis
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                                                                                                                                                                                                       Grey
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S 밁 á

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ADO44075
ID ADO44
XX ADO44
XX ADO44
XX ADO44
XX AMinc
XX B6 px
XW cervi
XW anal
XX Human
XX W0200
XX W0200
XX W0200
XX W0400
XX W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The epitopes for inclusion in an epitope-base vaccine may be selected from conserved regions of viral or tumour-associated antigens, which reduces the likelihood of escape mutants, also immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-base vaccines. An additional advantage is the ability to combine selected epitopes (CTI and HTI) and to modify the composition of the epitopes achieving enhanced immunogenicity, the major benefit of the vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent polypeptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exposure to a pathogen or immunogen, and as reagents to evaluate immune recall responses or evaluate the efficacy of a vaccine. The vaccine compositions are useful for removing warts or treating HPV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can also be used in a tetramer staining assay to assess peripheral blue mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen, and as reagents to evaluate immunogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    treatment or prophylaxis of HPV infection, in persons who have manifested symptoms e.g. genital warts or neoplastic growth. The manifest of the symptoms of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract canc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 149 AA;
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    WPI; 2004-316328/29
                                                                                        Smith L,
                                                                                                                                                                                                                                                                                    03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                  02-OCT-2003; 2003WO-US031726
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                                                                                                  Cassetti MC/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence of the E6 polypeptide of HPV31.
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Pred. No. 3.6e-50;
8; Mismatches 33;
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   New antibody composition for oncogenic strains of
                                                                                                                                                                                                                                                               23-DEC-2003;
                                                                                                                                                                                                                                                                                                                     23-DEC-2004; 2004US-00021949
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comprising a mixture of monoclonal human papilloma virus, useful for o
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Pred. No. 3.6e-50;
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RESULT 52
AEC98865
ID AEC98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC least three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins CC of at least three different oncogenic HPV strains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
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Best Local S
Matches 98
                                                            (INNO-)
(CHES/)
(NEWM/)
(MOTH/)
                                                                                                                                                              31-DEC-2003;
02-JUL-2004;
                                                                                                                                                                                                                                                                                                                                        Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                           01-DEC-2005
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               (BAKE/)
(SOUT/)
(BABE/)
                                                                                                                                                                                                                                              29-SEP-2005
                                                                                                                                                                                                                                                                            WO2005089164-A2
                                                                                                                                                                                                                                                                                                           Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                       HPV_31 Envelope protein E6
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                                                                                                                              (EPIM-)
CHEN/)
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98; Conserv
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SOUTHWOOD
BABE L M.
CHEN Y.
                                               MOTHE B.
BAKER D.
                                                                                              INNOGENETICS NV. CHESNUT R.
                                                                                                                              EPIMMUNE INC
                                                                             NEWMAN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                                                                                                                                              2003US-0533211P.
2004US-0584652P.
                                                                                                                                                                                                            2005WO-US000077
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63.0%; Score 523; DB 9;
64.9%; Pred. No. 3.6e-50;
Live 18; Mismatches 33
                                                                                                                                                                                                                                                                                                           type 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 149;
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RESULT 53
AEC96405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.EE1.214, and that CC are directly or indirectly joined to one another in the same reading CC multi-epitope construct, a polypeptide comprising an amino acid sequence cc encoded by the polynucleotide, a composition (comprising the polynucleotide, a composition (comprising the cc polynucleotide, vector or polypeptide and a carrier), a cell CC (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the colynucleotide, vector or polypeptide. The epitopes are derived from CC polynucleotide, vector or polypeptide. The epitopes are derived from CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The cepitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or colypeptide is useful in preparing a composition for inducing an immune composition for inducing an immune against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a invention.
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Matches
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(HUAN/)
(POWE/)
                                                                                                Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                    HPV protein E6 from HPV31.
                                                                                                                                                                                      01-DEC-2005
                                                                                                                                                                                                                        AEC96405
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149
29-SEP-2005
                                WO2005089164-A2
                                                                Human papillomavirus
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HUANG M T F.
POWER S D.
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Deyoung LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                             GVCTKCLRFYSKVSEFRWYRYSVYGTTLEKLTNKGICDLLIRCITCQRPLCPEEKQRHLD
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                                                                                                                                                                                    entry)
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Suang MTF,
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Power
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                                                                                                                                                                                                                                                                   construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the E1, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a defense against hypotein used to derive epitopes for the vaccine of the
                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen
                                                                                                                                                                                                                                                                 Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a new polynucleotide comprising a multi-epitope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 59; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2005-658982/67
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02-JUL-2004;
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121
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, Deyoung LM,
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                                                                                                                                                          1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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BAKER D.
SOUTHWOOD S.
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CHEN Y.
                                                                                                                                                                                                                  Similarity
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                      KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                  GVCTKCLRFYSKVSEFRWYRYSVYGTTLEKLTNKGICDLLIRCITCQRPLCPEEKQRHLD
                                                                                                                                  MFKNPAERPRKLHELSSALEIPYDELRLNCVYCKGQLTETEVLDFAFTDLTIVYRDDTPH
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                                                                                 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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 KKKRFHNIGGRWTGRCIACWR--RPRTETQV 149
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                                                                                                                                                                                                 63.0%; Score 523; DB 9; 1
64.9%; Pred. No. 3.6e-50;
Live 18; Mismatches 33;
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Power SD;
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RESULT 54
AAB98447
ID AAB98

AAB98447 standard; protein; 149

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine production. Peptides and corresponding nucleic acid compositions from the present invention are useful for stimulating an immune response to HPV by stimulating the production of CTL or HTL responses, specifically in the treatment or prophylaxis of HPV infection, in persons who have not manifested symptoms e.g. genital warts or neoplastic growth. The peptides can also be used in a tetramer staining assay to assess peripheral blood mononuclear cells for the presence of antigen-specific CTLs following exposure to a pathogen or immunogen, and as reagents to evaluate immune recall responses or evaluate the efficacy of a vaccine. The vaccine compositions are useful for removing warts or treating HPV infections. The epitopes for inclusion in an epitope-base vaccine may be selected.
                                                                                                                                                                                                                                                                                                                                         from conserved regions of viral or tumour-associated antigens, which reduces the likelihood of escape mutants, also immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of epitope-base vaccines. An additional advantage is the ability to combine selected epitopes (CTL and HTL) and to modify the composition of the epitopes achieving enhanced immunogenicity, the major benefit of the vaccine is that is safe and efficacious. AAB98391 to AAB98477 represent polypeptide sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV; epitope; T cell; identification; vaccine; infection; genital wart;
                                                                                                                                                                                                                                                                                         Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 26; 756pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      An isolated human papilloma virus (HPV) epitope, useful in vaccines treating HPV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1999; 99US-0172705P
15-AUG-2000; 2000US-00641528
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                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes an isolated prepared human papillomavirus
121
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                                                                                                                                                                                                                                   Similarity
                                                                 GICKLCLRFLSKISEYRHYNYSVYGNTLEQTVKKPLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                                           MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
LNKRFHNISGRWAGRCAACWRS--RRETAL 149
                            KKORFHNIRGRWTGRCMSCCRSSRTRRETOL 151
                                                                                        AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                        MFQDTEEKPRTLHDLCQALETTIHNIELQCVECKKPLQRSEVYDFAFADLTVVYREGNPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sidney J,
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                         B
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                                                                                                                                                                                                                62.7%; Score 520; DB 4; Length 149; 63.6%; Pred. No. 7.9e-50; tive 19; Mismatches 34; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŝ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chesnut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₽,
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RESULT 55
ADO44076
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                                                                                                                                                                                                                                                                                                        CC ADO44074 ADO44085 represent E6 polypeptides from human papillomaviruses. CC ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides. CC where the E7 polypeptide has mutations at any one or more of the amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids 20, 26 or 91 of the sequence given in CC cheer sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV) associated CC cancers, such as cervical cancer. The fusion proteins and nucleic acids cancers, such as cervical cancer. The fusion proteins and nucleic acids cancers, the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal CC tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
                                                                                                                                                                                                         Query Match
Best Local S
Matches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                             Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 79-80; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-OCT-2003; 2003WO-US031726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E6 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO44076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADO44076 standard; protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ADO44103
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121
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                                                                                                                                                                                                           96;
                                                                                                                                                                                                                             Similarity
                                                                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                     WEODPOERPRKTPOTCTETOTTHDITTECVYCKOOLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e.g. cervical
 LNKRFHNISGRWAGRCAACWRS--RRRETAL
                                KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                               GICKLCLRFLSKISEYRHYNYSVYGNTLEQTVKKPLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                  MEQDIEEKPRILHDLCQALETTIHNIELQCVECKKPLQRSEVYDFAFADLIVVYREGNPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E7 protein; fusion protein; HPV; HPV-associated cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence of the E6 polypeptide of HPV33
                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                        62.7%;
63.6%;
                                                                                                                                                                                                           19;
                                                                                                                                                                                                           Score 520; DB 8;
Pred. No. 7.9e-50;
9; Mismatches 34
                                                                                                                                                                                                           34;
                                                                                                                                                                                                                                          Length 149;
                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                             Gaps
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RRESULT 56
ARA598
AC ARA59
AC ARA59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC diagnostic kit (for detecting an HPV B5 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising the presence of an oncogenic HPV E6 protein a system for detecting the CC presence of an oncogenic HPV E6 protein a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a DDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins CC of at least three different oncogenic HPV strains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 16; 161pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-DEC-2003; 2003US-0532373P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPV (oncogenic strain) E6 amino acid sequence SEQ ID 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (ARBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody composition comprising a mixture of monoclonal oncogenic strains of human papilloma virus, useful for o
121
                                                        121 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                 96;
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                                                                                                                                                                                   AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                           MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                       GICKLCLRFLSKISEYRHYNYSVYGNTLEQTVKKPLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                                                                                                                                      MFQDTEEKPRTLHDLCQALETTIHNIELQCVECKKPLQRSEVYDFAFADLTVVYREGNPF
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                            62.7%;
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                                                                                                                                                                                                                                                                                                                                                                                 19;
                                                                                                                                                                                                                                                                                                                                                                           Score 520; DB 9;
Pred. No. 7.9e-50;
19; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Somoza DC,
                                                                                                                                                                                                                                                                                                                                                                              34; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 149;
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                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                           120
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RESULT 57 AEC96412

Best Local Similarity

Conservative

62.7%; Score 520; DB 9; 63.6%; Pred. No. 7.9e-50; tive 19; Mismatches 34

Length 149; Indels

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Gaps

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Query Match Matches

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The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (CHPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading the multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector or polypeptide and acarrier), a cell c polynucleotide, vector or polypeptide and acarrier), a cell c (comprising the polynucleotide, vector or polypeptide, inducing an c immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from CC different strains of HPV and are from the B1, E2, E6 and E7 proteins. The c epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or in the claims of the specification. The polynucleotide, vector or polypeptide in the tables referred to the claims of the specification. The polynucleotide, vector or polypeptide in the tables referred to the claims of the specification. The polynucleotide, vector or polypeptide in the claims of the specification. The polynucleotide, vector or polypeptide in the claims of the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen
                                                  polypeptide is useful in preparing a composition for inducing an immune response against human papillomavirus virus (HPV) and thus providing a defense against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the sequence is an HPV protein used to derive epitopes for the vaccine of the sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
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02-JUL-2004;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 61; 518pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2005
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BAKER D.
SOUTHWOOD S.
BABE L M.
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CHEN Y.
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INNOGENETICS NV.
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2004US-0584652P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Baker D,
Power SD;
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RESULT 58
AEC98866
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The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide and a carrier) and immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the E1, E2, E6 and E7 proteins. The
                                                                                                                                                                                      New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
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02-JUL-2004;
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                      The invention relates to an antibody composition comprising a mixtur monoclonal antibodies that specifically bind to E6 proteins of human papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least of the monoclonal antibodies specifically binds to E6 proteins of at least three different oncogenic HPV strains. Also included are a diagnostic kit (for detecting an HPV E6 polypeptide in a sample, composition above), a method of detecting an E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 protein in a sample and a system for detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against human papillomavirus virus (HPV) and thus providing a defense against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the sequence.
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                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 360; 161pp; English
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                                                                                                                                                                                                                                                                                                                                                                              diagnosing
                                                                                                                                                                                                                  a mixture of of human
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where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is an antibody that specifically binds to the E6 protein of at least three different oncogenic HPV strains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides,
                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKORFHNIRGRWTGRCMSCCRSSRTRRE 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVCKQCLRLLSKVSEYRYFNYSVYGNTLEEIVHKPLNEITIRCITCQRPLCPQEKQRHVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cassetti MC;
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                                                                                                                                                                                                                                                                                                                          Page 84-85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence of the E6 polypeptide of HPV58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cotein; fusion protein; HPV; HPV-associated cancer; immune response; lower gastrointestinal tract canc coductive system cancer; penile cancer; vulvar canc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP
                                                                                                                                                                                                                                                                                                                          101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
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Pred. No. 2.3e-47
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The invention relates to an antibody composition comprising a mixture of monoclonal antibodies that specifically bind to 86 proteins of human papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one of the monoclonal antibodies specifically binds to 86 proteins of at least three different oncogenic HPV strains. Also included are a diagnostic kit (for detecting an HPV 86 polypeptide in a sample, comprising the antibody composition above), a method of detecting an HPV 86 protein in a sample, a method of detecting the presence of an oncogenic HPV 86 protein in a sample and a system for detecting the presence of an oncogenic HPV 86 protein in a sample and a system for detecting the presence of an oncogenic HPV 86 polypeptide in a sample (comprising a first and a second binding partner for an oncogenic HPV 86 polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is an antibody that specifically binds to the 86 proteins of at least three different oncogenic HPV strains). The antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO 15; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2005-457781/46
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Pred. No. 3.9e-
20; Mismatches
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Best Local S
Matches 93
The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that
                                                              New polynucleotide comprises a multi-epitope construct comprising nuacids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                        Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     composition, kit, methods, and particularly cervical cancer.
                                                                                                                                                                                                                                                                                                                                     03-JAN-2005; 2005WO-US000077
                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus type 58
                                           Example 10; Page 349; 518pp; English
                                                                                                                                                                                                                                                                                                       31-DEC-2003; 2003US-0533211P.
02-JUL-2004; 2004US-0584652P.
                                                                                                                                                                                                                                                                                                                                                           29-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                WO2005089164-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEC98870 standard;
                                                                                                                                                                                                       (BAKE/)
(SOUT/)
(BABE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEC98870
                                                                                                                                                                                                                                        (/HTOM)
                                                                                                                                                                                                                                                                                 (EPIM-)
                                                                                                                                                               POWE/)
                                                                                                                                                                                               CHEN/)
                                                                                                                                                                                                                                                              CHES/)
                                                                                                                                                                                                                                                                         INNO-)
                                                                                                           2005-658982/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 LNKRFHNISGRWTGRCAVCWRP--RRRQTQV 149
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                                                                                                                     Deyoung I
                                                                                                                                                          MOTHE B.
BAKER D.
SOUTHWOOD S.
BABE L M.
CHEN Y.
DEYOUNG L M.
HUANG M T F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Envelope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93;
                                                                                                                                                                                                                                                  NEWMAN M J.
                                                                                                                                                                                                                                                            INNOGENETICS
CHESNUT R.
                                                                                                                                                                                                                                                                                  EPIMMUNE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVCKVCLRLLSKISEYRHYNYSLYGDTLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                          Newman MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein E6
                                                                                                                               ĽM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.8%;
                                                                                                                                                                                                                                                                         ₹
                                                                                                                              Huang
                                                                                                                               Mothe B, uang MTF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and system are useful for diagnosing er. The present sequence is an HPV E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 496; DB
Pred. No. 3.9e
20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        $
                                                                                                                               Baker
Power
                                                                                                                               SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 9;
.9e-47;
                                                                                                                                          Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 149
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                                                                                                                                          Babe
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                                                                                     nucleic
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RESULT 63
AEC96435
ID AEC96435
AC AEC96
XX AEC96
XX Humar
KW Humar
KW epitc
XX Humar
A (INNX Humar
A (INX Hum
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cc are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the completope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, a composition (comprising the polynucleotide, vector or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epicopes are derived from the coliferent strains of HPV and are from the El, E2, E6 and E7 proteins. The cepitopes may be linked via a GP-anchor/spacer peptide. The order of the cepitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune cressome against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a composition in the claims of the vaccine and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                                         (EPIM-)
(INNO-)
(CHES/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPV protein E6 from HPV58.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 149
                                                                                                                                                                                                                              (NEWM/)
                                                                                                                                                                                                                                                                                                                                                                          31-DEC-2003;
02-JUL-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          03-JAN-2005; 2005WO-US000077.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2005089164-A2
     (HUAN/
                                                           (DEYO,
                                                                                                                                           (BAKE/
                                                                                                                                                                                                       HIOM)
                                                                                         CHEN/
                                                                                                                   (BABE/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121
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MOTHE B.
BAKER D.
SOUTHWOOD S.
BABE L M.
CHEN Y.
DEYOUNG L M.
HUANG M T F.
POWER S D.
                                                                                                                                                                                                                                                                                       INNOGENETICS
                                                                                                                                                                                                                              NEWMAN M J.
                                                                                                                                                                                                                                                               CHESNUT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                          2003US-0533211P.
2004US-0584652P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ą,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 496; DB 9;
Pred. No. 3.9e-47;
0; Mismatches 36
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RESULT 64
ADO44081
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, a composition (comprising the polynucleotide, vector or polypeptide and a carrier), a cell CC (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the CC polynucleotide, vector or polypeptide. The epitopes are derived from CC different strains of HPV and are from the E1, E2, E6 and E7 proteins. The CC epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune CC defense against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a ference is an HPV protein used to derive epitopes for the vaccine of the convertion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                      Human papillomavirus type 52
                                                                                                                                                           E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
cervical cancer; immune response; lower gastrointestinal tract canc
                                                                                                                                                                                                                                                                                                                        ADO44081 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 66; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chesnut R, Newman M. Chen Y, Deyoung LM,
02-OCT-2003; 2003WO-US031726
                                   15-APR-2004
                                                                                                                                                                                                                 Amino acid
                                                                                                                                                                                                                                                   15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                          cancer; reproductive system cancer; penile cancer; vulvar cancer
                                                                                                                                                                                                                                                                                                                                                                                                                121 LNKRFHNISGRWIGRCAVCWRP--RRRQTQV 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                          KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MFQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AVCKVCLRLLSKISEVRHYNYSLYGDTLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MFQDAEEKPRTLHDLCQALETSVHBIELKCVECKKTLQRSEVYDFVFADLRIVYRDGNPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59.8%; Score 496; DB 9; ilarity 61.6%; Pred. No. 3.9e-47; Conservative 20; Mismatches 36
                                                                                                                                                                                                               sequence of the E6 polypeptide of HPV52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A,
                                                                                                                                                                                                                                                 (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        n MJ,
" Huang
                                                                                                                                                                                                                                                                                                                      protein; 148
                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mothe B,
Huang MTF,
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Power
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Southwood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>ب</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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RESULT 65
AEA98536
TX AX FX BX BX SX XX XX BX FX AX X
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADD44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and mucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, and cancer, and other cancers of the reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 148 AA;
                                            23-DEC-2004; 2004US-00021949
                                                                                                                                           Human papillomavirus; strain 52
                                                                                                                                                                           cancer; cervix tumor; cytostatic
                                                                                                                                                                                             Papillomavirus infection; virucide;
                                                                                                                                                                                                                          HPV (oncogenic strain) E6 amino acid sequence SEQ ID
                                                                                                                                                                                                                                                            08-SEP-2005
                                                                                                                                                                                                                                                                                                                            AEA98536 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 83; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-316328/29
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                                                                                                             US2005142541-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           121 KKORFHNIRGRWTGRCMSCCR 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEGDEGERERKTEGICTELGTTIHDIILECVYCKQQLLRREVYDEAFRDLCIVYRDGNEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 487; DB 8;
Pred. No. 3.9e-46;
9; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                              141
                                                                                                                                                                                              9
E
                                                                                                                                                                                             protein; diagnosis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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23-DEC-2003; 2003US-0532373P

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RESULT 66
AEC98868
ID AEC98
XX AEC98
XX O1-DE
XX HUMMAT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC monoclonal antibodies that specifically bind to E6 proteins of human C papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC least three different oncogenic HPV strains. Also included are a CC comprising the antibody composition above), a method of detecting an HPV E6 protein in a sample, a method of detecting the presence of an CC comprising the protein in a sample, a method of detecting the presence of an CC protein in a sample, a method of detecting the presence of an CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins CC of at least three different concogenic HPV E7 partner is an antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Simi
Matches 87;
                                                           31-DEC-2003; 2003US-0533211P
02-JUL-2004; 2004US-0584652P
                                                                                                                                                                                                                                                                                                                                                                                            Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                   03-JAN-2005; 2005WO-US000077
                                                                                                                                                                                                                                                                        WO2005089164-A2
                                                                                                                                                                                                                                                                                                                                Human papillomavirus type 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HPV_52 Envelope protein E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-DEC-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AEC98868
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 148 AA;
   (EPIM-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New antibody composition for oncogenic strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ARBO-) ARBOR VITA CORP.
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      EPIMMUNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANKREHNIMGRWTGRCSECWR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KKORFHNIRGRWTGRCMSCCR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GVCIMCLRFLSKISEYRHYQYSLYGKTLEERVKKPLSEITIRCIICQTPLCPEEKERHVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58.7%; >--
/ 61.7%; Pred. No. --
---ive 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Belmares MP,
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human papilloma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 487; DB 9;
Pred. No. 3.9e-46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mixture of monoclonal antibodies oma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schweizer
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RESULT 67 AEC96424

AEC96424 standard; protein;

TX 5 X F X F X B X

01-DEC-2005 HPV protein

E6 from HPV52

(first entry)

2 2 2 2

KKORFHNIRGRWTGRCMSCCR 141

ANKREHNIMGRWTGRCSECWR 141

19 19

AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD

MFEDPATRPRTLHELCEVLEESVHEIRLQCVQCKKELQRREVYKFLFTDLRIVYRDNNPY

60

GVCIMCLRFLSKISEYRHYQYSLYGKTLEERVKKPLSEITIRCIICQTPLCPEEKERHVN

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construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic Tlymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a defense against hyp infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the
                                                    Query Match
Best Local S
Matches 87
                                                                                                                          Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 10; Page 349; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2005-658982/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a new polynucleotide comprising a multi-epitope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BAKE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POWE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHEN/
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1 MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BABE L M.
CHEN Y.
DEYOUNG L M.
HUANG M T F.
POWER S D.
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BAKER D.
SOUTHWOOD S.
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Deyoung LM,
                                                                     Similarity
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NEWMAN M J.
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                                                      Conservative
                                                                                                                          AA;
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M.J.
                                                                     58.7%;
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                                                      19;
                                                    Score 487; DB 9;
Pred. No. 3.9e-46;
9; Mismatches 35
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Power SD;
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                                                                                      Length 148;
                                                      Indels
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                                                    Gaps
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Matches
                                                                                                                                                                                                                         Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynuclectide, a composition (comprising the polynuclectide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chesnut Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytocoxic Tlymphocyte (CTL) epitopes e.g., HPV16.B1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the
                                                                                                                                                                                                                                                                                               Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 64; 518pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-658982/67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-DEC-2003;
02-JUL-2004;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DEYO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHEN/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (BABE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIOM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (NEWM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHES/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polynucleotide comprises a multi-epitope construct comprising nucleic ds encoding the human papillomavirus (HPV) cytotoxic T lymphocyte b) epitopes, useful in preparing a vaccine against HPV.
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87; Conserv
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CHEN Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOUTHWOOD S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAKER D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEWMAN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHESNUT R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EPIMMUNE INC.
INNOGENETICS
                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
GVCIMCLRFLSKISEYRHYQYSLYGKTLEERVKKPLSEITIRCIICQTPLCPEEKERHVN
                                                                                               MFEDPATRPRTLHELCEVLEESVHEIRLQCVQCKKELQRREVYKFLFTDLRIVYRDNNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Newman MJ,
                                                                                                                                                                                               Conservative
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2004US-0584652P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ₩.
                                                                                                                                                                                                                       58.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , Mothe B, Huang MTF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stimulation; cytotoxic T-lymphocyte.
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                                                                                                                                                                                               19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                             Score 487; DB 9;
Pred. No. 3.9e-46;
9; Mismatches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker D,
Power SD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Southwood
                                                                                                                                                                                             35;
                                                                                                                                                                                                                                            Length 148;
                                                                                                                                                                                               Indels
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122

KQRFHNIRGRWTGRCMSCCRSSRT: | | | | | | | | | | |

63

VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121

PPNPEERPYKLPALCEEVNISIHEIELDCVYCERQLYRCEVYDFIFRDLCVVYRKGKPLG

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RESULT 68
AEA98878
ID AEA98
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                                        Matches
                                                     Query Match
Best Local
                                                                                                                                   of the monoclonal antibodies specifically binds to 86 proteins of at diagnostic kit (for detecting an HPV strains. Also included are a diagnostic kit (for detecting an HPV strains). Also included are a composition to the trains above), a method of detecting an HPV st polypeptide in a sample, a method of detecting the presence of an oncogenic HPV 86 protein in a sample and a system for detecting the presence of an oncogenic HPV st polypeptide in a sample (comprising a first and a second binding partner for an oncogenic HPV st polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is an antibody that specifically binds to the 86 proteins of at least three different oncogenic HPV strains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                        Sequence 148
                                                                                                                                                                                                                                                                                                                                                              monoclonal antibodies that specifically bind to E6 proteins papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where a
                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 359; 161pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-DEC-2003; 2003US-0532373P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus; strain 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papillomavirus infection; virucide; E6 protein; diagnosis; antibody; cancer; cervix tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HPV (oncogenic strain) E6 amino acid sequence SEQ ID 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AEA98878 standard; protein; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ARBO-) ARBOR VITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 ANKREHNIMGRWTGRCSECWR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121
                                      87;
     N
                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Garman JD,
     FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KKORFHNIRGRWTGRCMSCCR 141
                                        Conservative
                                                                                                        A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Belmares MP,
                                                     58.3%;
                                                                                                                                                                                                                                                                                                                                                                                                   an antibody composition comprising
                                      17;
                                                     Score 484; DB 9;
Pred. No. 8.4e-46;
                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schweizer J;
                                                                      Length 148;
                                        Indels
                                                                                                                                                                                                                                                                                                                                                                  where at least one
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                                                                                                                                                                                                                                                                                                                                                                                                a mixture of
                                                                                                                                                                                                                                                                                                                                                                                  of human
                                     Gaps
       61
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RESULT 69
AEA98538
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                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an antibody composition comprising a mixture of monoclonal antibodies that specifically bind to 86 proteins of human papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one of the monoclonal antibodies specifically binds to 86 proteins of at least three different oncogenic HPV strains. Also included are a diagnostic kit (for detecting an HPV E6 polypeptide in a sample, comprising the antibody composition above), a method of detecting an HPV E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 protein in a sample and a system for detecting the presence of an oncogenic HPV E6 protein and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is a PDZ domain protein and the second binding partner is a PDZ domain protein and the second binding partner is a PDZ domain protein and the Second binding partner is a PDZ domain protein and the Second binding partner is a PDZ domain protein and the Second binding partner is a PDZ domain protein and the Second binding partner is a PDZ domain protein and the Second binding partner is a PDZ domain protein and the Second binding partner is a PDZ domain protein and partner is a PDZ domain partner is
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Best Local S
Matches 89
                                                                                                                                                                                                                                                                                                                                                           Sequence 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papillomavirus cancer; cervix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AEA98538 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-457781/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lu PS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2003; 2003US-0532373P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-DEC-2004; 2004US-00021949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2005142541-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus; strain 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPV (oncogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AEA98538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 19; 161pp; English
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                                                                                                                                                                                           N
                                                                                                                                                                                                               1 MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                                                                                                                                                                                                                                                               ; 68
                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Garman JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARBOR VITA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NKRFHQIADQWTGRCTQCWRPSAT 146
                                                                                                                                            AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                        EKKRFHQIAEQWTGRCTRCWRPSAT 146
                                                       KKORFHNIRGRWTGRCMSCCRSSRT 145
                                                                                                        GVCQPCLKFYSKIREYRRYRQSVYGTTLENLTNKQLCNILIRCGKCQKPLCPLEKQKHVD
                                                                                                                                                                                        LFPNSEERPYKLQALCDEVNISIHDINLDCVFCQRGLYRSEVYDFAFSDLCIVYRKDKPY
                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection; virucide; E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            strain) E6 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein; 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Belmares MP,
                                                                                                                                                                                                                                                                           58.2%; Score 483; DB 9; 61.4%; Pred. No. 1.1e-45; tive 16; Mismatches 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein; diagnosis;
                                                                                                                                                                                                                                                                               40;
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                                                                                                                                                                                                                                                                                                                   Length 148;
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ADO44085
ID ADO4
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AC ADO4
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DT 15-3
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RESULT 70
RAR97563
ID AAR97563
AC AAR97
AC AVAR
AAR97563
ID 27-AU
AC AVAR
AAR97
AC AVAR
CC PAC AVAR
CC PEFE
CC PEFE
CC COF CT
CC AUG-C
XX
SA Seque
SQ Seque
RESULT 71
                                                                                                                                                                                Matches
                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                            A variant of the human papilloma virus (HPV) E6 or E7 protein which elicits a humoral and/or cellular immune response against HPV can be used in vaccines against HPV or to treat HPV infection. The variant is preferably a deletion mutant comprising at least half, and preferably two thirds of full length E6 or E7 protein starting from the N- or C-terminal, or is a full length E6 molety fused to a full length E7 molety. The variant optionally has a linkage molety and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This sequence is a fusion protein of the C-terminal end of E7 and the N-terminal end of E6. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-AUG-2003
11-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR97563;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR97563 standard; protein; 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 3; Page 18; 37pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vaccine variants of human papilloma virus antigens - contain variants of E6 and/or E7 protein, pref. deletion mutants, and are used to treat or prevent HPV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1996-309518/31.
N-PSDB; AAT31835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Edwards SJ, Cox J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-JUN-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papilloma virus E6/E7 protein variant
                                                                                                                                                                                                                                                 Sequence 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-DEC-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20-DEC-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     humoral immune response; cellular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papilloma virus; E6; E7; deletion mutant; HPV; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CSLC-) CSL LTD.
(UYQU ) UNIV QUEENSLAND.
                                                                                 19
                                                                                                                  77
                                                                                                                                                                                  66;
                                                                                                                                  1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                  Similarity
                                                                     AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYN 93
                                                                                                                  MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 136
                                                  AVCDKCLKFYSKISEYRHYCYSLYGTTLRSHHH 169
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                  AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (revised)
(first entry)
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                                                                                                                                                                                                  57.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                                                                                                    ω
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                                                                                                                                                                                                  Score 478; DB 2;
Pred. No. 4.8e-45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Frazer
                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immune response; vaccine
                                                                                                                                                                                                                Length 172;
                                                                                                                                                                                    Indels
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                                                                                                                                                                                    Gaps
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ADO44085; 15-JUL-2004

(first entry)

ADO44085 standard;

protein; 158

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RESULT 72
AEA98880
ID AEA98
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AC AEA98
XX
DT 08-SE
XX
DE HPV (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses. C2 ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E8 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and nucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                08-SEP-2005
                                                              AEA98880;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                             AEA98880 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 85-86; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2003; 2003WO-US031726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type 68.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AMHP ) WYETH HOLDINGS CORP
                                                                                                                                                                               123
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                                                                                                                                                                                                             121
                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acid
                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                             μ
                                                                                                                                                                                                                                                                                                                                                                            86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                             TKRRLHKIAGNFTGQCRHCWTSKREDRRRIRQETQV 158
                                                                                                                                                                                                                                                                                                                            MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                                                            KKORFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                                                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                         AACQSCIKFYAKIRELRYYSESVYATTLETITNTKLYNLLIRCMSCLKPLCPAEKLRHLT
                                                                                                                                                                                                                                                                                                         LFHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFSDLCVVYRDGVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cassetti MC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence
                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                         56.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the
                                                                                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u> 1</u>
                                                                                                                                                                                                                                                                                                                                                                                      Score 468.5; DB Pred. No. 5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polypeptide of HPV68
                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       DB 8;
                                                                                                                                                                                                                                                                                                                                                                          42;
                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7 polypeptides, (HPV)-associated
                                                                                                                                                                                                                                                                                                                                                                                                          158;
                                                                                                                                                                                                                                                                                                                                                                          5.
                                                                                                                                                                                                                                                                                                           62
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HPV (oncogenic strain) E6 amino acid sequence SEQ ID 361.

SEXEEXER

27-AUG-2003 11-JAN-1997

(revised) (first entry)

AAR97562

standard; protein;

172

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Human papilloma virus E6/E7 protein variant.

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RESULT 73
AAR97562
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic kit (for detecting an HPV E6 polypeptide in a sample, comprising the antibody composition above), a method of detecting an HP E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 protein in a sample and a system for detecting the presence of an oncogenic HPV E6 polypeptide in a sample (comprising a first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second binding partner is a PDZ domain protein and the E6 protein of at least three different oncogenic HPV strains). The antibody composition, kit, methods, and system are useful for diagnosing cancer, particularly cervical cancer. The present sequence is an HPV E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least of the monoclonal antibodies specifically binds to E6 proteins of at least three different oncogenic HPV strains. Also included are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an antibody composition comprising monoclonal antibodies that specifically bind to E6 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 361; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-DEC-2003; 2003US-0532373P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23-DEC-2004; 2004US-00021949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2005142541-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Papillomavirus infection; virucide; cancer; cervix tumor; cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (ARBO-) ARBOR VITA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JUN-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                               64
                                                                                                                                                                                                                                                                                 62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                           2 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garman JD,
                                                                                                                                                                                                                               ACQKCIKFHAKVRELRHYSNSVYATTLESITNTKLYNLSIRCMSCLKPLCPAEKLRHVNT 123
                                                                                                              KRRFHQIAGSYTGQCRHCWTSNREDRRRIRRETQV 158
                                                                                                                                                                   KORFHNIRGRWTGRCMSCCRSS----RTRRETOL 151
                                                                                                                                                                                                                                                                                                                                       FPNPAERPYKLPDLCTALDTTLHDITIDCVYCKTQLQQTEVYEFAFSDLFIVYRNGEPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 468.5; DB 9; Pred. No. 5e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΜP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Somoza DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9<u>8</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   composition comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein; diagnosis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Schweizer
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             where at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ن</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E6 proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 74
AD044080
ID AD044
XX AD044
XX AD044
XX AD044
XX AD041
XX E6 PI
KW E6 PI
KW E6 PI
KW Cervi
KW Anal
XX
Humar
XX
PN W0200
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elicite a humoral and/or cellular immune response against HPV can be used in vaccines against HPV or to treat HPV infection. The variant is preferably a deletion mutant comprising at least half, and preferably two thirds of full length E6 or E7 protein starting from the N- or C- terminal, or is a full length E6 moiety fused to a full length E7 moiety. The variant optionally has a linkage moiety and a foreign protein or peptide which facilitates the purification of, and enhances the immunogenicity of, the fusion protein. This is a fusion protein of the C-terminal end of E6 and the N-terminal end of E7. The protein is also a delicition where the purification of the C-terminal end of E6 and the N-terminal end of E7. The protein is also a delicition where the protein is also a delicition where the protein is also a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papilloma virus; E6; humoral immune response; ce
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 172 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A variant of the human papilloma virus (HPV) E6 or E7 protein which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 3; Page 17; 37pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vaccine variants of human poses and/or E7 protein, pref. prevent HPV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1996-309518/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-DEC-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO9619496-A1
                                                                           E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancer; anal cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                             15-JUL-2004
                                                Human papillomavirus
                                                                                                                                                Amino
                                                                                                                                                                                                                                           ADO44080 standard; protein; 151
                                                                                                                                                                                                                                                                                                                                                 111 CPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                        87;
                                                                                                                                              acid
                                                                                                                                                                                                                                                                                                                           56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UNIV QUEENSLAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT31834.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant generated from the sequence described in AAT31833. on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                                                                                                      GNPYAVCDKCLKFYSKISEYRHYCYSLYGTTLEQQINCQKPYNKPLCDLLIRC------
                                                                                                                                                                                                                                                                                                                                                                                                                   GNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQ------YNKPLCDLLIRCINXQKPL
                                                                                                                                                                                                                                                                                                                          CPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                              sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cox J,
                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94AU-00000157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Webb
                                               type 51
                                                                                                                                              of the E6 polypeptide of HPV51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; E7; deletion mutant; HPV; immune response; cellular immune response; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             papilloma virus antigens - contain variants of f. deletion mutants, and are used to treat or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 468; DB 2;
Pred. No. 6.3e-44;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Frazer I;
                                                                                                                                                                                                                                                ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 172;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           12;
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RESULT 75
AEA98543
ID AEA98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AD044074 AD044085 represent E6 polypeptides from human papillomaviruses. CC AD044098 is the consensus sequence derived from these polypeptides. The CS specification describes human papillomavirus E6 and E7 polypeptides, CC where the E7 polypeptide has mutations at any one or more of the amino acids 24, 26 or 91 of the sequence given in CC AD044073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of CC one or more of the amino acids corresponding to amino acids 63 or 106 of CC there sequence given in AD044072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV) associated CC cancers, such as cervical cancer. The fusion proteins are useful for generating immune responses CC encoding the fusion proteins are useful for generating immune responses CC cagainst HPV. They are also useful for treating lower gastrointestinal CC tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide comprising human papillomavirus E6 and useful for treating or preventing human papillomavirus cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           02-OCT-2003; 2003WO-US031726
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 82; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smith L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-OCT-2002; 2002US-0415929P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (AMHP ) WYETH HOLDINGS CORP
23-DEC-2004; 2004US-00021949
                              30-JUN-2005
                                                                                                                                     Papillomavirus
                                                                                                                                                                   HPV (oncogenic
                                                                                                                                                                                                 08-SEP-2005
                                                                                                                                                                                                                                                              AEA98543 standard;
                                                            US2005142541-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2004-316328/29.
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                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                61
                                                                                        papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEODEOEREKTEOTCIETOTTIHDIILECVYCKQQLLKREVYDEAFRDLCIVYRDGNEY
                                                                                                                                                                                                                                                                                                                                                                  KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                            AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                           EKKRÉHEÍAGRWTGQCANCWQRTRQRNETQV
                                                                                                                                                                                                                                                                                                                                                                                                 AVCKQCLLFYSKIREYRRYSRSVYGTTLEAITKKSLYDLSIRCHRCQRPLGPEEKQKLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cassetti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
K
                                                                                                                                                                                                 (first entry)
                                                                                                                                     infection; virucide;
                                                                                                                                                                   strain) E6 amino acid sequence SEQ ID 24
                                                                                                                        tumor;
                                                                                                                                                                                                                                                              protein; 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55.4%;
                                                                                          strain 51
                                                                                                                       cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 460; DB 8;
Pred. No. 4.2e-43;
                                                                                                                                        E
E
                                                                                                                                        protein; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                        151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E7 polypeptides, (HPV)-associated
                                                                                                                                           antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>.</u>.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60
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ARESULT 76
AD044079
ID AD044
XX AD044
XX AD044
XX AD15-JU
DT 15-JU
DX Amino
XX E6 pr
KW cervi
KW anal
XX AD040
XX Human
XX W0200
XX W0200
XX XX Y02-OC
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 polypeptide in a sample (comprising the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins of at least three different oncogenic HPV E7 and the second CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
            02-OCT-2003; 2003WO-US031726
                                          15-APR-2004.
                                                                                                 Human papillomavirus type
                                                                                                                                               cervical cancer;
                                                                                                                                                         E6 protein;
                                                                                                                                                                                        Amino acid
                                                                                                                                                                                                                     15-JUL-2004
                                                                                                                                                                                                                                              ADO44079;
                                                                                                                                                                                                                                                                          ADO44079 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 24; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New antibody composition comprising a mixture of monoclonal antibodies for oncogenic strains of human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-2003; 2003US-0532373P
                                                                                                                              cancer;
                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                                                                                                                                                                                                 121
                                                                                                                                                                                                                                                                                                                                                                                                             61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garman JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ARBOR VITA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KKORFHNIRGRWTGRCMSCCRSSRTRRETOL 151
                                                                                                                                                                                                                                                                                                                                                   EKKRFHEIAGRWTGQCANCWQRTRQRNETQV 151
                                                                                                                                                                                                                                                                                                                                                                                                             AVCKQCLLFYSKIREYRRYSRSVYGTTLEAITKKSLYDLSIRCHRCQRPLGPEEKQKLVD
                                                                                                                                                                                                                                                                                                                                                                                                                                    AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                        E7 protein;
                                                                                                                                                                                     sequence of the E6 polypeptide of HPV45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                         E7 protein; fusion protein; HPV; HPV-associated cancer; cer; immune response; lower gastrointestinal tract cancer; reproductive system cancer; penile cancer; vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       $
                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Belmares MP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%; Score 460; DB 9; 57.0%; Pred. No. 4.2e-43; tive 24; Mismatches 41
                                                                                                    45
                                                                                                                                                                                                                                                                             158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Somoza DC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schweizer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                           120
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             XX FX FX BX SX RX FX FX RX
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63 61

Human papillomavirus;

strain 45

(ARBO-) ARBOR VITA CORP 23-DEC-2003; 2003US-0532373P 23-DEC-2004; 30-JUN-2005 US2005142541-A1

2004US-00021949

Papillomavirus infection; virucide; cancer; cervix tumor; cytostatic.

93

protein; diagnosis; antibody;

HPV (oncogenic strain) E6 amino acid sequence SEQ ID

08-SEP-2005 AEA98548;

(first entry

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RESULT 77
AEA98548
ID AEA98
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                                                                                                                                                                                                                                                                                                                                                               CC AD044074-AD044085 represent E6 polypeptides from human papillomaviruses.
CC AD044098 is the consensus sequence derived from these polypeptides. The grecification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino cc acids corresponding to amino acids 24, 26 or 91 of the sequence given in CC AD044073 and the E6 polypeptide has no mutations or has mutations at any cone or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in AD044072 The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated CC cancers, such as cervical cancer. The fusion proteins and nucleic acids CC encoding the fusion proteins are useful for generating immune responses CC against HPV. They are also useful for treating lower gastrointestinal CC tract cancers, e.g. anal cancer, and other cancers of the reproductive system, including penile and vulvar cancers.
                                                                                                                                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                             Sequence
AEA98548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 81-82; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide comprising human papillomavirus E6 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2002; 2002US-0415929P
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                                                                                                                      122
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                                                                                                                                                        64 ACHKCIDFYSRİRELRYYSNSVYGETLEKITNTELYNLLIRCLRCQKPLNPAEKRRHLKD 123
                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                             87;
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                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AD044106.
                                                                                                                                                                                                                                                                                                                                                               158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or treating or e.g. cervical
                                                                                                                                                                            VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                             FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
standard; protein; 158
                                                                                                                      KORFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                            FDDPKQRPYKLPDLCTELNTSLQDVSIACVYCKATLERTEVYQFAFKDLCIVYRDCIAYA
                                                                                     KRRFHSIAGQYRGQCNTCCDQARQERLRRRRETQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cassetti
                                                                                                                                                                                                                                                                                             Conservative
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ਨ
                                                                                                                                                                                                                                                                                                          56.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preventing human papillomavirus (HPV)-associated cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORP.
                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                            Score 459.5; DB 8
Pred. No. 5.1e-43;
2; Mismatches 41
                                                                                                                                                                                                                                                                                                                            DB 8;
                                                                                     158
                                                                                                                                                                                                                                                                                             41;
                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                               158;
                                                                                                                                                                                                                                                                                            5
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RESULT 78
AEC98867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC least three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV E6 protein in a sample, a method of detecting the presence of an CC oncogenic HPV E6 protein in a sample and a system for detecting the presence of an CC oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide. CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins CC of at least three different concogenic HPV E7 and the second CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
   PRESENTATION OF THE PRESEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         용
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Best Local &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ę
                                                                                                                                                                                                                                                                                                          WO2005089164-A2
                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                         Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2005
                                                                                     31-DEC-2003; 2003US-0533211P
02-JUL-2004; 2004US-0584652P
                                                                                                                                                                              03-JAN-2005; 2005WO-US000077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEC98867 standard; protein; 158 AA.
(EPIM-) EPIMMUNE INC. (INNO-) INNOGENETICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACHKCIDFYSRIRELRYYSNSVYGETLEKITNTELYNLLIRCLRCQKPLNPAEKRRHLKD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRRFHSIAGOYRGOCNTCCDQARQERLRRRETOV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FDDPKQRPYKLPDLCTELNTSLQDVSIACVYCKATLERTEVYQFAFKDLCIVYRDCIAYA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            55.4%; Score 459.5; DB 9
56.1%; Pred. No. 5.1e-43;
tive 22; Mismatches 41
   ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    an antibody composition comprising a mixture of at specifically bind to E6 proteins of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comprising a mixture o human papilloma virus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ą,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of monoclonal antibodies
s, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schweizer
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AAR63866 ID AAR

AAR63866 standard;

protein;

RESULT 79

XXXPPPXX

16-OCT-2003 25-MAR-2003

(revised)

(first entry)

AAR63866;

28-JUN-1995 HPV18 E6/E7

proteins

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                                                                                                                                                                                                                                                                                                          The invention relates to a new polynucleotide comprising a multi-epitope CC construct comprising nucleic acids encoding the human papillomavirus CC (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and that CC are directly or indirectly joined to one another in the same reading CC frame, a vaccine minigene. Also included are a vector comprising the CC multi-epitope construct, a polypeptide comprising an amino acid sequence ce encoded by the polynucleotide, a composition (comprising the CC polynucleotide, vector and/or polypeptide and a carrier), a cell CC comprising the polynucleotide, vector or polypeptide, inducing an CC immune response against human papillomavirus virus (HPV) and making the CC epitopes may be linked via a GP-anchor/spacer peptide. The crited from CC epitopes may be linked via a GP-anchor/spacer peptide. The crited to comprising the specification. The polynucleotide, vector or polypeptide in the tables referred to in the claims of the specification. The polynucleotide, vector or composition for inducing an immune cesponse against human papillomavirus virus (HPV) and thus providing a defense against human papillomavirus virus (HPV) and thus providing a composition of the present sequence is an HPV infection and HPV-related cancers. The present in the vaccine of the convertion of the vaccine of the convertion.
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                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CHES/)
(NEWM/)
(MOTH/)
(BAKE/)
(SOUT/)
                                                                                                                                                                                                                                                                Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 10; Page 349; 518pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-658982/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUAN/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DEYO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHEN/
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                                                                                                                                                                                                                   Local
                               122 KORFHNIRGRWTGRCMSCCRSS----RTRRETOL 151
                                                                 64 ACHKCIDFYSRIRELRYYSNSVYGETLEKITNTELYNLLIRCLRCQKPLNPAEKRRHLKD
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NEWMAN M J.
MOTHE B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R, Newman MJ,
Deyoung LM,
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HUANG M T
POWER S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BABE L M.
CHEN Y.
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BAKER D.
                                                                                                                                                                                                                   Similarity
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                                                                                            VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                  FDDPKQRPYKLPDLCTELNTSLQDVSIACVYCKATLERTEVYQFAFKDLCIVYRDCIAYA
                                                                                                                                                        FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
KRRFHSIAGQYRGQCNTCCDQARQERLRRREETQV
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                                                                                                                                                                                                                  55.4%; Score 459.5; DB 9 56.1%; Pred. No. 5.1e-43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mothe
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Power
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                                                                                                                                                                                                                                 Length 158;
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RESULT 80
AAR79656
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Best Local (
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            13-JUL-1995
                                                                               Ubiquitin-conjugating enzyme; HPV-18 E6 protein; cell proliferation; cancer; psoriasis; fibrosis.
                                                                                                                    HPV-18 E6
                                                                                                                                         25-MAR-2003
06-DEC-1995
                                                                                                                                                                                                 AAR79656 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 27-28; 79pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papilloma virus detection assay - by amplification using self sustained sequence replication and hybridisation with a detector pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-NOV-1994.
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                                                        sapiens
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                                                                                                                                                                                                                                                                                                                       VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK
                                                                                                                                                                                                                                                            KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV
                                                                                                                                                                                                                                                                                  KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                                         ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                                                                                                                                                                                                                                                                      FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
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                                                                                                                   protein.
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(first en
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                                                                                                                                                                                                 protein;
                                                                                                                                          entry)
                                                                                                                                                                                                                                                                                                                                                                                                               54.9%; Score 455.5; DB 2
56.1%; Pred. No. 1.4e-42;
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                                                                                                                                                                                                                                                            158
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XX UDiqu
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23-MAY-1994;
27-MAY-1994;
13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HPV-18 E6 cDNA (given in AAQ97848) was amplified from a HeIa cell cDNA library using the primers given in AAQ97846-47. The gene was subcloned into a baculovirus vector for expression of recombinant E6 in Sf9 insect cells for use as a component of an in vitro ubiquitin conjugating system. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                                                                                                                                                                                   Ubiquitin conjugating enzyme; UbCE; ubiquitin-mediated proteolysis; cell-cycle regulatory protein; ubiquitination inhibitor; atherosclerosis; proliferative disorder; cancer; restenosis; tissue connective disorder; wound healing; fibrosis disorder; rheumatoid arthritis; scleroderma; insulin dependent diabetes mellitus; glomerulonephritis; cirrhosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying inhibitors of ubiquitin mediated proteolysis of cell cycle regulatory proteins - also new ubiquitin conjugating enzymes, their related nucleic acid, vectors, antibodies etc., useful for regulating e.g. cell proliferation.
04-JAN-1994;
23-MAY-1994;
                                                                                                                                                                                                                                                                                               diagnosis; therapy; E6.
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                                                                                                                                   19-OCT-1999
                                                                                                                                                                                                                                          Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPV-18 E6 protein sequence.
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DB; AAQ97848.
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87; Conserv
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94US-00247904.
94US-00250795.
94US-00305520.
  94US-00176937.
94US-00247904.
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56.1%;
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ARBOJIT 82
AABOJ176
ID AABOJ
XX AABOJ
XX AABOJ
XX AABOJ
XX I2-SE
DT 12-SE
DT 23-OC
XX HPV-1
XX HPV-1
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XW cell
XW HPV-1
XW HPV-1
XW HPV-1
XW HPV-1
XW WOUND
XX HUMAN
XX US606
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 level of ubiquitination. The ubiquitin-conjugating system comprises: (a) a reconstituted protein mixture including a ubiquitin conjugating enzyme (UDCE) produced by the expression of a nucleic acid which hybridizes under high stringency conditions to human UDCE, Candida albicans UDCE, or Schizosaccharomyces pombe UDCE coding sequences; (b) a regulatory protein; and (c) ubiquitin. The polymucleotides are useful for identifying ubiquitination inhibitors. The polymucleotides, on polypeptides, antisense compounds and antibodies against them may also be useful for the treatment and/or diagnosis of proliferative disorders (e.g. cancer, atherosclerosis, or restenosis) tissue connective disorders, controlling wound healing, and disorders characterized by fibrosis (e.g. rheumatoid arthritis, insulin dependent diabetes mellitus, glomerulonephritis,
                                                                  HPV-18 E6; ubiquitin mediated proteolysis; human; cellular protein half life; ubiquitination inhibitor; p53; cyclin; cell cycle regulator; myc deregulation; human papillomavirus; cell cycle regulator; myc deregulation; human papillomavirus; HPV-18 E6 protein; cervical cancer; skin cancer; epidermal hyperplasia; epidermal neoplasia; psoriasis; connective tissue disorder; wound healing; cytostatic; antiproliferative; anticancer; antipsoriatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cirrhosis, and scleroderma)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence is the human papillomavirus E6 protein. The invention relates to assays for identifying an inhibitor of ubiquitin-mediated proteolysis of a cell-cycle regulatory protein comprising contacting a candidate agent with an ubiquitin-conjugating system and measuring the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-590402/50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-1994;
13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Identifying ubiquitination inhibitors using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (-OTIM)
                                                                                                                                                                                                                                12-SEP-2003
23-OCT-2000
                                   Human papillomavirus; 18
                                                                                                                                                                                                                                                                                     AAB03176
                                                                                                                                                                                                                                                                                                                        AAB03176 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                               124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQRFHNIRGRWTGRCMSCCRSSR----TRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                                                                                                                                                               KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158
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                                                                                                                                                                                               protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                  (revised)
(first en
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94US-00305520.
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                                                                                                                                                                                                                                  entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 455.5; DB 2
Pred. No. 1.4e-42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                novel ubiquitin conjugating
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64

ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE

151

VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121 FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA

4

87;

Conservative

21;

Mismatches

42;

Indels

<u>ن</u>

63

Similarity

122 KQRFHNIRGRWTGRCMSCCRSSR-----TRRETQL

KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV

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cc ubiquitin-mediated proteolysis of a cell cycle regulatory protein capent. The eukaryotic cells is engineered eukaryotic cell with a candidate capent. The eukaryotic cells is engineered to express a recombinant human, candida albicans or Schizosaccharomyces pombe ubiquitin. Conjugating cenzyme (AAB03199-B03171), a cell cycle regulatory protein (such as p53) cand ubiquitin. The specification also discloses novel Candida albicans cell cycle regulatory protein (such as p53) cand chizosaccharomyces pombe ubiquitin conjugating capymes, hubcE and rapUBC (AAB03171), and two novel human ubiquitin-conjugating enzymes, caubCE and spUbCE (AAB03170, AAB03171), and two novel human ubiquitin-conjugating controlled cell degradation of intracellular proteins in eukaryotic cells. In particular, this system controlling the lavels of proteins involved in cell cycle important in controlling the lavels of proteins involved in cell cycle progression. Alterations in the development of cancers. For example, human cell cycle progression. Alterations in the development of cancers. For example, human capabillomaviruses such as HPV-18 encode a transforming protein. E6 (AAB03176), which combines with a cellular E6-associated protein (E6-AP; (AAB03177)) to stimulate the ubiquitination of p53, thus targetting it for connective tissue disorders and for controlling the wound healing connective tissue disorders and for controlling the wound healing conditions such as psoriasis, neoplastic epidermal conditions, skin cancers e.g., basal cell carcinomas, squamous cell carcinomas. The cells and cause apoptosis to occur. Inhibitors of balance of transformed cells and cause apoptosis to occur. Inhibitors of ubiquitin-cordinated degradation of cyclins are useful as antiproliferative agents. The present sequence represents HPV-18 E6 protein. (Updated on 12-SEP-2003 to standardise OS field)
Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-MAY-1994;
13-SEP-1994;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-JAN-1994;
23-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method of identifying ubiquitin-mediated proteolysis of a cell cycle re
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Col 97-100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chiu MI,
                                                                            Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identifying an inhibitor of ubiquitin mediated proteolysis of regulatory protein for treating cancers involves measuring ubiquitination levels of the protein in the presence of candidate agent in an eukaryotic cell.
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94US-00247904.
94US-00250795.
94US-00305520.
95US-00486663.
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                  54.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Berlin
                    Score 455.5; DB 3
Pred. No. 1.4e-42;
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                                       DB 3;
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                                       Length 158;
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                                                                                                                                                                                                                                                 CC treatment of prophylaxis of HPV infection, in persons who have not CC manifested symptoms e.g. genital warts or neoplastic growth. The peptides CC can also be used in a tetramer staining assay to assess peripheral blood CC mononuclear cells for the presence of antigen-specific CTLs following CC exposure to a pathogen or immunogen, and as reagents to evaluate immune CC recall responses or evaluate the efficacy of a vaccine. The vaccine CC compositions are useful for removing warts or treating HPV infections. CC The epitopes for inclusion in an epitope-base vaccine may be selected CC from conserved regions of viral or tumour-associated antigens, which CC reduces the likelihood of escape mutants, also immunosuppressive epitopes that may be present in whole antigens can be avoided with the use of CC epitope-base vaccines. An additional advantage is the ability to combine CC epitopes achieving enhanced immunogenicity, the major benefit of the CC vaccine is that is safe and efficacious. AAB99391 to AAB9477 represent construction of the present construction of the present construction of the present construction.
                                                                                                                                                 Query Match
Best Local :
                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes an isolated prepared human papillomavirus (HPV) epitope (I). (I) has antiviral activity, and can be used in vaccine production. Peptides and corresponding nucleic acid compositions from the present invention are useful for stimulating an immune response to HPV by stimulating the production of CTL or HTL responses, specifically in the
                                                                                                                                                                                                       Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 22; 756pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            An isolated human papilloma virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-381497/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sette A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-DEC-1999; 99US-0172705P.
15-AUG-2000; 2000US-00641528.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus; human leukocyte antigen; HLA; immune response; HPV; epitope; T cell; identification; vaccine; infection; genital wart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus protein HPV18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-DEC-2000; 2000WO-US033549.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neoplastic growth; antiviral.
                       62
                                                                                                                                87;
                                                         4
                                                                                                                                                   Similarity
VXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HPV infections
                                                       FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIFHA
                                                                                          FODPOERPRKLPOLCTELOTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                              54.9%; Score 455.5; DB 4;
56.1%; Pred. No. 1.4e-42;
tive 21; Mismatches 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          epitope, useful in vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celis
                                                                                                                              Indels
                                                                                                                                                               Length 158;
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                                                                                                                            Gaps
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62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEBKQRHLDK 121

ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE

FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA

64

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Matches Query Match Best Local (

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l Similarity 87; Conserv

Conservative

21;

Score 455.5; DB 8; Pred. No. 1.4e-42; 1; Mismatches 42;

Indels Length

Gaps

61 63

158; S

54.9%;

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RESULT 84
ADO44074
ID ADO44
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                                                  ADO44074-ADO44085 represent E6 polypeptides from human papillomaviruses. ADO44098 is the consensus sequence derived from these polypeptides. The specification describes human papillomavirus E6 and E7 polypeptides, where the E7 polypeptide has mutations at any one or more of the amino acids corresponding to amino acids 24, 26 or 91 of the sequence given in ADO44073 and the E6 polypeptide has no mutations or has mutations at any one or more of the amino acids corresponding to amino acids 63 or 106 of there sequence given in ADO44072. The polypeptides of the invention are useful for treating or preventing human papillomavirus (HPV)-associated cancers, such as cervical cancer. The fusion proteins and mucleic acids encoding the fusion proteins are useful for generating immune responses against HPV. They are also useful for treating lower gastrointestinal tract cancers, e.g. anal cancer, and other cancers of the reproductive
Sequence 158 AA;
                                      system,
                                                                                                                                                                                                                                                                                                                                Disclosure; Page 78; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                  cancers, e.g. cervical cancer.
                                                                                                                                                                                                                                                                                                                                                                                      New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-OCT-2003; 2003WO-US031726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervical cancer; immune response; lower gastrointestinal tract cancer, anal cancer; reproductive system cancer; penile cancer; vulvar cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-JUL-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2004-316328/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-OCT-2002; 2002US-0415929P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO44074 standard; protein; 158 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                    including penile and vulvar cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cassetti MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence of the E6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              polypeptide of HPV18
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151

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124 KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158

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RESULT 85
AEA98547
ID AEA98
XX AEA98
XX AEA98
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                                                                                           밁
                                                                                                                                                                                                                                                                          5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC class three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 protein as a system for detecting the CC presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, CC where the first binding partner is a DDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins of at least three different oncogenic HPV strains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New antibody composition for oncogenic strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lu PS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; cervix
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 28; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papillomavirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
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                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Garman JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KQRFHNIRGRWTGRCMSCCRSSR----TRRETQL
KQRFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                           ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158
                                                                                                                                                    VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                    FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                             FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection; virucide; E6 protein; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                  56.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising a mixture of monoclonal antibodies human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                         Score 455.5; DB 9
Pred. No. 1.4e-42;
1; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ξ
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                                                                                                                                                                                                                                                                                                                                            42;
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                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                                                                                                                                                                                                                                                                                                                        158;
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ARBSULT 86
ARBI1993
JID ARBI1193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC The invention relates to a method of producing a synthetic protein CC comprising an amino acid sequence that is at least 80% identical to a CC naturally occurring antigenic protein of a pathogen or tumor comprising CC chemically synthesizing two or more fragments, chemically ligating the C-cterminus of a fragment to the N-terminus of a neighboring fragment to comproduce the synthetic protein or its part and optionally repeating the C-cterminus of step to sequentially ligate a further neighboring fragment to obtained from the second step. The invention also relates to a composition comprising the protein and a method for treating or CC preventing human papillomavirus (HPV) associated disease by administering CC to the subject the protein or composition in a therapeutically effective amount. In producing a synthetic protein, the neighboring non-overlapping CC residues. The naturally occurring protein, the neighboring non-overlapping CC residues. The naturally occurring protein is an HPV protein e.g. E2, E6 CC residues. The naturally occurring protein is an HPV protein, e.g. E2, E6 CC residues. The naturally occurring protein is an HPV subscition is useful as a coccine for preventing or treating HPV associated disease, such as a confert. This sequence represents an HPV18 E6 protein used in the method conference in the invention.
                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                                                                                                                       Matches
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cancer; HPV18 E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing a synthetic protein of a pathogen or tumor comprises chemically synthesizing two or more fragments of 2-80 contiguous amino acids of sequence, the sequence of two or more fragments are neighboring and non-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-DEC-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPV18 E6
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention
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                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                              FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                            VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                   FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                       54.9%;
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                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                       Score 455.5; DB 9;
Pred. No. 1.4e-42;
1; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                       Length 158;
                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                       Gaps
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122

KORFHNIRGRWIGRCMSCCRSSR----TRRETQL 151

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       multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E6 and E7 proceins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the
                                                                                                                                                                                                                The invention relates to a new polynucleotide comprising a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.B1.214, and that are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the
                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2005-658982/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus type 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HPV_18 Envelope
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AEC98864 standard; protein; 158 AA.
                                                                                                                                                                                                                                                                                                          Example 10; Page 349; 518pp; English.
                                                                                                                                                                                                                                                                                                                                      New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHEN/)
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02-JUL-2004;
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                                                                                                                                                                                                                                                                                                                                                                     polynucleotide
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HUANG M T F.
POWER S D.
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SOUTHWOOD S.
BABE L M.
CHEN Y.
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2004US-0584652P.
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Power
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RESULT 88
AEC96398
AID AEC96
XX AEC96
XX AEC96
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KW Epitc
XX Human
XX Epit
PN W0200
XX Human
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                                                                                                                                                                                                                                                                                                                                    Chesnut Chen Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 158
construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes e.g., HPV16.E1.214, and t are directly or indirectly joined to one another in the same reading frame, a vaccine minigene. Also included are a vector comprising the
                                                                                                                                                                                     New polynucleotide comprises a multi-epitope construct comprising nucleic acids encoding the human papillomavirus (HPV) cytotoxic T lymphocyte (CTL) epitopes, useful in preparing a vaccine against HPV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papilloma virus infection; virucide; cancer; cytostatic; vaccine; epitope mapping; immune stimulation; cytotoxic T-lymphocyte.
                                                                                                                                                                                                                                                                                         WPI; 2005-658982/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-JUL-2004;
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                                                                                                                                         Disclosure; Page 57; 518pp; English.
                                                                                              The invention relates to a new polynucleotide comprising
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                                                                                                                                                                                                                                                                                                             c R, ...
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                                                                                                                                                                                                                                                                                                                                                                                                       SOUTHWOOD S.
BABE L M.
CHEN Y.
DEYOUNG L M.
HUANG M T F.
POWER S D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHESNUT R.
NEWMAN M J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPIMMUNE INC
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young LM,
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2004US-0584652P.
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56.1%; Pred. No. 1.4e-42;
tive 21; Mismatches 42
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                                                                                              9
                                                                                              multi-epitope
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Best Local :
                                                   A new DNA sequence encoding a fusion protein comprising a mutagenized HPV (human papillomavirus) E6 or E7 coding sequence and a sequence encoding a highly immunogenic fusion partner is useful to vaccinate against HPV infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multi-epitope construct, a polypeptide comprising an amino acid sequence encoded by the polynucleotide, a composition (comprising the polynucleotide, vector and/or polypeptide and a carrier), a cell (comprising the polynucleotide, vector or polypeptide), inducing an immune response against human papillomavirus virus (HPV) and making the polynucleotide, vector or polypeptide. The epitopes are derived from different strains of HPV and are from the El, E2, E6 and E7 proteins. The epitopes may be linked via a GP-anchor/spacer peptide. The order of the epitopes in the vaccine protein are disclosed in the tables referred to in the claims of the specification. The polynucleotide, vector or polypeptide is useful in preparing a composition for inducing an immune response against HPV infection and HPV-related cancers. The present sequence is an HPV protein used to derive epitopes for the vaccine of the
                  Disclosure;
                                                                                                                                         N-PSDB; AAL53422
                                                                                                                                                                                          Cid-Arregui A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus-18 (HPV18) EE6T-protein sequence.
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                                                                                                                                                                                                                                                              23-MAR-2001; 2001EP-00107271
                                                                                                                                                                                                                                                                                                                                                                      EP1243655-A1
                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus
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                                                                                                                                                                                                                                                                                               23-MAR-2001; 2001EP-00107271
                                                                                                                                                                                                                                                                                                                                   25-SEP-2002
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                                                                                                                                                                                                                             (DEKR-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                        papillomavirus-18; EE6T-sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          cytostatic; E6; E7 fusion protein; HPV; immunogenic; vaccine;
rtner; immunogenicity; HPV infection; neoplasm; HPV18;
              Fig
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                  4
              34pp;
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                                                                                                                                                                                          Hausen H;
                English.
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Pred. No. 1.4e-42;
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Best Local (
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25-MAR-2003
09-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a new DNA sequence encodes an B6 or E7 fusion protein of HPV, where at least 20% of the original codons are replaced by codons which lead to enhanced translation in a mammalian cell, containing a mutation which results in production of a truncated non-functional protein, and encoding a highly immunogenic polypeptide fusion partner capable of enhancing immunogenicity of the E6 or E7 protein in the mammalian host. The invention is used as a vaccine for the prevention or treatment of an HPV infection or a neoplasm associated with HPV infection. This sequence represents the human papillomavirus-18 (HPV18) EE6T-protein sequence of the invention
                     Disclosure; Fig 1b; 83pp;
                                                          Recombinant virus vectors encoding hu
                                                                                                 N-PSDB; AAQ29390.
                                                                                                                                                                                       14-MAR-1991;
                                                                                                                                                                                                                                          01-OCT-1992.
                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                            Human papillomavirus; 18.
                                                                                                                                                                                                                                                                                                                                                                                Virus vector;
                                                                                                                                                                                                                                                                                                                                                                                                       HPV 18 E6 protein fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR27728 standard;
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                                               cnem,
                                                                                                              WPI; 1992-349219/42.
                                                                                                                                      Boursnell MEG,
                                                                                                                                                                                                                                                                   WO9216636-A1
                                                                                                                                                                                                                                                                                                       Peptide
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                                             creating and vaccinating against them, such as cervical cancer.
                                                                                                                                                               (IMMU ) IMMUNOLOGY
                                                                                                                                                                                                               10-MAR-1992;
                                                                                                                                                                                                                                                                                                                                                                    immunotherapeutic.
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(revised)
(first en
                                                                                                                                                                                                                                                                                                                                                                                vaccinia virus; papillomavirus; HPV; human; amplification;
                                                                                                                                                                                        91GB-00005383
                                                                                                                                                                                                                92WO-GB000424
                                                                                                                                    Inglis SC,
                                                                                                                                                                                                                                                                                                     Location/Qualifiers
2. .259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
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                                                                                                                                                                                                                                                                                           "HPV-18 E6 protein"
                      English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                      Munro
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Pred. No. 1.6e-42;
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                                                           human papillomavirus proteins - for PV infections and conditions caused
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42;
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HPV-18

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AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG
                                                                                                                 Composition comprising induce immune response
                                                                                                                                                                                                                  Dalemans WLJ,
                                                                                                                                                                                                                                                                                    24-DEC-1997;
                                                                                                                                                                                                                                                                                                                    18-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                      WO9933868-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour; immunological fusion partner; CpG oligonucleotide; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPV fusion protein D1/3-E6-His/HPV18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 271 AA;
                                                                                                                                                                                                                                                     (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                   1999-405485/34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        prevention; treatment.
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                                                                                                                                                                                                                    Gerard
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Pred. No. 2.7e-42;
11; Mismatches 42
                                                                                                                                    E7
                                                                                 English.
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                                                                                                                                    or E6/E7
                                                                                                                                  fusion protein
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                                            This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY02641;
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                                                                                                                                                                                                                                                                       Disclosure; Fig 22; 95pp;
                                                                                                                                                                                                                                                                                                                            Human Papilloma Virus (HPV) fusion proteins - useful treatment or prophylaxis of HPV induced lesions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-AUG-1997;
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Haemophilus influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tumour;
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22-JUN-1999
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DB; AAX29789.
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87; Conserv
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(first entry)
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                                                                                                                                                                                                                                                                          English.
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Pred. No. 2.8e-42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                269
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RESULT 93
AED52653
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Best Local
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                                                                                                                The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                               Sequence 278
                                                                                                                                                                                                                                                                                                                                                                                                               04-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus type 18. Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  virucide; uteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fusion
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                                                                                                                                                                                                                                   Example 16; Fig 22; 96pp; English
                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                 22-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Haemophilus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
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FQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KORFHNIRGRWTGRCMSCCRSSR----TRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    btein; vaccine; papilloma; cytostatic; papillomavirus
uterine cervix tumor; E6; D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              influenzae; strain 772
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ilarity 56.1%;
Conservative
                                    Conservative
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                                             54.9%;
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Pred. No. 2.8e-
21; Mismatches
                                             Score 455.5;
Pred. No. 2.1
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                                    Mismatches
                                   2.8e-42;
hes 42;
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                                                        DB 9;
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Matches 87
                                                                                                                                                                                                                   AAX78791-X78801 represent nucleic acid sequences which encode novel constructs comprising an E6 or E7 protein or E6/E7 fusion protein from HPV (represented in AAY25375-Y25386). These constructs are optionally linked to an immunological fusion partner and an immunomodulatory CpG oligonucleotide. The products of the invention can be used to induce arimmune response in a patient to an HPV antigen. They can also be used i preventing or treating HPV induced tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY25386
                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                             Composition comprising induce immune response
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                                                                                                                                                                                                                                                                                                                                                                                                                     Dalemans
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fusion protein; E6 protein; E7 protein; E6/E7; immu immunological fusion partner; CpG oligonucleotide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HPV fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   papillomavirus.
                                                                                                                                               87;
                                                                                                                                                                                                                                                                                                                                                                                AAX78801.
                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                     XII; Page 61-62; 62pp;
                                                                                                                                                                                               383
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                                               ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
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                 KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                              VXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLDK 121
                                                                                                           FQDFQERPRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFYA
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KRRFHNIAGHYRGOCHSCCNRARQERLORRRETOV
                                                                                              FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
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nilarity 56.1%;
Conservative 21
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                                                                                                                                               Score 455.5; DB 2
Pred. No. 4.1e-42;
1; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                         E7
                                                                                                                                                                                                                                                                                                                     English.
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                                                                                                                                               42;
                                                                                                                                                                       2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immunomodulator; tumour;
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                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     immune response;
                                                                                                                                                                        383;
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RESULT 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents a chimeric B6 or B7 protein or B6/E7 fusion protein from Human papillomavirus (HPV) linked to an immunological fusion partner, in this case, a fragment of the Haemophilus influenzae B protein D. The sequence also contains a histidine tag at the C-terminus of the encoded protein. The protein can be used in a vaccine, for immunotherapeutically treating HPV induced tumour lesions (benign or malignant) and preventing HPV viral infection. (Updated on 17-OCT-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus. Haemophilus influenza Chimeric.
                          AED52657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig 25; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Papilloma Virus (HPV) fusion proteins - useful in vaccines treatment or prophylaxis of HPV induced lesions.
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22-JUN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                          standard; protein; 383
                                                                                                                                                                                                                        KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                  ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCOKPLNPABKLRHLNE
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 383;
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                                                                                                                                                                                                                                                                                                                                                                                              174
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RESULT 97
AEA9850
ID AEA98
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AC AEA98
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DT 08-SE
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DE HPV 0
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                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 87
                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to human Papilloma virus (HPV) fusion proteins, linked to an immunological fusion partner that provides T helper epitopes to the HPV antigen. Vaccine formulations comprising the fusion proteins are useful in the treatment or prophylaxis of HPV induced lesions (papillomas, warts and cervical cancer). HPV 16 (and HPV 18) E6 and E7 proteins (singly, as an E6-E7 fusion or mutated) were fused to either Haemophilus influenzae D protein (20-127), the C-terminus of Streptococcus pneumoniae Lyth protein (CLyth) or thioredoxin. The present sequence represents an HPV-H. influenzae D protein, fusion protein of the
                                                                                                                                                                                                                                                                                                                                                                    Sequence 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type 18. Synthetic.
                                       08-SEP-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 17; Fig 25; 96pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tyrrell AWR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haemophilus influenzae; strain 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pusion protein; vaccine; papilloma; cytostatic; papillomavirus infection; virucide; uterine cervix tumor; E7; E6; D protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-2005
            HPV (oncogenic strain)
                                                                                          AEA98550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN9801903-I4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2005-557648/57
)B; AED52656.
                                                                                                                                                                                                                                                                115
                                                                                                                                                                                                            175 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCOKPLNPAEKLRHLNE 234
                                                                                                                                                                                                                                      62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein D1/3-E6-E7-His/HPV18
                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                  87; Conserv
                                                                                                                                                                      | KQRFHNIRGRWTGRCMSCCRSSR-----TRRETQL 151
                                                                                                                                                                                                                                                               FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA 174
                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                     VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                           KRRFHNIAGHYRGOCHSCCNRARQERLQRRRETOV
                                                                                                                                                                                                                                                                                                                  54.9%; Score 455.5; DB 9 llarity 56.1%; Pred. No. 4.1e-42; Conservative 21; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                      B
                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98IN-CH001903
                                                                                       protein; 162
               9
E
            amino acid
             sequence
                                                                                                                                                                                                                                                                                                                                          DB 9;
                                                                                                                                                                                                                                                                                                                   42;
                                                                                                                                                           269
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                                                                                                                                                                                                                                                                                                                                             383;
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RESULT 98
ADL90077
ID ADL90
XX
AC ADL90
XX
DT 17-JU
XX
XX
KW Immun
XX
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                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an antibody composition comprising a mixture of CC monoclonal antibodies that specifically bind to E6 proteins of human CC papilloma virus (HPV) strains 16, 18, 31, 33 and 45, where at least one CC of the monoclonal antibodies specifically binds to E6 proteins of at CC least three different oncogenic HPV strains. Also included are a CC diagnostic kit (for detecting an HPV E6 polypeptide in a sample, CC comprising the antibody composition above), a method of detecting an HPV CC E6 protein in a sample, a method of detecting the presence of an oncogenic HPV E6 polypeptide in a sample (comprising a CC first and a second binding partner for an oncogenic HPV E6 polypeptide, CC where the first binding partner is a PDZ domain protein and the second CC where the first binding partner is a PDZ domain protein and the second CC binding partner is an antibody that specifically binds to the E6 proteins of at least three different oncogenic HPV Extrains). The antibody CC composition, kit, methods, and system are useful for diagnosing cancer, CC particularly cervical cancer. The present sequence is an HPV E6 protein.
                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 86
                                  Human papillomavirus 18-E6 protein, SEQ ID
                                                                                                                                                                                                                                                                                                                                                         Sequence 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 31; 161pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2005-457781/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Papillomavirus infection; virucide; E6 protein; diagnosis; antibody;
             Immune response; immunoglobulin; Ig; E6
                                                           17-JUN-2004
                                                                                                       ADL90077 standard; protein; 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ARBO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibody composition oncogenic strains of
                                                                                                                                                                   127
                                                                                                                                                                                        121
                                                                                                                                                                                                               67
                                                                                                                                                                                                                                       13
                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                             86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARBOR VITA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cervix
                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Garman JD,
                                                                                                                                                                                                                                                                            MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                 SKRRFHKIAGNFTGQCRHCWTSKREDRRTRQETQV 162
                                                                                                                                                                                     KKQRFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                               AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                              LFHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFGDLNVVYRDGVPL
                                                                                                                                                                                                                AACQSCIKFYAKIRELRYYSESVYATTLETITNTKLYDLSIRCMCCLKPLSPAEKLRHLN
                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2004US-00021949
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                                                          (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Belmares
                                                           entry)
                                                                                                                                                                                                                                                                                                                      54.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           strain 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     comprising a mixture of monoclonal antibodies human papilloma virus, useful for diagnosing
                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                            Score 451.5; DB 9;
Pred. No. 4.1e-42;
1; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΜP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Somoza
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                                     17.
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                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                 Length 162;
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                                                                                                                                                                                                                                                                                                             Gaps
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RESULT 99
ADO44078
ID ADO44
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for generating an immune response to an antigen in a patient. The method comprises administering to the patient an immunoglobulin (Ig) or its portion where the Ig has at least one peptide epitope of the antigen attached to the Ig or its portion and administering the immunoglobulin or its portion in conjunction with a RNA segment. The present sequence is an antigen sequence, used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Generating an immune response to an antigen, useful for generating desired T cell responses comprises administering an immunoglobulin one peptide epitope of the antigen attached to the immunoglobulin.
                                                                                                                                                                                                                                             E6 protein; E7 protein; fusion protein; HPV; HPV-associated cancer; cervical cancer; immune response; lower gastrointestinal tract cancanal cancer; reproductive system cancer; penile cancer; vulvar cancer; penile cancer; vulvar cancanal cancer; reproductive system cancer; penile cancer; vulvar cancanal cancer; reproductive system cancer; penile cancer; vulvar cancer; penile cancer; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 1G; 154pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2004-295415/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-SEP-2002;
14-MAR-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                   Amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADO44078;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADO44078 standard;
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                                                                                                                                                      Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-2004
15-APR-2004
                                                                                                                                                                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ASTRAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCOKPLNPAEKLRHLNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  158 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KRRPHKIAGHYRGOCHSCCNRARQERLORRRETOV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEDPTRRPYKLPDLCTELNTSLQDIEITCVÝCKTVLELTEVFEFAFKDLFVVÝRDSIPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                               sequence of the E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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2003WO-US007995
                                                                                                                                                                                                                                         reproductive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; 158
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                                                                                                                                                              type 39
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                                                                                                                                                                                                                                         system cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 449.5; DB 1; Pred. No. 6.7e-42 21; Mismatches 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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02-OCT-2003; 2003WO-US031726 03-OCT-2002; 2002US-0415929P

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RESULT 100
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AC ADV856
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XX Cytost
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XX Human
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Matches 86
 31-JAN-1995;
31-JAN-1996;
05-JUN-2000;
09-AUG-2001;
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                                                                                                                                                                                                             Human papillomavirus.
                                                                                                                                                                                                                                                                     Cytostatic; Virucide; Antibacterial; Antiparasitic; Vaccine; infection;
                                                                                                                                                                                                                                                   cancer; antigen.
                                                                                                                                                                                                                                                                                                       Human papillomavirus E6 protein, SEQ ID
                                                                                                                                                                                                                                                                                                                                                 10-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                       ADV85646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptide comprising human papillomavirus E6 and E7 polypeptides, useful for treating or preventing human papillomavirus (HPV)-associated cancers, e.g. cervical cancer.
                                                                                             12-MAR-2004;
                                                                                                                                     23-DEC-2004.
                                                                                                                                                                         US2004258688-A1
                                                                                                                                                                                                                                                                                                                                                                                                                         ADV85646 standard; protein;
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1 Similarity 55.5%; Pred. No. 6.7e-42;
86; Conservative 19; Mismatches 45;
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96WO-US001383.
2000US-00586704.
2001US-00925284.
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Search completed: May 27, Job time: 359.727 secs

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                                                                                                                                                                                                                                                                                                              receptor DEC-205. The method comprises exposing dendritic cells from the mammal to either: a conjugate comprising a preselected antigen covalently bound to an antibody to DEC-205; or a recombinant anti-DEC-205 antibody genetically engineered to contain at least one preselected antigen on at least one preselected site on the antibody molecule; and promoting maturation of the dendritic cells. The sequence encoding an anti-DEC-205 antibody (fragment) is preferably selected from ADV8563; which encode the heavy or light chain variable region of an anti-DEC-205 antibody. The antigen is targeted to antigen presenting cells through the inclusion of the anti-DEC-205 antibody, making antigen presentation chighly efficient. The immunity induced is robust and long lasting, even from a single dose at low concentration. The method of the invention is useful for immunizing a mammal to prevent or treat a disease such as a cuiral, bacterial or other infection or cancer. The immunization present sequence is a HPV protein sequence which can be
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a method (M1) for promoting highly efficient antigen presentation in a mammal, by targeting a presenced antigen to an endocytic receptor on an antigen-presenting cell, e.g. a dendritic cell. An example of a dendritic cell is the cell endocytic receptor DEC-205. The method comprises exposing dendritic cells from the
                                                                                                                                                                                                                                                                                                          Sequence 158 AA;
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(NUSS/)
(STEI/)
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                                    122 KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
                                                                          64 ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCQKPLNPAEKLRHLNE
                                                                                                        62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
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NUSSENZWEIG M.
STEINMAN R M.
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KRRFHKIAGHYRGOCHSCCNRAROERLORRRETOV
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ilarity 55.5%;
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21; Mismatches 43
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re greater than or equal to the score of the result being printed,
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ALIGNMENTS

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RESULT 2

WGWI35

EG protein - human papillomavirus type 35

E( species: human papillomavirus type 35

A,Note: host Homo sapiens (man)

C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C;Accession: E40824; S36521

R,Marich, J.E.; Ponteler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.

Virology 186, 770-776, 1992

A,Title: The phylogenetic relationship and complete nucleotide sequence of

A, Paference number: A40824; MUID:92124753; PMID:1310198
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C;Species: hu
C;Date: 28-Ma
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C;Superf
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A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
A;Accession: A03682
A;Molecule type: DNA
A;Residues: 1-158 <SEE>
A;Residues: 1-158 <SEE>
                       A; Reference number: S36469
A; Accession: S36521
                                                                                       A;Cross-references: UNIPROT:P27228; UNIPARC:UPI R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993
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                                                                  A;Description: Primer-directed sequencing of
                                                                                                                                                                               A; Molecule type: DNA
                                                                                                                                                                                                       A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI000000138B; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-158 <KEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P03126; UNIPARC:UPI000000138B; GB:K02718; NID:g333031; PIDN R;Kennedy, I.M.; Haddow, J.K.; Clements, J.B. J. Virol. 65, 2093-2097, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                            ;Residues: 1-149 <MAR>
  Statue:
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preliminary
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Pred. No. 2.7e-71;
1; Mismatches 2;
                                                                                                                                     UNIPARC: UPI00001383CF; GB:M74117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: K02718; NID: g333031;
                                                                    human papillomavirus types
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E6 protein - human papillomavirus C;Species: human papillomavirus ty C;Bate: 30-Jun-1987 #sequence_revi C;Aate: 30-Jun-1986 R.E. J. Virol. 58, 991-995, 1986

#sequence_revision

30-Jun-1987 #text_change 09-Jul-2004

type

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nucleotide

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0f

human

papillomavirus

type 33, ž W6WL33 RESULT 4

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A;Cross-references: UNIPROT:P17386; UNIPARC:UPI00001383CB; GB:J04353; NID:g333048; PIDN: C;Comment: This protein may be involved in the oncogenic potential of this virus. C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; zinc finger F;300-66/Region: zinc finger CCCC motif F;103-139/Region: zinc finger CCCC motif
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A;Cross-references: UNIPARC:UPI00001383CF; EM
A;Experimental source: strain 35H
C;Superfamily: papillomavirus E6 protein;
C;Keywords: DNA binding; early protein; zinc
F;30-66/Region: zinc finger CCCC motif
F;103-139/Region: zinc finger CCCC motif
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A;Title: Nucleotide sequence of human papillomavirus type A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: A32444
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A; Residues: 1-149 < GOL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: A32444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
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                                 KKORFHNIRGRWIGRCMSCCRSSRTRRETQL 151
                                                                                             AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                    MFKNPAERPRKLHELSSALEIPYDELRLNCVYCKGQLTETEVLDFAFTDLTIVYRDDTPH
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KKKRFHNIGGRWTGRCIACWR--RPRTETQV 149
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Pred. No. 5.7e-48;
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Pred. No. 9.9e-43;
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RESULT 6
A61237
E6 protein - human papillomavirus type 52
E6 proteis: human papillomavirus type 52
C;Species: human papillomavirus type 52
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 03-May-1996
C;Accession: A61237
R;Takamil, Y:; Kondoh, G:; Saito, J.; Noda, K.; Sudiro, T.M.; Sjahrurachman, Int. J. Cancer 48, 516-522, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change
C;Accession: B36779
R;Kirii, Y: Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
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A;Accession: A03633
A;Molecule type: DNA
A;Residues: 1-149 <COL>
A;Cross-references: UNIPROT:P06427; UNIPARC:UPI00001383CD;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
C;Keywords: DNA binding; early protein; zinc finger
C;Keywords: DNA binding; early protein; zinc finger
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A; Residues: 1-149 < KIR>
A; Cross-references: UNIPROT: P26555; UNIPARC: UPI000000081B; GB: D90400; NID: g222386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Human papillomavirus type 58 DNA;
A;Reference number: A36779; MUID:92024102;
A;Accession: E36779
A;Status: translation not shown
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Species: human papillomavirus type 58
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                                                                                                                                                                                                                                                                       KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                          AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFEEKQRHLD 120
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                                                                                                                                                                                                                                                                                                                   AVCKVCLRLLSKISEYRHYNYSLYGDTLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
                                                                                                                                                                                                                                                                                                                                                                                                         MFQDAEEKPRTLHDLCQALETSVHEIELKCVECKKTLQRSEVYDFVFADLRIVYRDGNPF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.8%; Score 496; DB 1; 61.6%; Pred. No. 3.7e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62.7%; Score 520; DB 1; 63.6%; Pred. No. 1.9e-42; tive 19; Mismatches 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence.
; PMID:1656594
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C;Species: human papillomavirus type 34 (C;Date: 20.-Feb-1995 #sequence_revision C;Accession: S36515 R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, Aug A;Description: primer_directed sequenci

sequencing of

r of hu

human

papillomavirus

E6 protein - human papillomavirus type 34 C;Species: human papillomavirus type 34

20-Feb-1995

#text_change

09-Jul-2004

S36515

A;Reference number: S36469
A;Accession: S36515
A;Molecule type: DNA
A;Residues: 1-148

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A; Molecule type: DNA
A; Residues: 1-148 <DEL>
A; Cross-references: UNIPROT: P36814; UNIPARC: UPI00001383DD;
C; Superfamily: papillomavirus E6 protein
C; Keywords: DNA binding; early protein; nucleus; zinc finge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E6 protein - human papillomavirus type C;Species: human papillomavirus type 52 C;Date: 20-Feb-1995 #sequence_revision
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S36573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Cloning and characterization of human papillomavirus type 52 from cervical A;Reference number: A61237; MUID:91258022; PMID:1646174 A;Accession: A61237
                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: S36573
R;Dellus, H:; Hofmann, B.
submitted to the EMBL Data Library, August
A;Description: Primer-directed sequencing
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C/Superfamily: papillomavirus E6 protein
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A; Residues: 1-148 < TAK>
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A;Accession: S36573
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Best Local Similarity
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                                                                                121 KKORFHNIRGRWTGRCMSCCR
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87; Conserv
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                                                                                                                                          AVXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPBBKQRHLD 120
                                                 ANKREHNIMGRWTGRCSECWR
                                                                                                                     GVCIMCLRFLSKISEYRHYQYSLYGKTLEERVKKPLSEITIRCIICQTPLCPEEKERHVN
                                                                                                                                                                                     MEEDPATRPRILHELCEVILESVHETRIQCVQCKKELQRREVYKELETDLRIVYRDNNPY
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                                                                                                                                                                                                                                                         Score 487; DB 2;
Pred. No. 2.6e-39;
9; Mismatches 35
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Pred. No. 2.6e-39;
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of human
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A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E40415
R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991
A;Title: Biologic properties and nucleotide sequence analysis of human papi.
A;Reference number: A40415; MUID:91303675; PMID:1649326
A;Accession: E40415
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W6WL51
E6 protein -
                                                                                      C;Accession: S36561
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August A;Description: Primer-directed sequencing C
                                                                                                                                                               E6 protein - human papillomavirus type 45
C;Species: human papillomavirus type 45
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:P26554; UNIPARC:UPI00001383DC; GB:M62877 C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; zinc finger F;30-66/Region: zinc finger CCCC motif F;103-139/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P36811; UNIPARC:UPI00001383CE; EMBL:X74476; NID:g396989; PID C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; nucleus; zinc finger
A; Molecule type: DNA
A; Residues: 1-158 < DEL>
A; Cross-references: UNI
                                                                            A; Reference number: S36469
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                                                           A; Accession:
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;Species: human papillomavirus type 51
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Best Local
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Best Local :
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                                                           S36561
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                                                                                                                                                                                                                                                                                                         EKKRFHEIAGRWTGQCANCWQRTRQRNETQV 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                           MFEDKRERPRTLHELCEALNVSMHNIQVVCVYCKKELCRADVYNVAFTEIKIVYRDNNPY
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 UNIPROT: P21735; UNIPARC: UPI00001383D8; EMBL: X74479; NID: g397022;
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Pred. No. 5.1e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 460; DB 1;
Pred. No. 1e-36;
4; Mismatches 41
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y of human
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                                                                                                                                                                   #text_change
                                                                                              papillomavirus
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   PID
RESULT 12
W6WLPR
E6 protein .
C;Species: l
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A;Residues: 1-158 <COL>
A;Cross-references: UNLPARC:UPI000002COFB; GB:X05015; NID:g60975; PIDN:CAA28664.1;
A;Cross-references: UNLPARC:UPI000002COFB; GB:X05015; NID:g60975; PIDN:CAA28664.1;
A;Gen. Virol. 67, 1909-1916, 1986
A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and A;Title: The expression of human papillomavirus type 18 E6 protein in bacteria and A;Contents: annotation; identification of the protein
C;Cuperfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;32-68/Region: zinc finger CCCC motif
F;105-141/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: Identification of early proteins of the human papilloma viruses type A;Reference number: A91068; MUID:87218459; PMID:3034571 A;Accession: A26165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E6 protein - human papillomavirus type 18 C;Species: human papillomavirus type 18 C;Decies: human papillomavirus type 18 C;Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text_change 09-Jul-2004 C;Accession: A26165; G26251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cole, S.T.; Danos, O.
J. Mol. Biol. 193, 599-608, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P06463; UNIPARC:UPI000002C0FB; GB:X04773; NID:960876; PIDN:C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: G26251
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Nucleotide sequence and comparative analysis of the A; Reference number: A92937; MUID:87283882; PMID:3039146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-158 < SEE>
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Best Local
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es 87; Conserv
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                                                      122 KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
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                                                                                                                                                            62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPBEKQRHLDK 121
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                                                                                                      ACHKCIDFYSRIRELRHYSDSVYGDTLEKLTNTGLYNLLIRCLRCOKPLNPAEKLRHLNE 123
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                                                                                                                                                                                                                FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
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KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV
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ilarity 56.1%;
Conservative 2
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                                                                                                                                                                                                                                                                                                                            Score 455.5; DB 1;
Pred. No. 2.8e-36;
21; Mismatches 42;
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Pred. No. 1.
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PID:g

human papillomavirus type ME1 uman papillomavirus type ME180

ME180 (provirus)

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A;Note: host Homo sapiens (man)
C;Pate: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: C40509
R;Reuter, S.; Delius, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervical c:
A;Reference number: A40509; MVID:91374616; PWID:1716694
A;Reference number: A40509
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-158 <REU>
A;Cross-references: UNIPAOT:P27962; UNIPARC:UPI000000082F; GB:M73258
C;Superfamily; papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger CCCC motif
F:105-141/Beation. zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E6 protein - human papillomavirus type 39
E7 (Species: human papillomavirus type 39)
E8 protein - human papillomavirus type 39
E8 protein - human papillomavirus type 39
E8 proteis: host Homo sapiens (man)
E9 protein - human papillomavirus type 39
E9 protein - human papillomavirus type 39
E9 protein - A38502
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                                                                     KORFHNIRGRWTGRCMSCCRSSR----TRRETOL 151
                                                                                                                                                            ACQSCIKFYAKIRELRYYSDSVYATTLENITNTKLYNLLIRCMCCLKPLCPAEKLRHLNS 123
                                                                                                                                                                                                                         VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                        FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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                                                                                                                                                                                                                                                                                                               FHNPAERPYKLPDLCTTLDTTLQDITIACVYCRRPLQQTEVYEFAFSDLYVVYRDGEPLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 449.5; DB 1;
Pred. No. 1.1e-35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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158
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RESULT

RESULT 16 W6WL56 E6 protein

human

papillomavirus

type

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C;Accession: S36544
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human
A;Beference number: S36469
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86 protein - rhesus papillomavirus (type 1)

C;Species: rhesus papillomavirus
C;Species: al-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: A38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-150 <DEL>
A;Residues: 1-150 <DEL>
A;Cross-references: UNIPROT:P36807; UNIPARC:UPI00001383C5; EMBL:X74472; NID:g396956; PIDN
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E6 protein - human papillomavirus type C;Species: human papillomavirus type 26 C;Date: 20-Feb-1955 #sequence_revision C;Accession: S36544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT:P22159; UNIPARC:UP100001383EE; EMBL:M37717 C;Superfamily: papillomavirus E6 protein; C;Keywords: DNA binding; early protein; transforming protein; zinc finger C;Keywords: DNA binding; early protein; transforming protein; zinc finger E;60-96/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: Characterization of the complete RhPV 1 genomic sequence and an integration A;Reference number: A38503; MUID:91135018; PMID:1847267 A;Accession: A38503
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A; Residues: 1-191 < OST>
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Best Local
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121
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                                                                                                                                                                                                                              1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                     l Similarity
83; Conserv
                                                                                            AACKRCVIFYSKITEYRRYTCSVYGATLEALTKKSLCNLLIRCHRCQMPLGPEEKQRIVD 120
                                            KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                      MFEDPRERPRILHELCESINTILQNIQVQCVYCKETIQWADVYNFAICDLRVVYRDRSPY 60
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EKRRFHEIAGOWKGLCTNCWR-PRRQTETQV
                                                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                                                                                                                                                                                                                                                                                         52.6%; Score 436.5; DB 2; 55.0%; Pred. No. 1.7e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23; Mismatches
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Pred. No. 1.6e-34;
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  150
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$36503

E6 protein - human papillomavirus type 30

C;Species: human papillomavirus type 30

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: $36503

R;Delius, H.; Hofmann, B.

submitted to the EMBL Data Library, August 1993

A;Description: Primer-directed sequencing of human papillomavirus types.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Molecule type: DNA
A;Residues: 1-155 <DEL>
A;Residues: 1-155 <DEL>
A;Cross-references: UNIDARC:UPI00001383B0; EMBL:X74483; NID:g397053; PIDN:CAA52596.1;
A;Cross-references: UNIDARC:UPI00001383B0; EMBL:X74483; NID:g397053; PIDN:CAA52596.1;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
F;33-69/Region: zinc finger CCCC motif
F;106-142/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-155 <105>
A;Cross-references: UNIPROT:P24836; UNIPARC:UPI00001383E0
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
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A;Title: Human papillomavirus type 56: a new virus detected in cervical cancers A;Reference number: A33377; MUID:90063558; PMID:2555440
A;Accession: A33377
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C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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A; Residues: 1-153 < DEL>
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A; Accession: S36503
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A; Accession: S36579
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|Spate: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
                                                                                                                                                                                                      Matches
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Best Local :
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Best Local
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                                                                                                                                                                                                                         Similarity
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  KORFHNIRGRWTGRCMSCCRSSRTRRET
                                                                           VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
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                                          VCNFCLLFYSKVRKIRHYNYSLYGASLVALTKKELFDLLIRCYRCQQPLTPEEKQLHCEY
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                                                                                                                        FENTGERPRTVHHLCEVQETSLLELQLQCVYCKKELSSSEVYNFACKDLRLVYREDSPYA
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56.4%; Pred. No. 1.6e-33;
htive 17; Mismatches 47
                                                                                                                                                                                                                      46.48;
                                                                                                                                                                                                      26; Mismatches
                                                                                                                                                                                                                         Score 385.5;
Pred. No. 1.3
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Best Local
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RESULT 18
$36527

B6 protein - human papillomavirus type 53
C; Species: human papillomavirus type 53
C; Species: 20-Feb-195 #sequence_revision 20-Feb
C; Accession: $36527
R; Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 19
A; Description: Primer-directed sequencing of
A; Reference number: $36469
                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: DNA
A;Residues: 1-155 <TAW>
A;Residues: 1-155 <TAW>
A;Residues: 1-155 <TAW>
A;Residues: UniproT:Q80955; UNIPARC:UPI00001383E6
A;Cross-references: UNIPROT:Q80955; UNIPARC:UPI00001383E6
A;Note: Sequence extracted from NCBI backbone (NCBIN:78637, NCBIP:7C;Superfamily: papillomavirus E6 protein
C;Superfamily: papillomavirus E6 protein; transforming protein; zinc
C;Keywords: DNA binding; early protein; transforming protein; zinc
F;33-69/Region: zinc finger CCCC motif
F;106-142/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-154 <DEL>
A;Cross-references: UNIPROT:P36815; UNIPARC:UPI00001383DE;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. Clin. Microbiol. 29, 2656-2660, 1991
A;Title: Characterization of human papillomavirus type 66
A;Reference number: A44890; MUID:92129556; PMID:1663515
A;Accession: A44890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E6 protein - human papillomavirus type 66
C;Species: human papillomavirus type 66
C;Date: 31-Mar.1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C;Accession: A44890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A.R.; Beaudenon, S.; Favre, M.; Orth, G.
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                                                                                                                                     AVXDKCLKFYSKISBYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFEEKQRHLD 120
                                                KKORFHNIRGRWTGRCMSCCRSSRTRRETO 150
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HKRRFHYIAYAWTGSCLQCWRHT-SRQATE 152
                                                                                                      AVCRVCLLFYSKVRKYRYYKYSVYGATLESITKKQLSDLSIRCYRCQCPLTPEEKQLHCE 123
                                                                                                                                                                                                                  IFSNTQERPRSLHHLSEVLQIPLLDLRLSCVYCKKELTSLELYRFACIELKLVYRNNWPY
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51.1%;
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Pred. No. 5.4e-29;
                                                                                                                                                                                                                                                                                                                        Score 372.5; DB 2;
Pred. No. 2.2e-28;
0; Mismatches 53;
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of human
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A,Title: DNA sequence and genome organization of genital human papillomavirus type A;Reference number: A90975; MUID:84131949; PMID:6321162
A;Reference number: A90975; MUID:84131949; PMID:6321162
A;Reference number: DNA
A;Residues: 1-150 <8CH>
A;Residues: 1-150 <8CH>
A;Cross-references: UNITROT:P06462; UNIPARC:UPI000000028A; GB:X00203; NID:g60955; PC;Superfamily: papillomavirus E6 protein C;Reywords: DNA binding; early protein; zinc finger F;31-67/Region: zinc finger CCCC motif F;104-140/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E6 protein - human papillomavirus type 6b C;Species: human papillomavirus type 6b C;Species: human papillomavirus type 6b C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004 C;Accession: E20558 R;Schwarz, E.; Durst, M.; Demankowski, C.; Lattermann, O.; Zech, R.; WolfspenBO J. 2, 2341-2348, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: human papillomavirus type 43
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: A34144
R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F.
J. Virol. 63, 2829-2834, 1989
A;Title: Cloning and partial DNA sequencing of two new human papillomavirus types
A;Reference number: A34144; MUID:89259065; PMID:2542593
A;Accession: A34144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
W6WL43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:P19709; UNIPARC:UPI00001383D6; GB:M27022; NID:g341596; C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-155 < LOE>
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W6WL6
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Best Local S
Matches 51
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Best Local
                                                         132 WIGRCMSC 139
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    human papillomavirus type

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                                                                                                                                                                                 13 IDQLCKTFNLSMHTLQINCVFCKNALTTAEIYSYAYKHLKVLFRGGYPYAACACCLEFHG 72
                                                                                                                                                                                                                     12 LPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYS 71
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                                                                                                                                      KISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KIHSVWKGYCLHCWKSCMEKRRRSET 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCFEEKQRHLDKKQRFH
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                   WKGRCLHC
                                                                                                KINQYRHFDYAGYATTVEEETKQDILDVLIRCYLCHKPLCEVEKVKHILTKARFIKLNCT 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQFHGKISQYRHFDYAAYADTVEEETKQTVFDLCIRCCKCHKPLSPVEKVQHIVQKAQFF 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QNARTIFELCDÉCNITLPTLQIGCIFCKKWLLTTEVLSFAFRDLRVVWRDGYPFAACLAC
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                                                                                                                                                                                                                                                                                 Score 304; DB 1; Length 150; Pred. No. 7.3e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 326.5; DB 1;
Pred. No. 5.4e-24;
?7; Mismatches 55;
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                48;
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W6WL44
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F;31-67/Regi
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A; Residues: 1-150 <LOE>
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A; Residues: 1-153 <HIR>
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R;Hirsch-Behnam, A.
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131
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                                                                                                                                                                                                                                                              Similarity
DTWKGRCFHCWIS
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RESULT 22
$15621
Sib621
E6 protein - human papillomavirus type 57
E7; Species: human papillomavirus type 57
C7; Species: human papillomavirus type 57
A7; Note: host Homo sapiens (man)
C7; Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C7; Accession: $15621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E6 protein - human papillomavirus type 44
C;Species: human papillomavirus type 44
A;Note: host Homo sapiens (man)
C;Date: 30-Sep-1990 #sequence_revision 30-Sep-1990 #text_change 09-Jul-2004
C;Accession: B34144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Virol. 63, 2829-2834, 1989
A;Title: Cloning and partial DNA sequencing of two new human papillomavirus types
A;Reference number: A34144; MUID:89259065; PMID:2542593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P22158; UNIPARC:UPI00001383E1; EMBL:X55965; N C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; transforming protein; zinc finger C;Keywords: DNA binding; early protein; transforming protein; zinc finger C;CCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:P19710; UNIPARC:UPI00001383D7; GB:M27023; NID:g341597; PIDN:
C;Superfamily: papillomavirus E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Loerincz, A.T.; Quinn, A.P.; Goldsborough, M.D.; Schmidt, B.J.; Temple, G.F. J. Virol. 63, 2829-2834, 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M. Virus Res. 18, 81-98, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                             F;104-140/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;102-138/Region: zinc finger CCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Keywords: DNA binding; early protein; transforming protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 AAAKURQYRHWHYSCYGDTVETETGIPIPQLFMRCYICHKPLCWEEKEALLVGNKRFHKI 127
                                                                                                                                                                                                                                                10 RKLPQLCTBLQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9 PRKLPQLCTBLQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK 68
                                                                                                     QKVNQFRHFNYAGYAVTVEBETNKSILDVLIRCYLCHKPLCHVEKVRHILDKARFIKLQ
                                                GRWTGRCMSCCRS 142
                                                                                                                                                        YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
                                                                                                                                                                                                              QSIDQLCKECNIPMENLQILCVFCRKTLSTAEVYSFAYKQLYVVYRGNFPFAACAICLEL
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                                                                                                                                                                                                                                                                                                                                             36.3%;
143
                                                                                                                                                                                                                                                                                                                          28;
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Pred. No. 9.3e-22;
3; Mismatches 51
                                                                                                                                                                                                                                                                                                                    Score 301; DB 1;
Pred. No. 1.4e-21;
8; Mismatches 52
                                                                                                                                                                                                                                                                                                                       52;
                                                                                                                                                                                                                                                                                                                                                                       Length
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A; Molecule type: DNA
A; Residues: 1-150 < DAN-
A; Residues: 1-150 < DAN-
A; Residues: 1-150 < DAN-
A; Cross-references: UNIFROT: P04019; UNIPARC: UPI00001383B7; GB: M14119; NID: g333026; PIDN: A; Cross-references: UNIFROT: P04019; CFSUperfamily; papillomavirus E6 protein
C; Keywords: DNA binding; early protein; zinc finger
C; Keywords: DNA binding; early protein; zinc finger
F; 311-67/Region: zinc finger CCCC motif
F; 104-140/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B6 protein - human papillomavirus type 11
C;Species: human papillomavirus type 11
C;Accession: A03684
R;Dartmann, K.; Schwarz, E.; Gissmann, L.; zur Hausen, H.
Virology 151, 124-130, 1986
A;Reference number: A94338; MUID:86181601; PMID:3008427
A;Accession: A03684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E6 protein - human papillomavirus type 2a
C;Species: human papillomavirus type 2a
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15614
R;Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:P25484; UNIPARC:UPI0000164A75; EMBL:X55964 C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; transforming protein; zinc fine F;35-71/Region: zinc finger CCCC motif F;108-144/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Virus Res. 18, 81-98, 1990
A;Title: A comparative sequence analysis of two human papillomavirus (HPV)
A;Reference number: S15614; MUID:91188699; PMID:1964523
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A; Residues: 1-159 <HIR>
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Best Local Similarity
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                                                                                      CACCLELQGKINQYRHFNYAAYAPTVEEETNEDILKVLIRCYLCHKPLCEIEKLKHILGK 123
                                                                                                                             XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKK 122
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                                                                                                                                                                                                               ODPOERPRKLPOLCTELOTTIHDIILECVYCKOOLLRREVYDFAFRDLCIVYRDGNPYAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRNIFLLCKEYGLELEDLRLLCVWCKRPLSEADIWAFAIKELFVVWRKGFPFGACGKCLI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK 68
                                                                                                                                                                        KDASTSATSIDQLCKTFNLSLHTLQIQCVFCRNALTTAEIYAYAYKNLKVVWRDNFPFAA 63
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                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                   35.4%; Score 294; DB 1; 35.8%; Pred. No. 6.6e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35.8%; Score 297.5; DB 1 41.7%; Pred. No. 3.2e-21;
                                                                                                                                                                                                                                                              33;
  140
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E6 protein - human papillomavirus type 27 (;Species: human papillomavirus type 27 (;Species: human papillomavirus type 27 (;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09 (;Accession: S36497 R.Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993 A.)Pescription: Primer-directed sequencing of human papillomavirus A.,Reference number: S36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E6 protein - human papillomavirus type 7
(;Species: human papillomavirus type 7
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: S36584
R;Delius, H.; Hofmann, B.
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S36497
                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P36800; UNIPARC:UPI00001383B3; EMBL:X74463; NID:g397060; PID:C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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S36584
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C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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A; Residues: 1-159 < DEL>
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A;Residues: 1-154 <DEL>
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                                                                                                                                                                                                                                                                                                                                Local Similarity 37.1%;
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130
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                                                GRWTGRCMSC---CRSSRTRRET 149
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DSWTGYCLHCWKKCMEKGQRSET 152
                                                                                                   YGKVNQYRNFRYAAYAPTVEEETGLTILEVRIRCCKCHKPLSPVEKTNHIVKKTQFFKLQ 129
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42.7%; Pred. No. 1.1e-20;
ative 21; Mismatches 54
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sequencing of human
                                                                                                                                                                                                                                                                                                             30;
                                                                                                                                                                                                                                                                                                     Score 290.5; DB 2; Length 154;
Pred. No. 1.5e-20;
10; Mismatches 57; Indels 3
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protein 28

human

papillomavirus

type 40

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C;Species: human papillomavirus type 40
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #te
C;Accession: S36555
R;Deliue, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papar, Primer enumber: S36469
A;Accession: S36555
A;Molecule type: DNA
A;Residues: 1-154 <DEL>
$36509

R6 protein - human papillomavirus type 32
C;Species: human papillomavirus type 32
C;Date: 20-Feb-1995 #sequence_revision 20-
C;Accession: $36509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Compar A;Reference number: A42955; MUID:92391075; PMID:1325697
A;Accession: A36818
A;Molecule type: DNA
A;Residues: 1-150 <VAN>
A;Residues: 1-150 <VAN>
A;Cross-references: UNIPARC:UPI00001383ED; EMBL:X62844; NID:g61010; PIDN:CAA44655.1; PIIC C;Superfamily: papillomavirus E6 protein
C;Ksuperfamily: papillomavirus E6 protein; transforming protein; zinc finger F;31-67/Region: zinc finger CCCC motif
F;104-140/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B6 protein - pygmy chimpanzee papillomavirus (type 1)
C;Species: pygmy chimpanzee papillomavirus
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 16-Jul-1999
C;Date: 30-Bill
C;Accession: A36818
R;van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.;
Virology 190, 587-596, 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P36812; UNIPARC:UPI00001383D3; EMBL:X74478; NID:g397014; C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; nucleus; zinc finger
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 34.8%;
Similarity 37.1%;
                                                                                                                                                                                        CEWKGRCFHCWTS
                                                                                                                                                                                                                                      GRWTGRCMSCCRS 142
                                                                                                                                                                                                                                                                                                                   YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GRWTGRCMSC---CRSSRTRRET
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
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                                                                                                                                                                                                                                                                                    QGKVNQYRHFDFAAYAVTVEEEINKSIFDVRIRCYLCHKPLCDVEKLRHILEKARFIKLN 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      34.7%; Score 288; DB 1; 38.3%; Pred. No. 2.5e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 288.5; DB 2
Pred. No. 2.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                20-Feb-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-Feb-1995 #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54;
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                        09-Jul-2004
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R; Philipp,
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E6 protein - human papillomavirus type 42
C;Species: human papillomavirus type 42
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: E39451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Accession: A42955
R;van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, Virology 190, 587-596, 1992
A;Title: Human papillomavirus type 13 and pygmy chimpanzee A;Reference number: A42955; MUID:92391075; PMID:1325697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT
W6WL13
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C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                                Ś
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Keywords: DNA binding; early protein; transforming protein; F;31-67/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,Cross-references: UNIPROT:002269; UNIPARC:UPI00001383B9; EMBL:X62843; NID:g60295; PIDN C;Superfamily: papillomavirus E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-150 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
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A; Residues: 1-142 < DEL >
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A;Description: Primer-directed sequencing of human papillomavirus types
                                                                                                                           W6WL42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                   10 RKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKF 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                              49;
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                                                                                                                                                                                                                                                  GRWTGRCMSCCRS 142
                                                                                                                                                                                                                                                                                                                                YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRGRWTGRCMSC 139
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                                                                                                                                                                                                             SSWKGRCFHCWSS
                                                                                                                                                                                                                                                                                            QGKINQFRHFDFAGFAVTVEEDTKQSILDVLIRCYLCHKPLCEVEKLRHILQKARFIKLN 130
                                                                                                                                                                                                                                                                                                                                                                            KTIDQLCKECNLSMHSLQILCVFCRKTLSTAEVYAFQYKSLYIVWRGQFPFAACACCLEI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32.9%; Score 273; DB 1; 36.8%; Pred. No. 6.6e-19;
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Sapp,
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  M.; Cole,
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Pred. No. 7e-20;
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    S.T.; Streeck, R.E
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A;Reference number: A39451; MUID:92087479; l
A;Accession: E39451
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-150 <PHT-
A;Crosci
E6 protein - human papillomavirus type 3
(;Species: human papillomavirus type 3
(;Species: human papillomavirus type 3
(;Date: 20-Feb-195 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
(;Accession: S36550
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: human papillomavirus type 10
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36532
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer_directed sequencing of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-148 < LDEL»
A; Cross-references: UNIPROT: P36802; UNIPARC: UPI00001383B6; EMBL: X74465;
A; Cross-references: UNIPROT: P36802; UNIPARC: UPI00001383B6; EMBL: X74465;
C; Superfamily: papillomavirus E6 protein; nucleus; zinc finger
C; Keywords: DNA binding; early protein; nucleus; zinc finger
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E6 protein - human papillomavirus type 10

C;Species: human papillomavirus type 10

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
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C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
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A; Accession: $36532
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Similarity 41.7%;
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                                                                                                                                                                                                                                                                                                                LKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFH 126
                                                                                                                                                                                                                                                                                                                                                                                      ERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKC
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                                                                                                                                                                                                                                                                                   LLLQGIVRRLKYWDYSYYVEGVEEETKQSIYTQLIRCYMCHKPLVREEKDRHRNERRRLH
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Pred. No. 1.1e-15;
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Pred. No. 2e-18;
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PMID:1309278
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A; Description: Primer-directed sequencing of human papillom A; Reference number: $36469 A; Accession: $36479 A; Molecule type: DNA A; Residues: 1-141 < DEL> A; Residues: 1-141 < DEL> A; Cross-references: UNIPROT: P36805; UNIPARC: UPI00001383BC; C; Superfamily: papillomavirus E6 protein C; Keywords: DNA binding; early protein; nucleus; zinc finge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-152 <DEL>
A; Cross-references: UNIPROT: P36799; UNIPARC: UPI00001383B0; EMBL: X74462;
C; Superfamily: papillomavirus E6 protein
C; Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                  E6 protein - human papillomavirus type (7;Species: human papillomavirus type 17 (7;Date: 20-Feb-1995 #sequence_revision C;Accession: S36479 R;Delius, H.; Hofmann, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P36813; UNIPARC:UPI00001383DB; C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; nucleus; zinc finge
                                                                                                                                                                     R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-138 <DEL>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68 KFYSKISEYRHYCYS-VYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFH 126
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Pred. No. 1.3e-07;
0; Mismatches 65
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Pred. No. 6.7e-15;
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RESULT 38
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A,Reference number: A43550
A;Recession: A43550
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-156 <HIR>
A;Residues: 1-156 <HIR>
A;Cross-references: UNIPROT:P27555; UNIPARC:UPI00001383D4; EMBL:X56147; NID:g60942; C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; transforming protein; zinc finger
E;42-78/Region: zinc finger CCCC motif
                  A;Molecule type: DNA
A;Residues: 1-140 <DAN>
A;Residues: 1-140 <DAN>
A;Cross-references: UNIPROT:P06929; UNIPARC:UPI00001383BE; GB:V01116;
A;Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
                                                                                                             A; Title: Human papillomavirus 1a complete DNA sequence: A; Reference number: A90970; MUID:84182467; PMID:6325156 A; Accession: B17475
                                                                                                                                                                        E6 protein - human papillomavirus type la C;Species: human papillomavirus type la C;Date: 30-Sep-1987 #sequence_revision 30 C;Accession: B17475 R;Danos, O.; Katinka, M.; Yaniv, M. EMBO J. 1, 231-236, 1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993
C;Accession: A43550
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E6 protein -
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                                                                                                                                                                                                                                                                                                                                                                           RIGGIWRGTCVRC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TRVLARLEFTARHEVSCAASRLPHFIGQSLSDLEVRCVRCLALLQSVEKDYILREDLSVH 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFH 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ERPRKTPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKC 66
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29.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.5%; Score 137; DB 1; 1
26.3%; Pred. No. 6.2e-06;
tive 23; Mismatches 75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 143.5; DB 2;
Pred. No. 1.4e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                 30-Sep-1987 #text_change 09-Jul-2004
    la and bovine
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type
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papillomavirus
                                                                                                                                                          얁
                                                            GB:X03321;
                                                                                                                                                        genome organizat
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                                                        NID:g60
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A;Molecule type: DNA
A;Residues: 1-161 <DEL*
A;Residues: 1-161 <DEL*
A;Cross-references: UNIFROT:P28833; UNIPARC:UPI00001383C4; EMBL:X74471; NID:g396948;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
                                                                                                                                                                                                                                        R;Delius, H.; Hofmann, B.
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
submitted to the EMBL Data Library, August 1993
                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S36491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:P11302; UNIPARC:UPI000017495C;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;17-55/Region: zinc finger CCCC motif
F;90-129/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E6 protein - bovine papillomavirus type 2
C;Species: bovine papillomavirus type 2
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
C;Accession: H31169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Watches 37; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A92993; MUID:83189357; PMID:6302319
A;Contents: annotation
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
                                                                                                                                                                                                             A; Description: Primer-directed A; Reference number: S36469 A; Accession: S36491
                                                                                                                                                                                                                                                                                                                                              E6 protein - human papillomavirus type 25
C;Species: human papillomavirus type 25
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-139 < GRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Groff, D.E.; Mitra, R.; Lancaster, W.D. submitted to GenBank, May 1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: H31169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A94519
                                                                                                                                                                                                                                                                                                                           C; Accession: S36491
Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSLLEFVLYYQESYEVPETEETLDRPLLQTELRCVTCTKKLSVAEKLEVVSNGERVHRVR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEAQLLHGKSLDRLCIRCCYCGGKLTKNEKORHVLYNEPFCKTRSNIIRGRCYDCCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                        15.9%;
25.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.2%;
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Pred. No. 6.3e-06;
  Score 132; DB 2;
Pred. No. 1.9e-05;
4; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 134.5; DB 1; Pred. No. 9.7e-06;
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                                                                                                                                                                                                                                                                                                                                                   #text_change 09-Jul-2004
                                                                                                                                                                                                                                                         papillomavirus
                                           Length 161
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:M20219;
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RESULT 42
S36473
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$28510
E6 protein -
                                                                                                   R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August 1993 A;Description: Primer-directed sequencing of hu
                                                                                                                                                             E6 protein - human papillomavirus type 15 c;Species: human papillomavirus type 15 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: $36473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPARC:UPI0000178416; EMBL:X65201
A;Note: the source is designated as Mastomys natalensis papillomavirus
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
F;95-171/Region: zinc finger C3HC4 motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 1-207 <VAN>
A;Cross-references: UMIPROT:P30735; UNIPARC:UPI00001383EA; EMBL:X65201; NID:g60575; A;Note: the source is designated as Mastomys natalensis papillomavirus R;van Ranst, M.; Tachezy, R.; Pruss, J.; Burk, R.D.
Nucleic Acids Res. 20, 2889, 1992
A;Title: Primary structure of the E6 protein of Micromys minutus papillomavirus and A;Reference number: S22955; MUID:92310995; PMID:1319576
A;Accession: S22956
                                                              A; Reference number: S36469
A; Accession: S36473
                   A; Molecule type: DNA
A; Residues: 1-141 < DEL>
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A; Residues: 77-204 < VAN2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: S28510; S22956
R;van Ranst, M.A.
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;Date: 12-Mar_1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                      CARVCASLDLFLHH-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELQTTIH---
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                                                                                                                                                                                                                                                                                                                                                                KQRHLDKKQRFHNIRGRWTGRCMSC 139
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                                                                                                                                                                                                                                                                                                                                      KLECAERGESFAKVRGQWRARCRIC 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
  UNIPROT: P36804; UNIPARC: UPI00001383BB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.6%; Score 129.5; DB 2; 22.1%; Pred. No. 4.2e-05; 22.1%; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -DIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                      ONSRPLADVLRDENLTLHGLKARCRVCMKILSVTE 179
                                                                                                       human
                                                                                                     papillomavirus types
                                                                                                                                                                                     #text_change 09-Jul-2004
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  EMBL: X74468;
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NID:g396924;
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E6 protein - human papillomavirus type 18
C;Species: human papillomavirus type 18
C;Species: human papillomavirus type 18
C;Accession: 156705
R;Inagaki, Y.; Tsunokawa, Y.; Takebe, N.; Nawa, H.; Nakanishi, S.; Terada, M.;
J. Virol. 62, 1640-1646, 1988
A;Title: Nucleotide sequences of cDNAs for human papillomavirus type 18 transcr
A;Reference number: I56705; MUID:88188247; PMID:2833614
A;Accession: I56705
A,Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                  E6 protein - cottontail rabbit papillomavirus
C;Species: cottontail rabbit papillomavirus
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change
C;Accession: A03686
                                                                                                                                                                                                                                                                                                                      R;Giri, I.; Danos, O.; Yaniv, M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A;Title: Genomic structure of the cottontail rabbit (Shope)
A;Reference number: A94027; MUID:85166175; PMID:2984661
A;Accession: A03686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-57 < RES>
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                                                                                                                                                                                                                       C; Keywords:
                                                                                                                                                                                                                                          A;Cross-references: UNIPARC:UPI0000000953
C;Superfamily: papillomavirus E6 protein
                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-273 <GIR>
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les 36; Conserv
                                                                                                                                                             Local
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                    69
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                                                                                                                                        Similarity
37; Conserv
                                                                                                                                                                                                                     DNA binding; early protein; zinc
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FYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRC-INXQKPLCPEE---KQRH-----L 119 : | | : : | : : | : : 119
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                                                          PRSLEKLQQILQISLEDLPFGCIFCGKLLGAAEKQLFKCTGLCIVWHKGWPYGTCRDCTV 65
                                                                                                  PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK 68
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                                                                                                                                        Score 127; DB 1; 1
Pred. No. 9.5e-05;
1; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 128.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 127; DB 2; ]
Pred. No. 2.1e-05;
4; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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3.6e-05;
71;
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                                                                                                                                            14;
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E6 protein - human papillomavirus type 19
C;Species: human papillomavirus type 19
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #te
C;Accession: $36485
R;Deliue, H; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papa, A;Reference number: $36469
A;Accession: $36469
A;Rolecula type: DNA
A;Residues: 1-166 <DEL>
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S36538
E6 protein
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S36485
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C;Species: human papillomavirus type 12
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36538
R;Delius, H.; Hofmann, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-157 <DEL>
A;Residues: 1-157 <DEL>
A;Cross-references: UNIPROT:P36803; UNIPARC:UPI00001383B8; EMBL:X74466; NID:g396910;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; nucleus; zinc finger
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                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P36806; UNIPARC:UPI00001383BD; EMBL:X74470 C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; nucleus; zinc finger
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 149
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 RDSWKGICRLC 159
                                    RGRWTGRCMSC 139
                                                                       ATATFEFNEFYEHTVTGREIEFVTGKSVFDIDVRCQNCMRYLDSIEKLDICGRRLPFHKV 148
                                                                                                          FYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNI 128
                                                                                                                                              PATIAGLAALLEIPLDDCLVPCNFCGKFLSHLEACEFDDKRLSLIWKGHLVYACCRWCCT 88
                                                                                                                                                                                 PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ELPTTIKELADLLDIPLVDCLVPCNFCGKFLDFLEVCDFDKKQLTLIWKGHFVTACCRSC
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                                                                                                                                                                                                                      14.8%; Score 123; DB 2; Length 166; 24.4%; Pred. No. 0.00014; Live 24; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: C18151
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LEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGR-WTGRCMSCCR-SSRT 145
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A; Cross-references: UNIPROT:P06931; UNIPARC:UPI0000033CF0; GB:X02346; GB:J02044; R; Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
A; Title: Comparative analysis of the human type 1a and bovine type 1 papillomavir A; Reference number: A92993; MUID:83189357; PMID:6302319
A; Contents: annotation
R; Androphy, E.J.; Schiller, J.T.; Lowy, D.R.
Science 230, 442-445, 1985
Science 230, 442-445, 1985
A; Title: Identification of the protein encoded by the E6 transforming gene of bov A; Reference number: A94282; MUID:86018841; PMID:2996134
A; Contents: annotation; identification of the protein
C; Comment: This protein is present in the cell nucleus and the cellular membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E6 protein - human papillomavirus type 9
C;Species: human papillomavirus type 9
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E6 protein - bovine papillomavirus type 1
C;Species: bovine papillomavirus type 1
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: C18151
R;Chen, E.Y.; Howley, P.M.; Levinson, A.D.; Seeburg, P.H.
Nature 299, 529-534, 1982
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submitted to the EMBL Data Library, August 1993
A;Description: Primer_directed sequencing of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Title: The primary structure and genetic organization of A, Reference number: A93289; MUID:83012974; PMID:6289124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-137 < CHE>
                                                                                                                                                                                                                                ;Superfamily: papillomavirus E6 protein; transforming protein; zinc
                                                                                                                                                Local Similarity
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LDCLWCREPLTEVDAFRCMVKDFHVVIREGCRYGACTICLENCLATERRLWQGVPVTGEE 74
                                                    LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT 87
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                                                                                                                                             14.3%;
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Pred. No. 0.00029;
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W6WL8

B6 protein - human papillomavirus type 8

C;Species: human papillomavirus type 8

C;Species: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
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A;Residues: 1-155 <FUC>
A;Cross-references: UNIPROT:P06428; UNIPARC:UPI00001383B4; GB:M12737; NID:g333074
A;Note: this ORF is not annotated in GenBank entry PPH8CG
                                                                                                                                                                                                                                                                                               A;Reference number: )
A;Accession: A03685
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                     R;Fuchs, P.G.; Iftner, T.; Weninger, J.; Pfister, H.
J. Virol. 58, 626-634, 1986
A;Title: Epidermodysplasia verruciformis-associated human papillomavirus 8: genomic sequal, Reference number: A93019; MUID:86200410; PMID:3009874
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                                                                                                                                                       C;Superfamily: papillomavirus E6 protein (;Keywords: DNA binding; early protein; 2 F;39-75/Region: zinc finger CCCC motif F;112-148/Region: zinc finger CCCC motif
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C;Keywords: DNA binding; early protein; transforming
F;40-76/Region: zinc finger CCCC motif
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A; Residues: 1-156 < KIY>
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C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
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Best Local S
Matches 34
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                                                                             Matches
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Best Local :
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                                   ERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXD--
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                                                                           Score 118; DB 1;
Pred. No. 0.0004;
27; Mismatches 6
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PMID:2162112
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C.Species: human papillomavirus type 5b
A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C;Accession: E40480
R;Yabe, Y.; Sakai, A.; Hitsumoto, T.; Kato, H.; Ogura, H.
Virology 183, 793-798, 1991
A;Title: A subtype of human papillomavirus 5 (HPV-5b) and its subgenomic sec A;Reference number: A40480; MUID:91306467; PMID:1649510
A;Accession: E40480
                                                                                                                                                     A;Cross-references: UNIPARC:UPI000017495B
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;41-77/Region: zinc finger CCCC motif
F;114-150/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                     E6 protein - human papillomavirus type 5
C;Species: human papillomavirus type 5
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Feb-1997
C;Accession: F26277
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A; Residues: 1-157 <ZAC>
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A; Residues: 1-157 < YAB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPBEKQRHLDKK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34;
                                                                  ch 13.6%;
l Similarity 24.1%;
33; Conservative 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ω
3 QDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDEAFRDLCIVYRDGNPYAV 62 : | | | : | :::| :| :| :| :| :| :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human papillomavirus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CRVCCGATATYEFNOFYEQTVLGRDIELASGLSIFDIDIRCQTCLAFLDIIEKLDCCGRG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KDKAELPSTIRDLAETLGIPLIDCIIPCNFCGKFLNYLEACEFDYKKLSLIWKDYCVFAC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFHKVRGGWKGVCRLC 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RFHNIRGRWTGRCMSC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KCLKFYSKISEY-RHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQ 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14.0%;
ilarity 24.8%;
Conservative 2
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                                                                       22;
                                                                  Score 113; DB 1;
Pred. No. 0.0012;
12; Mismatches 8;
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Pred. No. 0.00063;
                                                                       82;
                                                                                                              Length 157
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                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                           human papillomavirus type
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                                                                       Gaps
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A;Status: nucleic acid sequence not shown
A;Rolecule type: DNA
A;Residues: 20-147 <VAN2>
A;Cross-references: UNIPARC:UPI0000178417; EMBL:X65200
A;Cross-references: UNIPARC:UPI0000178417; EMBL:X65200
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
F;38-74/Region: zinc finger
F;311-147/Region: zinc finger
A;Molecule type: DNA
A;Residues: 1-135 <GRO>
A;Residues: UNIPROT:P03128; UNIPARC:UPI00001383EB;
C;Superfamily: papillomavirus E6 protein
C;Keywords: DNA binding; early protein; zinc finger
                                                                                                                                             E6 protein - deer papillomavirus
C;Species: deer papillomavirus
C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Date: 38-May-1986 #sequence_revision 28-May-1986 #text_change 09-Jul-2004
C;Accession: A03687
R;Groff, D.E.; Lancaster, W.D.
J. Virol. 56, 85-91, 1985
A;Title: Molecular cloning and nucleotide sequence of deer papillomavirus.
A;Reference number: A93013; MUID:85293253; PMID:2993669
A;Accession: A03687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E6 protein - Old World harvest mouse papillomavirus (fragment) C;Species: Old World harvest mouse papillomavirus C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 09-Jul-2004 C;Accession: S28509; S22955 R;van Ranst, M.A. submitted to the EMBL Data Library, April 1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 20, 2889, 1992
A;Title: Primary structure of the E6 protein of Micromys
A;Reference number: S22955; MUID:92310995; PMID:1319576
A;Accession: S22955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: S28509
A; Accession: S28509
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A; Residues: 1-154 < VAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASEK---LDAKCELQTFILVRHMWRTSCRAC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RDGNPYAVXDKCLKFYSKISEYRHYCYSV---YGTTLEQQYNKPLCDLLIRCINXQKPLC 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QRFHNIRGRWTGRCMSC 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KDKAELPLSIRDLAEALGIPVIDCLIPCNFCGNFLNYLEACEFHYKRLSLIWKDYCVFAC 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KD----CCFKGACIKCRRKLAFAEROKYQVCVGEADLVEAMVGSHVINLTVRCSECLALLT 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PQ-ERPRKLPQLCTE------LQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CRVCCGATATYEFNQFYEQTVLGRDIELASGLSIFDIDIRCQTCLAFLDIIEKLDCCGRG 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKK 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PQPTRPYSFMELCREYTLEQLLKFLNVTLDTLMLPCHFCSSFMDLNNKASYLASQLKVIV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 86; DB 2;
Pred. No. 0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         minutus papillomavirus
                                                               GB:M11910; NID:g333021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22;
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                                                                  PIDN:
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        B6-I protein - human papillomavirus typ (Species: human papillomavirus type 33 (Species: human papillomavirus type 37 (C;Date: 20-Feb-1995 #sequence_revision C;Accession: $23825; $23829 R;Snijders, P.J.F.; van den Brule, A.J.
                                                                                                                                                                             RESULT
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57

den Brule, A.J.C.; Schrijnemakers,

type e 33

33

(fragment)

30-Jan-1998 #text_change 09-Jul-2004

H.F.J.; Raaphorst,

P.M.C.;

3

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RESULT
S19909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-32 <SNI-2
A;Cross-references: UNIPROT:Q81885; UNIPARC:UPT00000F932A; EMBL:X64086; NID:g60282;
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
S19906
                                                                                                                                         A;Molecule type: mRNA
A;Residues: 1-35 <SN1-2
A;Cross-references: UNIPROT:Q81887; UNIPARC:UPI00000EBD75; EMBL:X64087; NID:g60286;
C;Superfamily: papillomavirus E6 protein
C;Keywords: early protein
                                                                                                                                                                                                                                                                        R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers, H.F.J.; Raaphorst, submitted to the EMBL Data Library, January 1992
A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data Library, January A, Description: HPV type 33 in a tonsillar ca A, Reference number: S19906 A, Accession: S19906
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R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers,
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                                                                                                                                                                                                                                       A;Reference number: S19906
A;Accession: S19909
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                  ;Accession: S19909
                                                                                                                                                                                                                                                                                                                                                                     6-III protein - human papillomavirus type 33 (fragment);Species: human papillomavirus type 33
                                                                                                                                                                                                                                                                                                                                                 ;Date: 30-Jun-1992 #sequence_revision
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Best Local
                                                                                      Query Match
Best Local (
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                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
 w
                                                                     l Similarity
16; Conserv
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                     LCTELQTTIHDIILECVYCKQQLLRRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCTELQTTIHDIILECVYCKQQLLRRE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTTLEQ--QYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LYCVFCYCVLGKVEARRCYDKKIR---TVVRGGLRCAVCTACLEKGLYLERVLNAPQPVY 65
LCQALETTIHNIELQCVECKKPLQRSE 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LCQALETTIHNIELQCVECKKPLQRSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QGSIEEPDPFIQKAC---IRCMYCGGILTRDEKDRHRYFEELYVIFRNQVLGRCYTCTR
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                                                                       Conservative
                                                                                      10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10.1%; Score 83.5; DB 1; 28.6%; Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               in a tonsillar carcinoma generates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Mismatches
                                                                       4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.
                                                                                    Score 83; DB 2
Pred. No. 0.21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 83; DB 2
Pred. No. 0.19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                   30-Jun-1992 #text_change 09-Jul-2004
                                  41
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                                                                                                          Length 35;
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                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its putative E7
                                                                       0;
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                                                                       Gaps
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E6 protein - European elk papillomavirus (,Species: European elk papillomavirus (,Species: European elk papillomavirus C,Date: 31-Mar-1989 #sequence revision 31-Mar-1989 #text_change 09-Jul-2004 C,Accession: A29499; F94457; F94506 C,Accession: A29499; F94457; F94506 R,Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U. Gene 50, 195-205, 1986 R,Thitle: Organization and expression of the transforming region from the Eu. A;Reference number: A91567; MUID:87219878; PMID:3034730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 58
T02749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data
A;Description: HPV type 33
A;Reference number: S19906
A;Accession: S23825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: T02749

R;Grafi, G.; Burnett, R.J.; Helentjaris, T.; Larkins, B.A.; deCaprio, J.A.; Sellers, submitted to the EMBL Data Library, March 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G1/S transition control protein RB - maize (fragment) N;Alternate names: retinoblastoma-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: UNIPROT:Q81883; UNIPROT:Q81884; C;Superfamily: papillomavirus E6 protein C;Keywords: DNA binding; early protein; zinc finger
  A; Cross-references:
                      A; Molecule type: DNA
A; Residues: 1-135 < AHO>
                                                              A; Reference number: A91567; A; Accession: A29499
                                                                                                                                                                                                                                                             M6WLEP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q41763; UNIPARC:UPI000017784A; EMBL:U52099;
A;Experimental source: strain W64A+; endosperm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Description: A maize cDNA
A;Reference number: Z14715
A;Accession: T02749
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A; Residues: 1-47 < SNI >
                                                                                                                                                                                                                                                                                 RESULT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Residues: 1-471 <GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: translated from GB/EMBL/DDBJ
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDGNPYAVXDKCLK-----FYSKISEY-----RHYC-----YSVYGTTLEQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DDNSDPRSPKRSCNEFRNTVVERNLQTPPPKQSHMVSTSLKAKCHPLQSTFASPTVC---
                                                                                                                                                                                                                                                                                                                                                                                     ---YNKPLCDLLIRCINXQKPLCPEE 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DPQERPRKLPQLCTELQTTIHDIILECVYCKQQ-----LLRREVY----DFAFRDLCIVY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCTELQTTIHDIILECVYCKQQLLRRE 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LCQALETTIHNIELQCVECKKPLORSE 29
                                                                                                                                                                                                                                                                                                                                             TLFFNRHIDQLILCCLYGVAKVCQLE
                                                                                                                                                                                                                                                                                                                                                                                                                                 NPVGGNEKCADVTIHIFFSKILKFPAIRIRNLCERVQCVEQTERVYNVFKQILEQQT
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  UNIPROT: P11331; UNIPARC: UPI00001383EC; GB: M15953;
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23.3%; Pred. No. 5.4;
tive 23; Mismatches 48; Indels 4
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                                                                                                                                                                                                                                                                                                                                               326
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NID:g333025;
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                                                                                                          European
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zyxin - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence
C:Accession: G02845
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A;Reference number: A94457
A;Accession: F94457
A;Molecule type: DNA
A;Residues: 1-135 <ERI>
A;Cross-references: UNIPARC:UPI00001383EC; GB:M15953; NID:g333025;
R;Pettersson, U.
submitted to GenBank, August 1987
                                                                                                                                                                                                                                                                                                       A;Gene: zyx
C;Keywords: duplication
C;Keywords: duplication
F;384-436/Domain: LIM metal-binding repeat
F;444-495/Domain: LIM metal-binding repeat
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A;Molecule type: mRNA
A;Residues: 1-572 <BEC's
A;Cross-references: UNIPROT:Q15942; UNIPARC:UPI00000424F2; EMBL:X94991; NID:g1155087
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: G02
R; Beckerle, M.C.
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A;Accession: F94506
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: G02845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data A; Reference number: H01748
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Best Local :
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137
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                                                                                                                                   44 DFAFRDLCI-VYRD-----GNPYAVXDKCLKFYSKISEYRHYCYS------VYGTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28 LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT 87
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                                                                                                                                                                                                      1 MFQD---PQERPRKLPQLC------TELQTTIHDIILECVYCKQQLLRREVY 43
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MSC 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTCIWCKKGLDKVDAKRCHEKKIRIACRNGKHCAVCTSCLE:
                                                                                                   SLEGAPYCEGCYTDTLEKCNTCGEP--ITDRMLRATGK--AYHPHCFTCVVCARPLEGTS
                              FIVDQANRPHCVPDYHKQYAPRCSVCSEPIMPEPGRDETVRVVALDKNFHM--
                                                               -LEQQYNKPLC-----DLLIRCINXQKPLCPE----EKQRHLDKKQRFHNIRGRWTGRC 136
                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                        Score 77.5;
Pred. No. 10
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homology <LIM2>
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CiSpecies: Homo sapiens (man)
C;Date: 16-Uul-1999 #sequence-
C;Date: 16-Uul-1999 #sequence-
C;Accession: T09483
R;Smedley, D.P.; Hamoudi, R.; Clark, J.; Warren, W.; Abdul-Rauf, M.; Somers, submitted to the EMBL Data Library, November 1997
A;Description: RAMP, a novel gene encoding a Cys-rich protein.
A;Reference number: Z16688
A;Accession: T09483
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T09483
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C;Date: 22-Jan-1994 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11515
R;Woychik, R.P.; Maas, R.L.; Zeller, R.; Vogt, T.F.; Leder, P.
Nature 346, 850-853, 1990
A;Title: 'Formins': proteins deduced from the alternative transcripts of the limb A;Reference number: S11515; MUID:90363291; PMID:2392150
A;Accession: S11515
  RESULT
S44810
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A;Residues: 1-699 <SME>
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                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPARC:UPI0000169706; EMBL:AF035374; NID:g2665702; PID:g2665703
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
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                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;Molecule type: mRNA
;Residues: 1-1468 <WOY>
;Cross-references: UNIPROT:Q05860; UNIPARC:UPI000027927; EMBL:X53599; NID:g52877; PIDN
                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
Gene: RAMP
                                                                                                                                                                                                                                                                                                                                                                                          position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61
                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                               77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76
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                                                                                                                                                                                                                                                                        25 DIILECVYCKQQLLRR-----EVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEY 76
                                                                                                                                                                                                                                                                                                               37;
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                                                                                                                 KQRHLDKK------QRFHNIRGRW---TGRCMSCCRSSRTRRE 148
                                                                                                                                                      VTYCEYCQEEKTLHETVNFSGVKRPFCSEGCKLLYKQDFARRLGLRCVTCNYCSQLCKKG 465
                                                                                                                                                                                               RHYC-YSVYGTTLEQQYN-----KPLCD-----
                                                                                                                                                                                                                                   DIQLKCNYCKNSFCSKPEILEWENKVHQFCSK-----TCSDDYKKLHCI 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NILG 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIRG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRHYCYSVYG----TTLEQQYNKPLCDLLIRCINXQKPL-----CPEEKQRHLDKKQRFH 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISE 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CT-LQ--LHNPIABLCYISFYLPKGEVRGFSYKGTVTLDRSNNAF------
                                                                                                                                                                                                                                                                                                                                                                                          13q11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.3%; Score 77.5; lilarity 27.4%; Pred. No. 25; Conservative 14; Mismatches
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      537
                                                                                                                                                                                                                                                                                                                               9.3%; Score 77; DB 22.2%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                                                                                                               Mismatches
                                                                             -WYYKAARC-DCCKSQGTLKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
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                                                                                                                                                                                               -----LLIRCI--NXQKPLCPEE 114
                                                                                                                                                                                                                                                                                                               49;
                                                                                                                                                                                                                                                                                                                                                 Length 699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1468;
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                                                                                                                                                                                                                                                                                                               64;
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                                                                                                                                                                                                                                                                                                            Gaps
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                RESULT
T21125
hypothetical protein F19H8.2 -
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C;Species: Homo sapiens (man)
C;Date: 09-Dec-1997 #text_change 09-Jul-2004
C;Accession: S71522; I38074
C;Accession: S71522; I38074
R;Hofferbert, S.; Burfeind, P.; Hoyer-Fender, S.; Lange, R.; Haidl, G.; Engel, Hum. Mol. Genet. 2, 2167-2170, 1993
A;Title: A homozygous deletion of 27 basepairs in the coding region of the hum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
S71522
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C;Species: Caenorhabditis elegans
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Sep-1997
C;Accession: S44B10
R;Antonacci-Fulton, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-400 < ANT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, September 1993 A;Description: Sequence of the C. elegans cosmid F
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                                                                                     밁
                                                                                                                                                                                                                                                                     A; Description: provides the sperm tail with stabilizing and zinc binding properties A; Note: one of the main component of the sperm tail
                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: UNIPROT:Q14990; A;Note: the nucleotide sequence was
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000017B6C2; EMBL:L23648; NID:g388585; PID:g388589
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A; Introns: 107/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: I38074; MUID: 94154698; PMID: 8111388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   outer dense fiber protein 2 - human
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                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: ODF2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: nucleic acid sequence not shown; translation not
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                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196
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                                                                                          26 RCIDEFSTRCLCDLYM--HPYCCCDLHPYPYCL------CYS------KRSRSC 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 DPQERPRKLPQ------LCTELQTTIHDIILECVYCK---QQLLRREVYDFAFR 48
                                          PLCDLLIRCINXQKPLCPEEKQRHL------DKKQRFHNIRGRWTGRCM--SCCRSS 143
                                                                                                                                  REVYDFAFRDLCIVYRDGNPYAVXD-----KCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EPOSHIRESPOKETNLEKYSTGELCLYGRELVNDLNVKTSYLSTILKKVMERKPLN----
GLCDLYPCCLCDYKLYCLRPSLRSLERKAIRAIEDEKRELAKLR-RTTNRILASSCCSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PMDEEROKRAELEORFAIVISKTPPVEGHIWYQGKW 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLCPEEKQRHLDKKQRFHNI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----QGENPNDLADQCKNALQRMSDIRQIIEKRREPTWKRMTGEDYIELMLDDSELKK 305
                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                               14;
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                                                                                                                                                                                                     Score 75.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 76; DB 2; Length 400; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                  UNIPARC: UPI0000130BD2; EMBL: X74614; submitted to the EMBL Data Library,
                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                          DB 2;
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                                                                                                                                                                                                                            Length 250;
                                                                                                                                                                               Indels
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                                                                                                                                                                               37;
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August 1993
  124
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Caenorhabditis elegans

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RESULT 66
S56100
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submitted to the EMBL Data Library,
A;Reference number: Z19379
A;Accession: T21125
             alpha-fetoprotein precursor - gorilla
C;Species: Gorilla gorilla (gorilla)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         outer dense fiber protein - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Kim, Y.; Adham, I.M.; Haack, T.; Kremling, H.; Engel, W. Biol. Chem. Hoppe-Seyler 376, 431-435, 1995 A;Title: Molecular cloning and characterization of the bovine A;Reference number: S56100; MUID:96066278; PMID:7576240
C; Accession:
                                                                                            RESULT 67
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A; Residues: 1-262 < KIM>
                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: UNIPROT:045378; A; Experimental source: clone F19H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-303 <WIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Species: Caenorhabditis elegans;Date: 15-Oct-1999 #sequence_rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Gene: CESP:F19H8.2
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                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession:
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Best Local
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                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                         RCIDEFSTRCLCDLYM--HPYCCCDLHPYPYCL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RWTGRCMS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---RKYNLPEIEVNNSTLTSNSTHVQVSPLEQCLNFQK-ICAAKYKKHFACRQ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QERPRKLPQLCTELQ-----FA 46
                                                                                                                                                  GLCDLYPCCLCDVKLYCLRPSLRSLERKAIRAIEDEKRELAKLR-RTTNRILASSCCSSN
                                                                                                                                                                                    PLCDLLIRCINXQKPLCPEEKQRHL-----DKKQRFHNIRGRWTGRCM--SCCRSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TLEQQYNKPLCDL-------LIRCINXQKPLCPEEKQRHLDKKQRFHNIRG
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                                                                                                                                                                                                                                                         REVYDFAFRDLCIVYRDGNPYAVXD-----KCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.0%;
                                                                                                                                                                                                                                                                                                             9.0%;
                                                                                                                                                                                                                                                                                              14; Mismatches
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                                                                                                                                                                                                                                                                                                                 Score 74.5; DB Pred. No. 9.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               March 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIPARC:UPI0000075B82; EMBL:Z93378; PIDN:CAB07582.1
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                                                                                                                                                                                                                                                                                                                                  Length 262;
                                                                                                                                                                                                                                                                                              Indels
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N,Alternate names: AFP; alpha-1-fetoprotein; alpha-fetoglobulin C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 19-Feb-1984 #sequence revision 19-Feb-1984 #text change 09-Jul-2004 C;Accession: A26624; S37655; A93961; A91497; A23699; A61480; A90624; A90757; A93042; A03; R;Accession: A26624; S37655; A93961; A91497; A23699; A61480; A90624; A90757; A93042; A03; R;Gibbs, P.E.M.; Zielinski, R.; Boyd, C.; Dugalczyk, A. Biochemistry 26, 1332-1343, 1987 Biochemistry 26, 132-1343, 1987 Bioch
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C; Superfamily: serum albumin; serum albumin repeat homology
C; Keywords: embryo; fetus; globulin; glycoprotein; metal binding; plasma
F; 1-18/Domain: signal sequence #status predicted <SIG>
F; 19-609/Product: alpha-fetoprotein #status predicted <MAT>
F; 29-207/Domain: serum albumin repeat homology <SA1>
F; 221-394/Domain: serum albumin repeat homology <SA2>
F; 413-592/Domain: serum albumin repeat homology <SA3>
F; 413-592/Domain: serum albumin repeat homology <SA3>
F; 221-394/Jomain: serum albumin repeat homology <SA3>
F; 221-394/Jomain: serum albumin repeat homology <SA3>
F; 221-394/Jomain: serum albumin repeat homology <SA3>
F; 227/Binding site: copper (His) #status predicted
F; 299-114, 113-124, 148-193, 192-201, 224-270, 269-277, 289-303, 302-313, 384-393, 416-462, 461-472, F; 249/Binding site: bilirubin (Lys) #status predicted
F; 251/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Accession: A26624
A;Molecule type: DNA
A;Residues: 1-609 <GIB>
A;Residues: 1-609 <GIB>
A;Cross-references: UNIPROT:P02771; UNIPARC:UPI0000012A9; GB:M16110; NID:g773678; PIDN:I
A;Cross-references: UNIPROT:P02771; UNIPARC:UPI0000012A9; GB:M16110; NID:g773678; PIDN:I
R;MCVey, J.H.; Michaelides, K.; Hansen, L.P.; Ferguson-Smith, M.; Tilghman, S.; Krumlauf
Hum. Mol. Genet: 2, 379-384, 1993
A;Tille: A G->A substitution in an HNF I binding site in the human alpha-fetoprotein gen
A;Reference number: S37655; MUID:93278385; PMID:7684942
A;Accession: S37655
                                                                                                                                                                                                                        A;Cross-references: UNIPARC:UPI000016A4DF; EMBL:Z19532; NID:g28527; PIDN:CAA79592.1; A;Note: the authors translated the codon TAT for residue 26 as Thr R;Morinaga, T.; Sakai, M.; Wegmann, T.6, Tamaoki, T. Tamaoki, T. Proc. Natl. Acad. Sci. U.S.A. 80, 4604-4608, 1983
A;Title: Primary structures of human alpha-fetoprotein and its mRNA.
A;Reference number: A93961; MUID:83273664; PMID:6192439
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A;Title: Structure of the gorilla alpha-fetoprotein gene and the divergence A;Reference number: A37970; MUID:91169517; PMID:1706310
A;Molecule type: mRNA
A;Residues: 1-609 <MOR>
A;Cross-references: UNIPARC:UPI00000012A9; GB:J00077; NID:g311348; PIDN:CAA24758.1;
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A; Residues: 1-28 < MCV >
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;Residues: 1-609 <RYA>
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Pred. No. 21;
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A;Mclecule type: protein
A;Mclecule type: protein
A;Residues: 'S',20-24,'Q',26-30,'A',32-35,'E',37-39 <RUO>
A;Cross-references: UNIPARC:UPIO0017442C
R;Sakai, M; Morinaga, T; Urano, Y.; Watanabe, K.; Wegmann, T.G.; Ta
J. Biol. Chem. 260, 5055-5060, 1985
A;Title: The human alpha-fetoprotein gene. Sequence organization and
A;Reference number: A92520; MUID:85182629; PMID:2580830
A;Contents: annotation; gene, exons and introns
R;Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 38, 3483-3486, 1978
A;Title: Copper(II)-binding ability of human alpha-fetoprotein.
A;Reference number: A90758; MUID:79001617; PMID:80265
A;Contents: annotation; metal binding
R;Aoyagi, Y.; Ikenaka, T.; Ichida, F.
Cancer Res. 39, 3571-3574, 1979
Cancer Res. 39, 3571-3574, 1979
                                                                                                                                                                                                                                                                                                                                                                                             Cancer Res. 39, 3571-3574, 1979
A;Title: alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-binding abi. A;Title: alpha-Fetoprotein as a carrier protein in plasma and its bilirubin-binding A;Reference number: A90759; MUID:80001710; PMID:89900
A;Contents: annotation; bilirubin binding
C;Comment: aPP is synthesized by the fetal liver and yolk sac. It occurs in the plasma of the company of the serum level in adults is usually less than 40 mg/ml. A otrace amounts after birth. The serum level in adults is usually less than 40 mg/ml. A otrace amounts after birth. The serum level in adults is usually less than 40 mg/ml. A
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A;Residues: 429-556 <BEA>
A;Cross-references: UNIPARC:UPI0000174421; GB:J00076
R;Cross-references: UNIPARC:UPI0000174421; GB:J00076
R;Pucci, P.; Siciliano, R.; Malorni, A.; Marino, G.; Tecce, M.F.; Ceccarini, C.;
Biochemistry 30, 5061-5066, 1991
Biochemistry 30, 5061-5066, 1991
A;Title: Human alpha-fetoprotein primary structure: a mass spectrometric study.
A;Reference number: A23699; MUID:91242409; PMID:1709810
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A; Residues: 'S', 20-30, 'A', 32-37, 'A' <AOY>
A; Residues: 'S', 20-30, 'A', 32-37, 'A' <AOY>
A; Crose - references: UNIPARC: UPI000017442B
A; Ruoslahti, E.; Pihko, H.; Vaheri, A.; Seppala, M.; Virolainen, Johns Hopkins Med. J. Suppl. 3, 249-255, 1974
Johns Hopkins Med. J. Suppl. 3, 249-255, 1974
A; Title: 20. Alpha fetoprotein: structure and expression in man.
A; Reference number: A93042; MUID:75018719; PMID:4138095
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A;Title: Comparative chemical structure of human alpha-fetoproteins A;Reference number: A90757; MUID:78001760; PMID:71198
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A;Residues: 19-45;63-97;102-107;122-184;187-249;255-489;507-609 <TEC>
A;Residues: 19-45;63-97;102-107910000174422; UNIPARC:UPI0000174424; UNIPARC:UPI0000174425
A;Cross-references: UNIPARC:UPI0000174422; UNIPARC:UPI0000174424; UNIPARC:UPI0000174425
R;Yachnin, S.; Hsu, R.; Heinrikson, R.L.; Miller, J.B.
Biochim. Biophys. Acta 493, 418-428, 1977
A;Title: Studies on human alpha-fetoprotein. Isolation and characterization of monomerical
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A;Residues: 'S',20-22,'S',24-35 <YAC>
A;Cross-references: UNIPARC:UPI000017442A
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A;Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
A;Residues: 19-45;60-97;102-107;122-184;187-249;255-489;507-609 <PUC>
A;Crose-references: UNIPARC:UPI0000174422; UNIPARC:UPI0000174423; UNIPARC:UPI0000174424;
A;Tecce, M.F.; Terrana, B.; Giuliani, M.M.; Ceccarini, C.
T. Nucl. Med. Allied Sci. 34, 213-216, 1990
A;Tille: Characterization of in vitro expressed human alpha-fetoprotein as highly reprocaping the procaping of the procaping o
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A;Title: Structure and evolution
A;Reference number: A91497; MUID:
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A;Map position: 4g11-4g13
A;Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3; 353/2; 397/3; 430/2; 476/3;
C;Superfamily: serum albumin; serum albumin repeat homology
                                                                                                                                                                                        A;Gene: GDB:AFP
A;Cross-references: GDB:119660; OMIM:104150
                                                                                                                                                                                                                                                                                                                   properties.
C; Genetics:
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A;Gene: afp
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A;Mene: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3
A;Introns: 29/1; 46/2; 90/3; 161/2; 205/3; 238/2; 281/3
C;Superfamily: serum albumin; serum albumin repeat home
C;Keywords: 91ycoprotein
C;Keywords: 91ycoprotein
F;1-19/Domain: signal sequence #status predicted <SIG>
F;1-19/Domain: signal sequence #status predicted .
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F;413-592/Domain: serum albumin repeat homology <SA3>
F;413-592/Domain: serum albumin repeat homology <SA3>
F;24/Binding site: copper (His) #status experimental
F;99-114,113-124,148-193,192-201,224-270,269-277,289-303,302-313,384-393,416-462,461-472
F;249/Binding site: bilirubin (Lys) #status predicted
F;251/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-609 < NIS>
A; Cross-references: UNIPROT: Q28789;
C; Comment: This protein is a plasma
o similar properties and structure.
C; Genetics:
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                                                                                                                                                                  -----RDGNPYAVXDKCLKFYSKISEY--RHYCYSVYGTTLEQQYNKPLCDLLIRC 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                               9.0%;
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                                                                                                                                                                                                                                                                                                                                                                                           26;
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 74.5;
Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 74.5;
Pred. No. 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIPARC:UPI00012A6FA; GB:U21916; NID:g841311; PIDN protein produced in the fetal and neonatal liver and
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-Feb-1996 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          238/2; 281/3; 353/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zielinski, R.; Dugaiczyk, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                           44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 609;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <MAT>
                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RGQCIIHAENDEKPEGLS 327
                                                                                                                                                                                                                                             RGQCIIHAENDEKPEGLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     structural similarity
                                                                                                                                                                                                                                                                                                                                                                                           41;
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                                                                                                                                                                                                                                             327
                                                                                          384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54
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FQTENPLECQDKGEEELQKYIQESQ

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C;Accession: F96784
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Southwick, A.M.; Sun, H.; Tallon, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: F96784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Accession: T45119
R;Popovici, C.; Adelaide, J.; Ollendorff, V.; Chaffanet, M.; Guasch, G.; Jacrot, M.; Lex Proc. Natl. Acad. Sci. U.S.A. 95, 5712-5717, 1998
A;Title: Fibroblast growth factor receptor 1 is fused to FIM in stem-cell myeloprolifera A;Reference number: Z22919; MUID:98245146; PMID:9576949
A;Accession: T45119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FIM protein [imported] - human
C;Species: Homo sapiens (man)
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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A; Residues: 1-1379 < POP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-524 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q9UBW7; UNIPARC:UPI000016AF9A; EMBL:Y13472; NID:g3135791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Gene: F1B16.6
                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            position: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80 CYSVYG---TTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
                                                                                                                                                                                                                                                                         25 DIILECVYCKQQLLRR-----EVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEY 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43 YDFAFRDLC--IVYRDGNPYAVXD---KCLKFYSKISE------YRHY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27;
                                                                                                                                                                                                                                                                                                                                  37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 8.9%; Score 74; DB Similarity 24.3%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                      KORHLDKK----
                                                                                                       VTYCEYCQEEKTLHETVNFSGVKRPFCSEGCKLLYKQDFARRLGLRCVTCNYCSQLCKGG
                                                                                                                                                           RHYC-YSVYGTTLEQQYN-----KPLCD-----
                                                                                                                                                                                                                     DIQLKCNYCKNSFCSKPEILEWENKVHQFCSK-----TCSDDYKKLHCI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOYHYONLSNOLSYNNLNPSTMSDENGKSLSVHOHHSDQILPSSVYNNNGNNGVGFYNNY
ATKELDGVVRDFCSEDCCKKFQD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RYETSGFVSSVLRSRYLKPTQQLLDEVVSVRKDLKLGNKKMKNDKGQDFHN
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                          8.9%;
                                                   -----QRFHNIRGRW---TGRCMSCCRSSRTRRE 148
                                                                                                                                                                                                                                                                                                                             16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17; Mismatches
                                                                                                                                                                                                                                                                                                                                                          Score 74; DB 2; Length 1379; Pred. No. 51;
                                                                                                                                                                                                                                                                                                                                Mismatches
-WYYKAARC-DCCKSQGTLKE
                                                                                                                                                              ----NXQKPLCPEE
                                                                                                                                                                                                                                                                                                                                50;
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  781
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                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                 114
                                                                                                                                                                                                                     679
RESULT 74
JC7686
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A;Cross-references: UNIPROT:Q89370; UNIPARC:UPI00000F6ADB; EMBL:U42580; NID:g4028896; A;Experimental source: specific host Chlorella strain NC64A C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     proline-rich protein A35L - Chlorella virus PBCV-1
C;Species: Chlorella virus PBCV-1
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999
C;Accession: T17525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 31-Dec-2004
C;Accession: A72220
C;Accession: A72220
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hi, Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,
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A; Residues: 1-549 < GRA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the EMBL Data Library, May 1999
A;Reference number: Z18806
A;Accession: T17525
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
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A;Title: Evidence for lateral gene transfer between Archaea and A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: A72220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Graves, M.V.; Van Etten,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q9X221; UNIPARC:UPI00000C1227; GB:AE001810; GB:AE000512; A;Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-357 < ARN>
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                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       A35L
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146 RQIQAEAEGKAAAEFQGEYRNCLLYSRYKEPPQV 179
                                               122 KORFHNIRGR----WTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 ALEYADRNLYDIAHDIIKFMLDIDENYAPAYELKGSLLVEQ 144
                                                                                                                                       67 LKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLI----RCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                    36 TEEEQTLYQYYCKATDMYPKDTEWESKCEDLAYKYPELKLRHDMCNLWQDEYFCGMRDRN
                                                                                                                                                                                                                                 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 CIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQ 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    46
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3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 QERPRKLPQLCTELQTTIHDIILECVYCK-----QQLLRRE---VYDF-----AFRDL 50
                                                                                          EQLYPERS----YCYDSDGNIDKTQ---PFCVKLCETTPGKCISQAE---AEERRKQREK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KENIMKEVOTCEKLEKVVH--LDETVYEPLIFPEFOEWLREENITPKDFKNVSLKGLYDL 103
                                                                                                                                                                                                                               TELOTTIHDIILEC--VYCKQQLLRREVYDFAFR-----DLCIVYRDGNPYAVXDKC 66
                                                                                                                                                                                                                                                                               Conservative
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Library, May 1999
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Pred. No. 15;
                                                                                                                                                                                                                                                                                                  Score 73.5;
Pred. No. 23;
                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                            BB
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                                                                                                                                                                                                                                                                                                                       Length 549;
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                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                               29;
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F;324-374/Domain: LIM metal-binding repeat homology <LIM1>
F;383-433/Domain: LIM metal-binding repeat homology <LIM2>
F;383-433/Domain: LIM metal-binding repeat homology <LIM3>
F;442-492/Domain: LIM metal-binding repeat homology <LIM4>
F;501-551/Domain: LIM metal-binding repeat homology <LIM4>
F;31,118,181/Binding site: phosphate (Tyr) (covalent) #stat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Salgia, R.; Li, J.L.; Lo, S.H.; Brunkhorst, B.; Kansas, G.S.; Sobhany, E.S.; Sun, Y. J. Biol. Chem. 270, 5039-5047, 1995
A;Title: Molecular cloning of human paxillin, a focal adhesion protein phosphorylated A;Reference number: A55933; MUID:95197488; PMID:7534286
A;Accession: A55933
                                                                                                                                                                                                                                                                                                                     A; Map position: 12q24-12q24
C; Keywords: cell adhesion; c:
F; 46-55/Region: proline-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activator of cAMP-responsive element modulator, testis - human C;Species: Homo sapiens (man) C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004 C;Accession: JC7686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-557 < SAL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
C;Accession: A55933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Contents: Testis
A; Accession: JC7686
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A;Title: Cloning and expression of activator of CREM in testis in
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                                          Ś
                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: GDB:702105
                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:PXN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Alternate names: peroxisomal membrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     paxillin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Keywords: spermatogenesis; testis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 6q
A; Introns: 53/3; 112/3; 168/3; 231/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of human spermatogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Palermo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cross-references: UNIPROT:P49023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Homo sapiens (man)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reference number: JC7686; MUID:21226154; PMID:11327716
                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                          Similarity
                                                QLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKI 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCTELQTTIHDIILECVYCKQQLL----RREVYDFAFRDLCIVYRD----
QVVTAMGKTWHPEHFVCTHCQEEIGSRNFFE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LCEEQFMSRDDYPFCMDCYNHLYANKCVACSK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LCPEEKORHLDKKORFHNIRGRWTGRCMSCCR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SGN----YCVPCFEK--EFAHYCNFCKKVITSGGTTFCDQLWHKECFL--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -GNPYAVXDKCLKFYSKISEYRHYC-----YSVYGTTLEQQYNKPLCDLLIRCINXQKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LCTECYS--NECSSKCFHCKRTIMPGSRKMEFKGNYWHETCFVCENCRQPIGTKPLISKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.8%; Score 73; DB 21.1%; Pred. No. 14;
                                                                                                                          8.8%;
20.7%;
                                                                                                                                                                                                                                                                                                                                                     cytoskeleton; peroxisome; phosphoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                          Score 73;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIPARC: UPI000002B0A7;
                                                                                                  Mismatches
                                                                                                                                                                                                  (covalent) #status
                                                                                                                             DB
26;
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•-
                                                                                                                                                Length 557
RDGQPYCEKD----YHNLF 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GB:U14588; NID: 9704347; PIDN
                                                                                                                                                                                                     predicted
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C;Date: 12-Feb-1999 #sequence revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: T01171; S72272
C;Accession: T01171; S72272
R;Ach, R.A.; Durfee, T.; Miller, A.B.; Taranto, P.; Hanley-Bowdoin, L.; Zambryski, P.C. Mol. Ccll. Biol. 17, 5077-5086, 1997
Mol. Ccll. Biol. 17, 5077-5086, 1997
A;Title: RRB1 and RRB2 encode maize retinoblastoma-related proteins that interact with A;Reference number: Z09601; MUID:97415586; PMID:9271385
A;Accession: T01171
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R;Salgia, R.; Li, J.L.; Lo, S.H.; Brunkhorst, B.; Kansas, G.S.; Sobhany, E.S.; Sun, Y. R;Salgia, R. E. Li, J. Li, Lo, S.H.; Brunkhorst, B.; Kansas, G.S.; Sobhany, E.S.; Sun, Y. J. Biol. Chem. 270, 5039-5047, 1995
A;Title: Molecular cloning of human paxillin, a focal adhesion protein phosphorylated A;Reference number: A55933; MUID:95197488; PMID:7534286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;326-376/Domain: LIM metal-binding repeat homology <LIM1>
F;385-435/Domain: LIM metal-binding repeat homology <LIM2>
F;3844-494/Domain: LIM metal-binding repeat homology <LIM3>
F;503-553/Domain: LIM metal-binding repeat homology <LIM4>
F;31,118/Binding site: phosphate (Tyr) (covalent) #status predicted
                                                          A;Description: cell cycle control; probably controls C;Superfamily: retinoblastoma-associated protein C;Keywords: cell cycle control
                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
A; Residues: 1-866 < ACH>
A; Residues: 1-866 < NCH>
A; Cross-references: UNIPROT:022344; UNIPARC:UPI00000A3DFE; EMBL:AF
A; Cross-references: UNIPROT:022344; UNIPARC:UPI0000A3DFE; EMBL:AF
R; Xie, Q.; Sanz-Burgos, A.P.; Hannon, G.J.; Gutierrez, C.
EMBO J. 15, 4900-4908, 1996
A; Title: Plant cells contain a novel member of the retinoblastoma
A; Reference number: S72272; MUID:97045098; PMID:8890163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N_iAlternate names: retinoblastoma susceptibility protein Rb1; retinoblastoma-related C_iSpecies: Zea mays (maize)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                    C; Function:
                                                                                                                                                                          A; Gene: RRB1; Rb1
                                                                                                                                                                                                                                           A;Cross-references: UNIPARC:UPI000002EEEB; EMBL:X98923; NID:g1617473; PIDN:CAA67422.1;
                                                                                                                                                                                                                                                                    A; Molecule type: mRN
A; Residues: 184-866
                                                                                                                                                                                                                                                                                                                               A; Accession: S72272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Molecule type: mRNA
;Residues: 1-559 <SAL>
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;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                            Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEYRHYCYSVYGTTLEQQYNKPLCDLLIRCIN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEYRHYCYSVYGTTLEQQYNKPLCDLLIRCIN
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Pred. No. 27;
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Length
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                                                                                                                     phase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: AF007793; NID: g2352794;
                                                                                                                        transition
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                                                                                                                                                                                                                                                                                                                                                                                             family of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Query Match Best Local Similarity

8.7%; 23.3%;

Score 72.5; Pred. No. 45;

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C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004 (C;Accession: G82108 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio ch A;Reference number: A82035; MUID:20406833; PMID:10952301
                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-422 <WIL>
A;Cross-references: UNIPROT:Q20082; UNIPARC:UPI000007F86E; EMBL:Z36752; PIDN:CAA85325.1;
A;Experimental source: clone F35H8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Nolecule type: DNA
A;Molecule type: DNA
A;Residues: 1-270 <HEI>
A;Cross-references: UNIPROT:Q9KQ28; UNIPARC:UPI000013B7DF; GB:AE004289; GB:AE003852; NII
A:Rxnerimental source: serogroup OI; strain NI6961; biotype El Tor
                                                                                                                                                                                                                                         submitted to the EMBL Data Library, August 1994
A;Reference number: Z19475
A;Accession: T21820
                                                                                                                                                                                                                                                                                                 R; Berks, M.
                                                                                                                                                                                                                                                                                                                                  hypothetical protein F35H8.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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                                                                         A; Introns: 24/1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              conserved hypothetical protein VC2176 [imported] - Vibrio cholerae (strain N16961 C;Species: Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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Best Local S
Matches 22
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 Best Local
Matches
                                                                                                              Gene: CESP:F35H8.3
                                                                                                                                Genetics:
                                    Query Match
                                                                                           position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               position:
                                                                                                                                                                                                                                                                                                                                                                                                                79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 -- IEHCPNDPAAELLKTQVN 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KQQLLRREVYDFAFR--DLCIVYRDGNPYAVXDKCLKFYS-----KISEYRHYCYSVYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TLFFNRHIDQLILCCLYGVAKVCQLE 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---NPVGGNEKCADVTIHIFFSKILKLAAIRIRNLCERVQCVEQTERVYNVFKQILEQQT 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTLEQQYNKPLCDLLIRCIN 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KSALLREERYTLALRCTDLALTFVPDDPYEIRDRGFIYQQLQCHQIAISDYQYF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RDGNPYAVXDKCLK-----FYSKISE-----YRHYC------YSVYGTTLEQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DDNADPRSPKRSCNESRNTVVERNLQTPPPKQSHMVSTSLKAKCHPLQSTFASPTVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DPQERPRKLPQLCTELQTTIHDIILECVYCKQQ-----LLRREVY----DFAFRDLCIVY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---YNKPLCDLLIRCINXQKPLCPEE 114
                                                                         52/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                       98/1; 191/3; 274/3; 368/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.7%;
8.7%; Score 72; DB
23.6%; Pred. No. 25;
Live 13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 72; DB
Pred. No. 16;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Mismatches
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16;
                   DB 2;
25;
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43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 270
                                    Length 422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pathogen Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gwinn, M.L.; Dodson, R.J
H.; Dragoi, I.; Sellers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41;
 38;
Gaps
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7;
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                                 A; Description: :
C; Superfamily: 1
C; Keywords: DNA
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H86477
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                                                                                             C; Function:
                                                                                                            A; Gene:
                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 81
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R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dew ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Liu, X. Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Ma Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; T. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: H86477

A;Accession: H86477

A;Accession: H86477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references:
C;Genetics:
                                                                                                                                                                                 A; Gene: F1504.1
A; Map position:
                                                                                                                                                                                                                                                                             A; Residues: 1-565 <STO:
                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
                                                     Query Match
Best Local Similarity 33...
"---hes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80
                                                                                                                                                                                                            F1504.19
  217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                219 LKDHSLLKPMFSCD--
VYSGVLEESSTSVTCAI---CID---DYCVGEKLRILPCKHKYHAVCIDSWLGRCRSFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TLEQQYNKPL--CDLLIRCINXQKPLCP-----EEKQRHLDKKQRFHNIRGRWTGRCMS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LYRCTNCKTYFGNKEVYO---RHIQEVHGDARPFRCFNCGMRFANKTSMTHH--
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                                         VYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNI-RGRWTGRCMSCC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCR 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CMR 262
                                                                                                                                                                                                                                                        UNIPROT:Q91QG6; UNIPARC:UPI00000A7592; GB:AE005172; NID:g8778343; PII
                                                                                                             33.9%;
                                                                                       6
                                                                                                             Score 71.5;
Pred. No. 37;
                                                                                         Mismatches
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                                                                                                                                        B
                                                                                       26;
                                                                                                                                   Length 565
                                                                                         Indels
                                                                                       7;
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                                                                                         Gaps
  269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Marziali,
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C;Species: Synechococcus sp.

A;Variety: PCC 7942
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
C;Accession: T11850
                                                                                                                                                                                                                                R;Bird, A.J.; Turner-Cavet, J.S.; Lakey, J.H.; Robinson, N.J. Biol. Chem. 273, 21246-21252, 1998
A;Title: A caboxyl-terminal Cys2/His2-type zinc-finger motif A;Reference number: Z17359; MUID:98362004; PMID:9694883
A;Accession: T11850
                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-616 <BIR>
                                                                                                                               A; Cross-references: UNIPROT: P74893; UNIPARC: UPI00001321F0;
                                                                                                                                                                                                     A;Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA primase (EC 2.7.7.-) -
interacts with DNA to synthesize the DNA primase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synechococcus sp.
                                                                                                                                                                                                             from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PCC 7942)
                           primer
                                                                                                                                  EMBL: X94247
                           RNA that initiates DNA replic
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                                                                                                                                                                                                                                                                                       DNA primase
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influences

Ö

replication; nucleotidyltransferase

71.5;

DB

2

Length

616;

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hypothetical protein SPBC31F10.14c - fission yeast (Schizosaccharomyces pombe) c;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004 C;Accession: T40217 R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Pohl, T. substitud to the EMBL Data Library, August 1997
                                                                                                                                                                                                                                                                                                            RESULT 83
T40217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Tachypleus tridentatus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A23689
R;Muta, T.; Hashimoto, R.; Miyata, T.; Nishimura, H.; Toh, Y.; Iwanaga, S.
J. Biol. Chem. 265, 22426-22433, 1990
A;Title: Proclotting enzyme from horseshoe crab hemocytes. cDNA cloning, disulfide A;Reference number: A23689; MUID:91093088; PMID:2266134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:P21902; UNIPARC:UPI00001313DC; C;Superfamily: serine proteinase easter; trypsin homology C;Keywords: hydrolase; serine proteinase estatus predicted <SIG> F;1-21/Domain: signal sequence #status predicted <SIG> F;128-370/Domain: trypsin homology <TRY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       S
                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                  A; Reference number: Z21913
A; Accession: T40217
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A; Residues: 1-375 < MUT>
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                                               A; Residues: 1-1630 < WOO>
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Best Local Similarity
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Matches 31; Conserv
Cross-references: UNIPROT:P87315; UNIPARC:UPI00006956C; EMBL:Z97204; PIDN:CAB10090.1 Experimental source: strain 972h-; cosmid c31F10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       228,326/Active site: His, Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   167
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             46;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCCRSSRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTLEQQYNKPLCDLLIRCINXQ--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VITASH----CVVNSAGTDVMPADVFSVRLGEHNLYSTDDDSNPIDFAVTSVKHHEHFVLA 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VYDFAFRDLCIVYRDG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PKQIPPNLPEVCGIHNTTTTRIIGGREAPIGAWPWMTAVYIKQGGIRSVQCGGALVTNRH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQERPRKLPQLCTELQTTIHDII-------LECVYCKQQLLR------RE 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LCPEEKQRHLDKKQRFHNI 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERPRKLPQLCTEL--QTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXD 64
                                                                                                                                                                                                                                                                                                                                                                                                        FNGPSSAVLREVQL 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYLN-----DIAILTLNDTVTFTDRIRPICLPYRKLRYDDLAMRKPFITG-W-GTTA 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAKQFY-----YCFSCGAGGNPIKFLMELGKQSFSEVVLDLAKRYQVPVRTLEVQQ-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DTPRLHPETIAAVKERADIVDIVSE-----QVVLKKRGKDFV--GLCPFHDDKSPSFTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 71;
Pred. No.
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7; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -KPLC-PEEKQRHLDKKQRFHNIRGRWTGRCM 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 375
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guanine nucleotide exchange factor unc-73a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: 11-Jan-2000 #sequence revision 11-Jan-2000 #text_change 09-Jul-2004 C;Accession: T42739; T42740; T34427; T34430; T34426 R;Steven, R.; Kubiseski, T.J.; Zheng, H.; Kulkarni, S.; Mancillas, J.; Ruiz Morales, Cell 92, 785-795, 1998 A;Title: UNC-73 activates the Rac GTPase and is required for cell and growth cone mig A;Accession: T42739 A;Accession: T42739 A;Accession: T42739 A;Accession: T42739 A;Ascatus: preliminary; translated from GB/EMBL/DDBJ
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D87749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology. A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_elegans/A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;anonymous, The C. elegans Sequencing Science 282, 2012-2018, 1998
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C;Species: Caenorhabditis elegans
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les 40; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                 932 DRNKLLKSAHGCYKTYETAVLPILNQLESEYHSPTVTDWCAGCTSSIDADRAAYVADLLS 991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 --SKISEYRHYCYSVYGTT-----LEQQYNKP-LCDLLIRCINX----QKPLCPEEKQ 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 DFAFRDLCIVYRDGNPYAVXDKCLKFYS-----KISEYRHYCYSVYGTTLEQQYNKPLC 97
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                                                                                                                                                                                                                                                                                                                                           KHMDYKERFGKGCTYALRNGDFLLRYIRR-STVNQSERKRHETKI 1035
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22.8%; Pred. No.
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Pred. No. 1.2e+02;
Pred. No. 52;
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C;Accession: C97723
R;Ogata, H.; Audic, S.; Renesto-Audiffren, Science 293, 2093-2098, 2001
A;Title: Mechanisms of Evolution in Ricket: A;Reference number: A97700; MUID:21442074; A;Accession: C97723
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 86
C97723
                                                                                                                                                                                                                                                                                                                                                  aspartate-tRNA ligase (EC 6.1.1.12) - Rickettsia conorii (strain Malish 7) C;Specias: Rickettsia conorii (C;Specias: Rickettsia conorii (C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 03-Jun-2002 C;Accession: C97723
                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-615 < KUR>
A; Cross-references: UNI
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A; Introns: 7/3; 64/2;
19/3; 2262/2; 2331/1;
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A; Residues: 'MVIKCFT', 1568, 'LRK', 1572-2488 <DU3>
A; Cross-references: UNIPARC: UPI000002A2LD; EMBL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Du, Z.; Le, T.
submitted to the EMBL Data Library, November 1996
A;Description: The sequence of C. elegans cosmid F55C7
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A;Cross-references:
A;Accession: T42740
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A;Residues: 1-2488 <DUZ>
A;Residues: 1-2488 <DUZ>
A;Cross-references: UNIPARC:UPI0000611F8; EMBL:U80436;
A;Experimental source: strain Bristol N2; clone F55C7
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;Residues: 1-1634,'QN',1637,'E' <ST2>
;Cross-references: UNIPARC:UPI00002A21C; EMBL:AF048835;
                                                                                           Gene: aspS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene: unc-73; F55C7.7a; unc-73; F55C7.7b; CESP:F55C7
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                                                                        Superfamily:
                                                                                                                      Genetics:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 932 DRNKLLKSAHGCYKTYETAVLPILNQLESEYHSPTVTDWCAGCTSSIDADRAAYVADLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 KQQLLR-----REVYD---FAFRDLC---IVYRDGNPY---AVXDKCLKFY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40;
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                                                                      lysine-tRNA ligase
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                                                                                                                                            UNIPARC: UPI0000164BE8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95/3; 230/3; 265/2; 335/3; 360/3; 488/3; 569/1; 2351/3; 2396/1; 2431/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.6%;
                                                                                                                                                                                                                                                         ution in Rickettsia conorii and Rickettsia MUID:21442074; PMID:11557893
    .58;
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Pred. No. 1.7e+02
    Score
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clone F55C7
                                                                                                                                         GB:AE006914; PIDN:AAL02725.1; PID:g15619236;
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  <u>ب</u>
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    615;
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A;Title: Comparative genomes of Clamydia pneumoniae and C. A;Reference number: A72000, MUID:99206606; PMID:10192388 A;Recession: D72127 A;Status: preliminary A;Molecule type: DNA A;Molecule type: DNA A;Residues: 1-449 <ARN A;Residues: 1-449 <ARN A;Experimental source: strain CWL029 A;Experimental source: strain CWL029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein CPj0041 [imported] - Chlamydophila pneumoniae (strain J138) C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (c;Species: Chlamydophila pneumoniae) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004 C;Accession: C86496 C;Accession: C86496 R;Shirai, M; Hirakawa, H.; Kimoto, M; Tabuchi, M; Kishi, F; Ouchi, K.; Shiba
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: C86496
A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                         hypothetical protein - Chlamydophila pneumoniae (strain C
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_
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A;Experimental source: strain J138
C;Genetics:
A;Gene: CPj0041
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                                                                                                                               A;Gene:
                                                                                                                                                   A; Experimental C; Genetics:
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                                                      . Similarity 27; Conserv
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                 REVYDFAFRDLCIVYR----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REVYDFAFRDLCIVYR-----DGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
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                                                        Conservative
                                                                        8.4%;
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                                                     Score 70; DB
Pred. No. 42;
13; Mismatches
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Pred. No.
-DGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
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                                                                                                                                                                                                                                                                                                                                         J.; Olinger, L.; Grimwood,
                                                                                                                                                                                          GB:AE001589;
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                                                        18;
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A;Residues: 1-708 <WIL>
A;Cross-references: UNIPROT:O62305; UNIPARC:UPI000017A3A1; EMBL:Z70279; PIDN:CAA94244.1;
A;Experimental source: clone K11E8
C;Genetics:
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C;Accession: A81544

C;Accession: A81544

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C;Accession: A81544
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submitted to the EMBL Data Library,
A;Reference number: Z19771
A;Accession: T23616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-Oct-2004
C;Accession: T23616
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T23616
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A81544
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C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
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A;Experimental source: strain AR39;
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Best Local Similarity
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Introns: 8/2;
                                                                                                                                                                                                                                                                                       Gene: CESP:K11E8.1c
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          401 YHPY----HC--FTNKMSNYERAAPSSHGSSTTKKIANAIADLVIR 440
                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95 PLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
                                                                                                                                                                    23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      h 8.4%; Score 70; DB Similarity 27.6%; Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AFCE----YEKAKLIGDEEKSAHAE--QRFQDIKNRW 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REVYDFAFRDLCIVYR-----DGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REVVDRFMRTTCNIRKIAMTFDRHVYSVAKTA---FEKAFGALETC--VY-ESMRESYRE 263
                                                                                       PQKFPRNC-----VHPFTTHPYYSPKESSKKKLFFTLLFEVCPHTSRSHILLRDNTKNI 400
                                                                                                                          PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLC----IVYRDG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REVVDRFMRTTCNIRKIAMTFDRHVYSVAKTA---FEKAFGALETC--VY-ESMRESYRE 263
                                             -NPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIR 102
                                                                                                                                                                                                                                           78/2; 100/2; 124/3; 186/1; 217/3; 258/3; 286/3; 401/2;
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -YEKAKLLGDEEKSAHAE--QRFQDIKNRW
                                                                                                                                                                  8.4%; Score 70; DB 2; Length 708; 21.7%; Pred. No. 64; ative 23; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIPARC:UPI00000D2F9A; GB:AE002232; GB:AE002161; NI
HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      March 1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Length 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                    24;
                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                 501/1; 536/1;
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1436 <TET>
A;Cross-references: UNITROT:Q9PKP1; UN
A;Experimental source: strain Nigg (Mc
C;Genetics:
A;Gene: TC0424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONSERVED hypothetical protein TC0424 [imported] - Chlamydia muridarum (strain Nigg) C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;Jate: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Ju1-2004 C;Accession: B81704 R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 200 A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39. A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 92
T15519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Bentley, D.
submitted to the EMBL Data Library, April 1996
specription: The sequence of C. elegans cosmid C15H9
A;Reference number: Z18364
A;Accession: T15519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C15H9.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004 C;Accession: T15519
                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-314 <BEN>
A;Residues: 1-314 <BEN>
A;Cross-references: UNIPROT:Q18029; UNIPARC:UPI000007A22F; EMBL:U56965; NID:g1945492;
A;Experimental source: strain Bristol N2; clone C15H9
吊
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                           A; Introns: 76/1; 177/3; 210/3; 268/2
                                                                                                                                                                                                                                                                                                                                                                   Map position: X
                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                           Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                  Watch 8.4%; Score 69.5; Local Similarity 26.3%; Pred. No. 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 8.4%; Score 70; DB 2; Local Similarity 21.9%; Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        403 VRIVTQKCLREELKDLLGKTDEELKPCDLSKIQRSVCLFATSVVSLLEGRMGVSEKSSIK 462
  284 IFRGSKCL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 --AVXDKCLK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                                                                                                                  9 PRKLPQLCTBLQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGN------P 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 QERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDG-NPY---- 60
                                                     YAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQ-YNKPLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QAK 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EIBETVYRELGSTILOLGGLSGGITPLIDNVHKAIROGRALSNELROSIOLHPERRFHRL 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDRIRSLAQ-----QKTLTAALLRKLYC-----EIED-AMHEICI--EDGISPYIQDQ 402
                                                                                                             PRKTSRVSTELKVSINFIIVSMFLLVQTLI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EYRHYCYSVYGTTLEQQYN-----KPLCDLLIRCINXQKPLCPEEKQR-HLDKKQRFHNI 128
                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                           11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Mismatches
  -AYMVSGSALRNAIVNLILC 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UNIPARC:UPI0000057904; GB:AE002309; GB:AE002160; NID (MoPn)
                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----FYSKIS 74
                                                                                                                ----YNICTLYEDNNLCLFLLFIAP 283
                                                                                                                                                                                                                           31,
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                                                        97
                                                                                                                                                                                                                                                                                Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                           31;
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                                                                                                                                                                                                                           Gaps
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RESULT
A71928
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T33884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: The sequence A;Reference number: Z21431 A;Accession: T33884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Becker, M.; Wamsley, P.; Twyman, B.; Beck, C.; Bradshaw, H. submitted to the EMBL Data Library, February 1999
A;Description: The sequence of C. elegans cosmid H14E04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-298 <STO>
A;Cross-references: UNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: B84474
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A;Experimental source: strain Bristol N2; clone H14E04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-327 <BEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein H14E04.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 31-Dec-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gene: At2g06010
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Gene: CESP:H14E04.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T33884
                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                 Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                 Introns: 11/2; 47/1;
Superfamily: cyclin,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Accession: B84474
                        95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          167 VGHNFQMNAIGWKWKLTSCLGGDGVSRIRNKTTL 200
                                                                                            122 AIVLPKRWGVTFETTSTKNGVVYDSEFILVEILDCCLVVHHASRPMCPPPPPREIFDK 179
                                                                                                                                           84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86 TTLEQQYNKPLCDLLIRCINXQKPLCPEEK-----QRHLDKK---QRF-----
                                                                                                                                                                                                                                        31 VYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSV-----
                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --HNIRGR---WTGRCMSCCRS---SRTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STNNQLYNEPTNDYHAKLV--LKPLCPERKWKFIYEPLHQEVRVLSKKIPVTRFLNLQVG
                                                                                                                                                                                           IYFKRFYLRQ-----SFRDMC-----PFLVASTALFLACKVEE--HTTLSVSSFLKNT 121
                                                                                                                                         ----YGTTLEQQYNKP----
                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNIPROT: Q8VY85; UNIPARC: UPI000017A73D; GB: AE002093; NID: g4388730;
                                                                                                                                                                                                                                                                                                                                                                                 84/2; 125/1; 167/2; 181/1; 215/1; C/H/G types
                                                                                                                                                                                                                                                                                                              8.3%; Score 69; DB 2; Length 327; 23.7%; Pred. No. 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8.3%;
30.9%;
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Pred. No.
                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                         --LCDLLIRCI---NXQKPLCPEEKQRHLDKK 122
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                                                                                                                                                                                                                                                                                       35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                       40;
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                                                                                                                                                                                                                                                                                     Gaps
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C;Species: Helicobacter pylori
A;Variety: strain J99
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C;Accession: A71928
R;Alm, R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.R.; Tves, C.; Gibson, R.; Mezberg, D.; Mills, S.D.; Jiang, Q.; Taylor, D.E.; Vovis, G.F.;
Nature 397, 176-180, 1999
A;Title: Genomic sequence comparison of two unrelated isolates of the human gastric pathon, Reference number: A71800; MUID:99120557; PMID:9923682
A;Accession: A71928
A;Accession: A71928
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Kim,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          outer dense fiber protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S56101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
S56101
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A;Cross-references: UNIPROT:Q9ZLVO; UNIPARC:UPI00000D3637; GB:AE001481; GB:AE001439; NID
A;Experimental source: strain J99
C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-262 «KIM»
A;Cross-references: UNIPROT:Q29438; UNIPARC:UPI0000130BD1; GB:X69514; NID:g1165005;
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: Molecular cloning and characterization of the bovine A;Reference number: S56100; MUID:96066278; PMID:7576240 A;Accession: S56101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , Y.; Adham, I.M.; Haack, T.; Kremling, H.; Engel, W. Chem. Hoppe-Seyler 376, 431-435, 1995
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                                                                                                            95 PLCDLLIRCINXQKPLCPEEKQRHL------DKKQRFHNIRGRWTGRCM--SCCRSS 143
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33; Conservative
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Pred. No. 2e+02;
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Pred. No. 3;
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tumor necrosis factor receptor 1 precursor (validated) - human N;Alternate names: P55 tumor necrosis factor receptor; TNF receptor type 1 N;Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding C;Species: Homo sapiens (man) C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004 C;Accession: A38208; A34899; A34900; A36555; C36555; A38281; S12057; JT0758; A602

A60231; A38

protein

GQHUT1

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A;Accession: C36555
A;Molecule type: protein
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-2
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-2
A;Residues: 30-38;41-53,'X',55-79,'XX',82-94,'NK';'XX',100-104;107-128;162-167,'X',169-2
A;Cross-references: UNIPARC:UPI00002D398; UNIPARC:UPI00002D836; UNIPARC:UPI00001736D8;
A;Note: the purified protein, called tumor necrosis factor binding protein, is a soluble R;Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.
Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990
A;Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of rela;Reference number: A38281; MUID:91017509; PMID:2170974
                                                                                                                                                                                                                                                     Gene i34, 209-216, 1993
A;Title: Cloning and partial characterization of the promoter A;Reference number: JT0758; MUID:94085779; PMID:8262379
A;Accession: JT0758
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A;Accession: A36555
A;Molecula type: mRNA
A;Residues: 1-455 <HIM>
A;Residues: 1-455 <HIM>
A;Cross-references: UNIPARC:UPI000002CE11; GB:M63121; NID:g339755; PIDN:AAA36754.1; PID:
                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000002CE11; EMBL:X55313; NID:g37223; PIDN:CAA39021.1; A;Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ender, R;Kemper, O.; Wallach, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPARC:UPI000002CE11; GB:M37764
A;Note: the authors translated the codon TGG for residue
R;Nophar Y; Kemper O.; Brakebusch, C.; Engelmann, H.;
EMBO J. 9, 3269-3278, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Note: part of this sequence, inc. R;Schall, T.J; Lewis, M.; Koller, Cell 61, 361-370, 1990
A;Title: Molecular cloning and exp. A;Reference number: A34900; MUID:99
                                                                                                R;Seckinger, P.; Vey, E.; Turcatti, G.; Wi
Bur. J. Immunol. 20, 1167-1174, 1990
A;Title: Tumor necrosis factor inhibitor:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: Soluble forms of tumor necrosis factor receptors le form of the receptor.
A; Reference number: S12057; MUID:91006021; PMID:1698610
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Cell 61, 351-359, 1990
A;Title: Molecular cloning a
A;Reference number: A34899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Fuchs, P.; Strehl, S.; Dworzak, M.; Himmler, A.; Ambros, Genomics 13, 219-224, 1992
A;Tille: Structure of the human TNF receptor 1 (p60) gene A;Reference number: A38208; MUID:92250049; PMID:1315717
                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-13 < KE
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-455 < NOP>
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A;Residues: 1-455 <GRA>
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DNA Cell Biol. 9, 705-715, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPARC:UPI000002CE11; GB:M33294; NID:g339744; PIDN:AAA03210.1; R;Himmler_A.; Maurer-Fogy. I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-455 <F
A; Molecule type: protein
A; Residues: 41-43,'X',45-53,'X',55-57
                                                 A; Accession: A60231
                                                                               A; Reference number: A60231;
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                                                                                                                                                                                                                 1-13 <KEM>
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                                                                                                                                                    G.; Wingfield,
                                                                               purification, pMID:2113477
                                                                                                                                                    P.; Dayer, J.M.
                                                                                                     NH-2-terminal
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A;Residues: 41-43,'X',45-53,'V',55-57,'XK',60
A;Cross-references: UNIPAC:UPI00001736E2
A;Experimental source: renal failure patient u
R;Engelmann, H.; Novick, D.; Wallach, D.
Biol. Chem. 265, 1551-1536, 1990
A;Title: Two tumor necrosis factor-binding pro
A;Reference number: A35010; MUID:90110215; PMI
A;Accession: A35010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;30-211/Domain: extracellular #status predicted <EXT>
F;41-201/Product: TNF binding protein I (tumor necrosis
F;44-82/Domain: NGF receptor repeat homology <NG2>
F;84-126/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;127-167/Domain: NGF receptor repeat homology <NG3>
F;168-196/Domain: NGF receptor repeat homology <NG4>
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A;Map position: 12p13.2-12p13.2
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNPR1); NGF receptor repeat homology.
C;Keywords: duplication; glycopyrotein; receptor; transmembrane protein
F;12-1/Domain: signal sequence #status predicted csIGo
F;22-455/product: tumor necrosis factor receptor 1 #status predicted cMAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: protein
A; Residues: 41-53; X', 55-144, 'X', 146-150, 'X', 152-186, 'X', 188-201
A; Cross-references: UNIPARC: UPI00001736E4
A; Experimental source: urine
C; Comment: This protein is one of two known receptors for both TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UPI00001736E3
A;Experimental source: normal urine
R;Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K.
Biosci. Biotechnol. Biochem. 58, 2266-2268, 1994
A;Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified
A;Reference number: JC2404; MUID:95128033; PMID:7765720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Experimental source: cancer patient serum R;Olsson, I.; Lantz, M.; Nilsson, E.; Peetre, Eur. J. Haematol. 42, 270-275, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPARC:UPI0000072FDB
R;Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci
Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990
A;Title: Purification and characterization of an inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Isolation and characterization of a tumor necrosis A;Reference number: A60594; MUID:89171156; PMID:2924890 A;Accession: A60594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein A; Residues: 41-45 < ENG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 41-60 <GAT>
A;Cross-references: UNIPARC:UPI00001736E1
                                                                                                                                                                                                                                                                                                                                                                                                                F_1212-234/Domain: transmembrane #status predicted <MEM>F_1235-455/Domain: intracellular #status predicted <INT>
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                                                                                                                                                                                                                                                                                                                                                                                 ;54,145,151/Binding site: carbohydrate (Asn)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A38258
                                                                                                                                                                                                                                                                                             Similarity
                                                         LEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSSRTRR 147
                                                                                                                                LSCSKCRKEMGQVEI-----SSCTVDRD----
                                                                                                                                                                                       LECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
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                                                                                                                                                                                                                                                                                         8.3%;
25.0%;
CLNGTVHLSCQEKONTVCTCHAGFFLR---ENECVSCSNCKKSLE 190
                                                                                                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                                         Score 68.5; | Pred. No. 58;
                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                          -TVCGCRK----NOYRHY----WSEN 139
                                                                                                                                                                                                                                                           46;
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                                                                                                                                                                                                                                                           Indels
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RESULT 99
A30817
RESULT 100
G02741
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A;Cross-references: FlyBase:FBgn0005642
A;Introns: 338/2; 740/1
C;Keywords: DNA binding; transcription regulation; zinc finger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Vincent, A.; Kejzlarova-Lepesant, J.; Segalat, L.; Yanicostas, Mol. Cell. Biol. 8, 4459-4468, 1988
A;Title: sry h-1, a new Drosophila melanogaster multifingered pro A;Reference number: A30817; MUID:89039875; PMID:3141791
A;Accession: A30817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 serendipity (sry h-1) locus protein - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster C;Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
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A;Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A;Reference number: Z20484; MUID:99102612; PMID:9847359
A;Accession: T28260
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C;Species: Melanoplus sanguinipes entomopoxvirus
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
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A; Residues: 1-868 < VIN>
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A; Residues: 1-519 < AFO>
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                                                            114 - EKORHLDKKORFHNIRGRWTGRCMSCCRSSRTRR 147
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                                                                                                                                                                                                                                                                65 KCLK----FYSKI-SEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPL-CPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AVXDKCL----KFYSKISEYR------HYCYSVYGTTLEQ-----QYNK 94
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                                                                                                         FQERSHLQRHQKYHAQTRSY--RCEKCGKMYKTER 426
                                                                                                                                                                                                                                                                                                                     8.3%; Score 68.5; DB 2; Length 868; larity 27.4%; Pred. No. 1.1e+02; Conservative 16; Mismatches 36; Indels 1
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22.6%; Pred. No. 66;
tive 19; Mismatches 54;
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skeletal muscle LIM-protein SLIM1 - human
()Species: Homo sapiens (man)
()Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
()Accession: JC4893; G02741
()Accession: JC4893; G02741
()Accession: JC4893; Accession: JC4893; G02741
()Accession: JC4893; Accession: J
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A;Title: Slim defines a novel family of LIM-proteins expressed
A;Reference number: JC4893; MUID:96354835; PMID:8753811
A;Accession: JC4893
A;Status: preliminary
Search completed: May 27, Job time: 33.1084 secs
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A;Residues: 1-280 <MO2>
A;Cross-references: UNIPROT:Q9Y630; UNIPARC:UPI000017C350; EMBL:U60115; NID:g1381807; PII
F;162-212/Domain: LIM metal-binding repeat homology <LIM>
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Best Local
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Run 3

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Maximum
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Perfect so
Sequence:
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Q919C8_HPV16
Q919C8_HPV16
Q919C8_HPV16
Q919C8_HPV35
Q4TUF9_HPV35
Q4TUF9_HPV31
VE6_HFV31
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Q917C6_HPV58
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EMBL; AJ388069; CAB45105.1; -; Genomic_DNA.
EMBL; AY089951; AAM11875.1; -; Genomic_DNA.
EMBL; AY089954; AAM11881.1; -; Genomic_DNA.
EMBL; AY108954; AAM11881.1; -; Genomic_DNA.
EMBL; AY112663; AAM51854.1; -; Genomic_DNA.
GO; GO:0042055; C:host_cell_nucleus; IEA.
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Martins C.R.F.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-2002) to
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Ma Z., Qian D., Ma J.,
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01-NOV-1996, sequence version
07-FBB-2006, entry version 25.
Early transforming protein E6.
Human papillomavirus
                   Alphapapillomavirus.
NCBI_TaxID=333760;
                                              Viruses;
                                                                                  01-NOV-1999,
07-FEB-2006,
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EMBL; U34127; AAA91674.1; -; Genomic_DNA.
EMBL; U34133; AAA91680.1; -; Genomic_DNA.
GO; GO:0042025; C:host c:ll nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern
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                                                         Human papillomavirus type
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Virol. 69:7743-7753(1995).
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                                                                                   entry version
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Pred. No. 2.4e-73;
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RESULT 4
QSWMP5 HPV16
ID QSWMP5 HPV16
AC QSWMP5;
DT 01-NOV-1999, 1
DT 01-PEB-2006, 0
DE E6 protein.
OS Human papillom
OC Viruses dsDNI
OC Alphapapillom
OC NCBI TAXID=33
RN [1]
RP NUCLEOTIDE SE
RP MEDLINE=20112;
RA Verheijen R.H
RT "Analysis of 1
RT p53 codon 72 |
RL J. Gen. Virol
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                   NUCLEOTIDE SEQUENCE.
MEDLINE=20112892; PubMed=10644829;
MEDLINE=20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst
verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relatio
"Analysis odon 72 polymorphism genotypes in cervical carcinogenesis."
p53 codon 72 polymorphism genotypes in cervical carcinogenesis."
J. Gen. Virol. 81:317-325(2000).
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01-NOV-1999, sequence versi
07-FEB-2006, entry version
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EMBL; AF486322; AAL96627.1; -; Genomic_DNA.
EMBL; AY686580; AAV91652.1; -; Genomic_DNA.
GO; GO:0042025; C:host_cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
Chen Z., Terai M., Fu L., Herrero R., DeSalle R., Burk R.D.;
"Diversifying selection in human papillomavirus type 16 lineages based
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                                                                                                                                                                                      Human papillomavirus type 16. Viruses; dsDNA viruses, no RN Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on complete genome analyses.";
J. Virol. 79:7014-7023(2005).
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Pred. No. 2.5e-73;
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MEDLINE=20112892; PubMed=10644829;
MEDLINE=20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.
Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
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Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
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Distributed under the Creative Commons Attribution-NoDerivs Li
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EMBL; AJ388061; CAB45114.1; -; Genomi
EMBL; AJ388066; CAB45124.1; -; Genomi
GO; GO:0042025; C:host cell nucleus;
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Pred. No. 4.7e-73;
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Matches 148
JB20_HPV16 PRELIMINARY; PR7
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Q8BB20; O1-MAR-2003, integrated into Unit
O1-MAR-2003, sequence version 1.
O7-FEB-2006, entry version 13.
Early transforming protein E6.
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MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern
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Viruses; dsDNA viruses, no RNA stage;
unclassified Papillomaviridae.
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J. Virol. 69:7743-7753(1995).
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IL; U34111; AAA91658.1; -; Genomic_DNA.
IL; U34121; AAA91668.1; -; Genomic_DNA.
IL; U34123; AAA91670.1; -; Genomic_DNA.
GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
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151 AA; 1:
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P03I26; Q71BI7;
21-JUL-1986, int
21-JUL-1986, seq
07-MAR-2006, ent
Schneider-Maunoury S., Pehau-Arnaudet G., Breitburd F., On "Expression of the human papillomavirus type 16 genome in a line derived from a vulvar intraepithelial neoplasia."; J. Gen. Virol. 71:809-817(1990).
                                                                                                                NUCLEOTIDE SEQUENCE [GENOMIC DNA].
STRAIN-Isolate European German 131;
Terai M., Fu L., Ma Z., Burk R.D.;
"Cloning and sequencing of non-European human papillomavirus (HPV)
"Cloning and sequencing of cervicovaginal cells by an overlappi."
                                                                                                                                                                               MEDLINE=85246220; PubMed=2990099; Seedorf K., Krammer G., Durst M., "Human papillomavirus type 16 DNA Virology 145:181-185(1985).
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Viruses, dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333760;
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GO; GO:0042025; C:bost cell nucleus;
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18319 MW; 7CBD23
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Alphapapillomavirus.
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J. Mol. Evol. 55:491-499(2002).
                                                                                                Submitted (AUG-2002) to the EMBL/GenBank/DDBJ
                                                                                                           variant complete PCR method.";
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                                                                                                                                                                                                                                                                                                                            Protein E6.
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                                                            MEDLINE=90218027; PubMed=2157796;
                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF
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Ayala F.J., Villarreal L.P.;
reifying selection in human papillomavirus type
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AC Q547J2; PPV16
DT 24-MAY-2005, s
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OS Human papillom
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EMBL; D00735; BAA00632.1; -; Genomic_DNA.
PIR; A03682; W6WLHS.
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"Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
Biochem. Biophys. Res. Commun. 296;962-969 (2002).
-I- FUNCTION: Transcriptional transactivator. Binds double stranded
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InterPro; IPR001334; E6.
   Alphapapillomavirus.
NCBI_TaxID=333760;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-22188366; PubMed=12200142; DOI=10.1016/S0006-291X(02)02041-7;
                                              Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3D-structure; Activator; DNA-binding;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERACTION WITH HUMAN FBLN1, AND INHIBITION OF E6-MEDIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       similarity).
SUBCELLULAR LOCATION: Nuclear matrix-associated.
SUBCELLANEOUS: HPV16, in comparison to HPV types 6
MISCELLANEOUS: HPV16, in comparison to HPV types 6
Often associated with malignant genital cancers in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein to degradation. Those two functions presumably contribute to transforming activity (By similarity). Interaction with human FBLNI protein also seems to be linked to cell transformation. SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase which interacts with human P53. Binds to human FBLNI and MPDZ (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: Belongs to the papillomaviruses E6 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-
protein ligase, the human TP53/p53 tumor suppressor protein by
targeting it to degradation. Binds and targets human MUPP1/MPDZ
 _TaxID=333760
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                                                                          integrated into UniProtKB/TrEMBL sequence version 1. entry version 5. protein E6.
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98.0%;
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                                RNA stage; Papillomaviridae;
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Pred. No. 4.9e-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDZ-binding (By similarity)
R -> G (in Ref. 2).
L -> V (in Ref. 2).
; 01FEF5ADCFDB37EB CRC64;
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RESULT 10
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EMBL; AY686581;
GO; GO:0042025;
GO; GO:0003677;
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STRAIN=E-P, E-G241T, E-G187T, and E-G538T;

MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;

Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., C Cheung J.L.K., Xu L.Y., Cheng A.F.;

"Human papillomavirus type 16 intratypic variant infection for cervical neoplasia in southern China.";

Infect. Dis. 186:696-700(2002).
                   Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
                                                                         01-DEC-2001, integrated into U
01-DEC-2001, sequence version
07-FEB-2006, entry version 16.
E6 protein (Fragment)
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EMBL;
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STRAIN-CV17722E, and Qv15521E;
PubMed-15890941; DOI-10.1128/JV1.79.11.7014-7023.2005;
PubMed-15890941; DOI-10.1128/JV1.79.11.7014-7023.2005;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Virol. 79
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Submitted (APR-2002) t
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"Diversifying selection in human papillomavirus type 16 lineages based
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
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AF486320;
AF486321;
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0; AAL96625.1; -; Genomic_DNA.
1; AAL96626.1; -; Genomic_DNA.
9; AAM29167.1; -; Genomic_DNA.
1; AAV91660.1; -; Genomic_DNA.
5; C:host_cell_nucleus; IEA.
7; F:DNA_binding; IEA.
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                                                   RNA
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Pred. No. 4.9e-73;
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SEQUENCE
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Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
NCBI_TaxID=333760;
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QBBB19;
Q1-mAR-2003, integrated into U
01-mAR-2003, sequence version
Q7-FEB-2006, entry version 13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AY089955; AAM11883.1; -; Genomic_DNA.GO; GG:0042025; C:host cell nucleus; IEA.GO; GG:0008677; F:DNA binding; IEA.InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=22242222; PubMed=12355268; DOI=10.1007/800239-002-2344-y; DeFilippis V.R., Ayala F.J., Villarreal L.P.; "Evidence of diversifying selection in human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF404697; AAL01351.1; -; Genomic DN GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003577; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Evol. 55:491-499(2002).
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AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                               MFQDPQERPRKLPQLCTELQTTIHNIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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llarity 98.0%;
Conservative
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                                                                                                                                                                                                                           Score 821; DB 2; Length 1: Pred. No. 7.4e-73; Indels 1; Mismatches 2; Indels
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RESULT 13
Q8QRD7_HPV16
ID Q8QRD7;
AC Q8QRD7;
DT 01-UUN-2002, i
DT 01-UUN-2002, i
DT 01-FEB-2006, e
DE E6 protein.
OS Human papillom
OC Viruses; dsDNA
OC Alphapapillom
OX NCBL_TaxID=333
RN (1)
CALPALN=E-C4427
RX MEDLINE=221829
RA Cheung J.L.K.,
RA Cheung J.L.K.,
RA Cheung J.L.K.,
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Q4VRN5_HPV16
ID Q4VRN5_HPV16
AC Q4VRN5;
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05-JUL-2005,
07-FEB-2006,
STRAIN=E-C442T;
MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
Chann P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K.,
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection
                                                                                                                         Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AY686583; AAV91676.1; -; Genomic DN GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA. SEQUENCE 158 AA; 19172 MW; 91ECF5ADD4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Qv18158E;
PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
Chen Z., Terai M., Fu L., Herrero R., DeSalle R., Burk F.
"Diversifying selection in human papillomavirus type 16
on complete genome analyses.";
J. Virol. 79:7014-7023(2005).
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                                                                               NUCLEOTIDE SEQUENCE
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Human papillomavirus type 16.
ארחים אירישים נעשפי, Papillomaviridae;
                                                                                                           NCBI_TaxID=333760;
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Distributed
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Pred. No. 7.8e-73;
1; Mismatches 2;
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91ECF5ADD4CED31E
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Best Local
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                                                                                                                                                                                                                                                                                                                                                           EMBL; AF486316; AAL96621.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
Alphapapillomavirus.
NCBI_TaxID=333760;
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QBQRD8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                                                SEQUENCE
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_HPV16
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NCE 158 AA; 19173 MW;
                                                                                                                                                                                                                                                                                                                                        PF00518;
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AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCDEEKQRHLD 120
                                                                                                                                  MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                                                                                                     MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                Conservative
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AA; 19188 MW;
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Pred. No. 9.8e-73;
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Pred. No. 9.8e-73;
2; Mismatches 2;
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Q89640
AC Q89
AC Q80
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Q77ZJ5
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Best Local Similarity
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J5 HPV16
Q77ZJ5 HPV16
Q77ZJ5;
                                                                                                                                                                         40 9PAPI
Q85640, 9PAPI PRELIMINARY; PRT; 151 AA.
Q89640;
O1-NOV-1996, integrated into UniProtKB/TrEMBL.
O1-NOV-1996, sequence version 1.
O7-FEB-2006, entry version 22.
Early transforming protein E6.
Human papillomavirus.
Viruses; daBNA viruses, no RNA stage; Papillomaviridae;
Unclassified Papillomaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF003019; AAB70736.1; -; Genomic DNJ
EMBL; AF003018; AAB70735.1; -; Genomic DNJ
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18221 MW; 60CD2A34DA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-JUL-2004, integrated into 0
05-JUL-2004, sequence version
07-FEB-2006, entry version 11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tornesello M.L., Buonaguro F.M. Beth-Giraldo E., Giraldo G., "Sequence variations and viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97437474; PubMed=9292007;
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J. Gen. Virol. 78:2199-2208(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98.7%;
98.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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Pred. No. 1.2e-72;
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NUCLEOTIDE SEQUENCE. MEDLINE=96079021; PubMed=7494284;

NCBI_TaxID=10566;

Yamada T., Wheeler C.M., Jenison S.A.;

papillomavirus type 16 variant lineages

Halpern A.L.,

Stewart A.C., Hildesheim

Α.,

in United States

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RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION OF THE RESULATION O
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Best Local S
Matches 147
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48 9PAPI

48 9PAPI

98 9648 9PAPI

98 9648; 012653; 012654; 012928; 012929;

101-NOV-1996, Integrated into UniProtKB/TrEMBL.

101-NOV-1996, Sequence version 1.

107-FEB-2006, entry version 21.

Early transforming protein E6.
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EMBL; AF469198; AAA015693.1; -; Genomic_DNA.
EMBL; U34115; AAA91662.1; -; Genomic_DNA.
EMBL; U34129; AAA91667.1; -; Genomic_DNA.
EMBL; U34124; AAA91671.1; -; Genomic_DNA.
EMBL; U34124; AAA91671.1; -; Genomic_DNA.
CO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA_binding; IEA.
GO; GO:0003677; F:DNA_binding; IEA.
                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                populations characterized by nucleotide L2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Viruses; dsDNA viruses, no RNA stage; unclassified Papillomaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ponglikitmongkol M., Vaeteewoottacharn K.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            populations characterized by nucleotide sequence analysis 12, and L1 coding segments."; U. Virol. 69:7743-7753(1995).
                                                                                                                                                              Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
MEDLINE=96079021; PubMed=7494284;
Yamada T., Wheeler C.M., Halpern
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted
                                                                                                                                                                                                    Farmer A.D.
                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                 "Human papillomavirus type 16 variant lineages in United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18348 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Distributed
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      U34110;
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Pred. No. 1.2e-
2; Mismatches
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   Genomic_DNA
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..2e-72;
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Q9W331 HPV16
ID Q5W931;
AC Q9W931;
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DT 01-NOV-199, i

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Best Local S
Matches 148
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Viruses; dsDNA viruses, no
Alphapapillomavirus.
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MEDLINE=20112892; PubMed=10644829;
MEDLINE=20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.
van Duin M., Snijders P.J., Weijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation
"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
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EMBL; AJ388058; CAB45108.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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147; Conserv
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                                                                                                                               AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                    MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                              MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFQDLCIVYRDGNPY
                                                                    KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
   KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
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97.4%;
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                                                                                                                                                                                                                                                                                                                                                                                          Score 819; DB -,
pred. No. 1.2e-72;
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151

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EMBL; U34109; AAA91656.1; -; Genomic_DNA.
EMBL; U34113; AAA91660.1; -; Genomic_DNA.
EMBL; U34113; AAA91682.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PP00518; E6; 1.
SEQUENCE 151 AA; 18221 MW; 60CD2A34DAF4
                                                                                                                                                                                      MFQDFQERFRKLFQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNFY
                                     KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
                                                                             AVCDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                  MFQDPQERPGKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                        Score 819;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                         60CD2A34DAF48CB7 CRC64;
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Q2DJN9 HPV
ID Q2EJN
AC Q2PJN
AC Q2PJN
AC Q2PJN
DT 24-JN
DT 07-FE
DE E6 pr
GN Name==
OS Humann
OC Virus
OC Alpha
OX NCBI
RN NUCLE
RN WICHE
RN WICHE
RN WICHON
RT "Clon
RI Submi
CC Copyr
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Best Local
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STRAIN-A8-P, A8-C193, and A8-A178;

MEDLINE-22182962; PubMed-12195358; DOI=10.1086/342048;

MEDLINE-22182962; PubMed-12195358; DOI=10.1086/342048;

Chann P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K.,

Cheung J.L.K., Xu L.Y., Cheng A.F.;

"Human papillomavirus type 16 intratypic variant infection for cervical neoplasia in southern China.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative transforming protein E6. Human papillomavirus type 16. Viruses; deDNA viruses, no RNA st
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8QHT0_HPV16 PRELIMINARY; PRT; 158 AA. Q8QHT0; Q1-JUN-2002, integrated into UniProtKB/TrEMBL.
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07-FEB-2006,
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QZPJN9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=E6;
                         Copyrighted
Distributed
                                                                                                 Terai M., Fu L., Ma Z., Burk R.D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Distributed under the Creative Commons Attribution-NoDerivs License
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                      by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
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Pred. No. 1.2e-72;
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Q80963;
01-NOV-1996,
01-NOV-1996,
07-FEB-2006,
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EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                  "Human papillomavirus type 16 variant lineages in United populations characterized by nucleotide sequence analysis L2, and L1 coding segments.";
J. Virol. 69:7743-7753(1995).
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Human papillomavirus
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GO; GO:0003677; F:DNA bi
InterPro; IPR001334; E6.
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GO; GO:0042025; C:host cell nucleus;
GO; GO:0003677; F:DWA binding; IEA.
InterPro; IPR001334; E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE.
MEDLINE=96079021; PubMed=7494284;
                                                                                                                                                Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18291 MW; 97C7028D5169382D CRC64;
                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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9PAPI
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AF486306;
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); AAL96605.1; -; Genomic_DNA.
1; AAL96606.1; -; Genomic_DNA.
2; AAL96607.1; -; Genomic_DNA.
6; AAL96611.1; -; Genomic_DNA.
8; AAL96613.1; -; Genomic_DNA.
1; AAQ10403.1; -; Genomic_DNA.
1; C:host_cell_nucleus; IEA.
7; F:DNA_binding; IEA.
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Pred. No. 1.5e-72;
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                                                                                                         Length 151;
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Best Local S
Matches 147
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Viruses; dsDNA viruses, no RNA
Alphapapillomavirus.
NCBI_TaxID=333760
                                                                                                                                  QBB564 PAPI PRELIMINARY;
QBB564;
QBB564;
QBB503, integrated into
QI-MAR-2003, sequence versio
QI-FEB-2006, entry version 1
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(P5 HPV16
QBQHP5_HPV16
Viruses; dsDNA viruses, no RNA stage; unclassified Papillomaviridae. NCBI_TaxID=10566;
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EMBL; AF486333; AAL96628.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:NNA binding; IEA.
InterPro; IPR001334; E6.
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STRAINES-G276T, and E-G276G442T;
MEDLINES-2182962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intrattypic variant infection for cervical neoplasia in southern China.";
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01-JUN-2002, integrated into U
01-JUN-2002, sequence version
07-PEB-2006, entry version 13.
                                                                                                                 E6 protein
                                                                                          Human papillomavirus.
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9PAPI
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NCE 158 AA;
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nilarity 97.4%;
Conservative
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; 19160 MW;
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Pred. No. 1.5e-72;
2; Mismatches 2;
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Matches 147
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Best Local
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01-NOV-1999, i
07-FEB-2006,
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                                                                                                                                          EMBL; AJ388064; CAB45120.1; -; Genomic_DNA.
EMBL; AJ388062; CAB45116.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
                                                                                                                                                                                                                                                              MEDLINE-20112892; PubMed=10644829; Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F. Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; Verheijen cf human papillomavirus type 16 E6 variants in relation p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325 (2000).
                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus. NCBI_TaxID=333760;
                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                           E6 protein
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GO; GO:0042025; C:host cell nucleus; IE
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
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SEQUENCE 151 AA; 18348 MW;
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AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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96.7%;
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                                                                                  2,
                                                                                  Score 817; DB 2;
Pred. No. 1.8e-72;
2; Mismatches 2;
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Pred. No. 1.8e-72;
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RESULT 25

Q919D4 HPV16
ID Q919D4;
DT 01-DEC-2001,
DT 01-DEC-2001,
DT 07-FEB-2006,
DE E6 protein (F)
DE Manan papillon
OC Viruses; dsDN
OC Alphapapillon
OC VIRUSES; dsDN
OC NCBI_TaxID=33;
RN [1]
RN (1]
RN WCLEOTIDE SER
RX MEDLINE=21846;
RA Watts K.J. T.
RT "Sequence var
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RL Int. J. Cance
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CC FMBL; AF404692
DR GO; GO:0004202
DR GO; GO:000367
DR JEAM; PF0051BR
PF NON TER
SQ SEQUENCE 16:
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QBQRD9
ID QBQRD9
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QBQRD9; integrated into U
01-JUN-2002, sequence version
07-FEB-2006, entry version 14.
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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                                                                                                                                                                           Viruses; dsDNA viruses, Alphapapillomavirus. NCBI_TaxID=333760;
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MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung J.L.K., Xu L.Y., Cheng A.F.;
                                                                                          STRAIN-As-A267
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
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J. Infect. Dis. 186:696-700(2002).
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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SECUENCE 158 AA; 1
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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Pred. No. 2.4e-72;
Mismatches 2;
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Pred. No. 2.4e-72;
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RESULT Q89887 Q89887 Q8 AC Q8 PDT 011 DT 01 DT 07 DE Ea COS Hu OC Vi
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Best Local S
Matches 146
                                                                                                          Q89887 9PAPI
Q89887;
01-NOV-1996,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9QDH9 HPV16
Q9QDH9;
01-MAY-2000,
01-MAY-2000,
                  01-NOV-1996, sequence version 07-FEB-2006, entry version 22. Early transforming protein E6. Human papillomavirus Viruses, no RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF187866; AAF13392.1; -; Genomic DNA.
EMBL; AF486304; AAL96609.1; -; Genomic DNA.
EMBL; AF486305; AAL96610.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan R.K.S., Lam C.W., Cheng T.H., Li W.W.H., Lo K.W.K., Chan Cheung J.L.K., Xu L.Y., Cheng A.F.; "Human papillomavirus type 16 intratypic variant infection and for cervical neoplasia in southern China.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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Lee H.P., Song Y.S.,
Submitted (SEP-1999)
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9PAPI
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HPV16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               518; E6;
158 AA;
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  Papillomaviridae.
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                    no RNA
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                                                                                                                  UniProtKB/TrEMBL
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                    stage;
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1. No. 2.4e-72;
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                      Papillomaviridae;
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Attribution-NoDerivs License
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Best Local S
Matches 147
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SEQUENCE
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RESULT 30
Q8QRD5 HPV16
ID Q8QRD5;
DT Q1-UN-2002, i
DT 01-UN-2002, i
DT 01-UN-2002, i
DT 01-FEB-2006, e
DE Transforming g
OS Human papillom
OC Viruses; dsDNA
OC Alphapapillom
OC NCBI TaxID=333
RN [1]
RP NUCLEOTIDE SEC
RC STRAIN=NA1;
RX MEDLINE=221829
RA Cheung J.L.K.,
RT "Human papillo
RA CHEUNG J. L.K.,
RT "Human J. L
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EMBL; U34107; AAA91654.1; -; Genomic_DNA.
EMBL; U34112; AAA91659.1; -; Genomic_DNA.
EMBL; U34116; AAA91663.1; -; Genomic_DNA.
EMBL; U34119; AAA91666.1; -; Genomic_DNA.
EMBL; U34119; AAA91679.1; -; Genomic_DNA.
EMBL; U34132; AAA91679.1; -; Genomic_DNA.
EMBL; U34132; AAA91679.1; -; Genomic_DNA.
EMBL; U34132; AAA91679.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
NUCLEOTIDE SEQUENCE.
STRAIN=Qv15351AA, and Qv15321AA;
PubMed=15890941; DOI=10.1128/JVI.79.11.7014-7023.2005;
PubMed=15890941; M Fn L. Herrero R., DeSalle R., Burk
                                                                                                                                                                                            MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung J.L.K., Xu L.Y., Cheung A.F.; Cheung J.L.K., Xu L.Y., Cheung A.F.; "Human papillomavirus type 16 intratypic variant infectior for cervical neoplasia in southern China."; J. Infect. Dis. 186:696-700(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transforming protein E6.
Human papillomavirus type 16.
Viruses, daBNA viruses, no RN
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=333760;
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J. Virol. 69:7743-7753(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 1835
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147; Conser
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ilarity 97.4%;
Conservative
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Pred. No. 2.9e-72;
1; Mismatches 3;
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RESULT 31

QBQRD6_HPV16 PRELIMINARY; PRT; 158 AA.

AC QBQRD6;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.

DT 07-PEB-2006, entry version 13.

DE 86 protein.

DE 86 protein.

OS Human papillomavirus type 16.

OC Viruses; dsDNA viruses, no RNA stage; Papillomav OC Alphapapillomavirus.

OX NCBI_TaxID=333760;
RN NUCLEOTIDE SEQUENCE.

RC STRAIN=E-T360T;
RX MEDLINE=22182962; PubMed=12195358; DOI=10.1086/3.

RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., L. RA Cheung J.L.K., Xu L.Y., Cheung T.H., Li W.W.H., L. RA Cheung J.L.K., Xu L.Y., Cheung T.H., Li W.W.H., L. RA Cheung J.L.K., Xu L.Y., Cheung T.H., Li W.W.H., L. RA Cheung J.L.K., Xu L.Y., Cheung A.F.;
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Best Local S
Matches 147
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EMBL; AY686582; AAV91668.1; -; Genomic_DNA.
EMBL; AY6086582; AAV91668.1; -; Genomic_DNA.
EMBL; AY098923; AAM29171.1; -; Genomic_DNA.
EMBL; AY112662; AAM29171.1; -; Genomic_DNA.
EMBL; AY112662; AAM21853.1; -; Genomic_DNA.
EMBL; AY1686579; AAV91644.1; -; Genomic_DNA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 19208 MW; B8E47F57F22ECZE
STRAIN=E-T360T;
MEDLINE=25182962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
Cruz M.R., Martins C.
Submitted (MAY-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
Terai M., Burk R.D.;
Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Diversifying selection in human on complete genome analyses."; J. Virol. 79:7014-7023(2005).
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97.4%;
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Pred. No. 3e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 3e-
1; Mismatches
                                                                                                                                           stage; Papillomaviridae;
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Attribution-NoDerivs License
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Q9QDH3;
01-MAY-2000,
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SEQUENCE
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF486319; AAL96624.1; -; Genomic DN. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F.DNA binding; IEA. InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF187869; AAF13398.1; -; Genomic DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-FEB-2006,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=333760;
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                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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146; Conserv
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                                                                                                                                      MPQDPQERPRKLPQLCTBLQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                              AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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      KKORFHNIRGRWTGRCMSCCRSSRTRRETQL
                                                     AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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AA; 19210 MW;
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                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 1 Viruses; dsDNA viruses, no Alphapapillomavirus
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MEDLINE-21846229; PubMed-11857370; DOI=10.1002/ijc.10103;

MEDLINE-21846229; PubMed-11857370; DOI=10.1002/ijc.10103;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type cervical cancer isolates from Australia and New Caledonia.";
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STRAIN=As-C131;
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E6 protein (Fragment)
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                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=333760;
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GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
m; PF00518; E6; 1.
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J. Gen. Virol. 78:2199-2208(1997).
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Tornesello M.L., Buonaguro F.M., Meglio A.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state
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151 AA; 18238 MW; BEF32A8B016CC88B CRC64;
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96.7%;
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L; Mismatches
                                                                                                                                                                                                                                                                                                     Score 812; DB 2;
Pred. No. 5.7e-72;
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Pred. No. 4.8e-72;
2; Mismatches 3
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Q9MP4 HPV16 PRELIMINARY;
Q9MP4;
Q9MP4;
01-NOV-1999, integrated into
01-NOV-1999, sequence versio
07-FEB-2006, entry version 1
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                                                                                                                   MEDLINE-97437474; PubMed-9292007;
MEDLINE-97437474; PubMed-9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo E., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
type 16 in penile carcinomas from Ugandan patients.";
J. Gen. Virol. 78:2199-2208(1997).
                                                                                                                                                                                                                                                                                                                               Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
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012336;
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Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
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  EMBL;
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                                                     Distributed under the Creative Commons Attribution-NoDerivs License
                                                                             Copyrighted by the UniProt Consortium,
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GC:0042025; C:host cell nucleus; IEA.
GC:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
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NCE 151 AA; 18387 MW;
  AF003016; AAB70733.1;
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-; Genomic_DNA
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Pred. No. 7.2e-72;
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Q9QDH7;
01-MAY-2000,
01-MAY-2000,
07-FEB-2006,
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GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18206 MW; 51C12/
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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128
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NCE 158 AA; 19215 MW; FC5BF2B06576864B CRC64;
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96.0%;
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                                                                                                                                                                                                                                                                                                                               Score 809; DB 2;
Pred. No. 1.2e-71;
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Pred. No. 9e-72;
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RESULT 39
Q8B821 HPV16
ID Q8B821 HPV16
AC Q8B821;
DT 01-MAR-2003, i
DT 01-MAR-2003, i

PRELIMINARY;

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integrated into UniProtKB/TrEMBL sequence version 1.

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Best Loc
Matches
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                                       NUCLEOTIDE SEQUENCE.

MEDLINE-20112892; PubMed-10644829;

Van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.

Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333760;
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O9WMP2;
01-NOV-1999, integrated into U
01-NOV-1999, sequence version
07-FEB-2006, entry version 18.
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Early transforming protein E6.
Human papillomavirus type 16.
V/resca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; dsDNA viruses, no RNA stage; Alphapapillomavirus. NCBI_TaxID=333760;
                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Distributed under the Creative Commons Attribution-NoDerivs License
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Pfam; PF00518;
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GO:0042025; C:host cell nucleus; IE
GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
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Evol. 55:491-499(2002).
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No. 1.4e-71;
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Q76TSO PAPI ID Q76TSO PAPI AC Q76TSO; DT 05-JUL-2004, DT 05-JUL-2004, DT 07-BB-2006, DE Early transfo OS Human papillor

05-JUL-2004, integral of JUL-2004, sequent of FEB-2006, entry versely transforming party of the sequence of th

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Q919A9;
01-DEC-2001, integrated into Uni
01-DEC-2001, sequence version 1.
07-FEB-2006, entry version 16.
E6 protein (Fragment).
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                         WADLINE=21846229; PubMed=11857370; DOI=10.1002/jjc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus cervical cancer isolates from Australia and New Caledonia.";
                                                                                                                                                                                                                                                    EMBL; AF404706; AAL01368.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Terai M.,
Submitted
[3]
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                                                                                                                        MUCLEOTIDE SEQUENCE:
MEDLINE=97437474; PubMed=9292007;
Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L.,
Beth-Giraldo B., Giraldo G.;
"Sequence variations and viral genomic state of human papillomavirus
"Sequence variations and rical genomic state of human papillomavirus
                                                                                                                                                                                                                                                                                                               Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN.
Alphapapillomavirus.
NCBI_TaxID=333760;
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NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MEDLINE=96079021; PubMed=7494284;
Wheeler C.M., Halpern
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EMBL; U34125; AAA91672.1; -; Genomic_DNA.
EMBL; U34130; AAA91677.1; -; Genomic_DNA.
EMBL; U34131; AAA91678.1; -; Genomic_DNA.
GO; GO:00042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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                         NUCLEOTIDE SEQUENCE.
Terai M., Ma Z., Bur
Submitted (JAN-2002)
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unclassified Papillomaviridae.
NCBI_TaxID=10566;
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151 AA; 1
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QBJMU8;
QBJMU8;
                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
Terai M., Fu L., Ma Z., Burk R.D.;
Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2002, integrated into UniProtKB/TrEMBL 01-OCT-2002, sequence version 1. 07-FEB-2006, entry version 12.
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                           SEQUENCE
                                                                 EMBL; AY098922; AAM29170.1; -; Genomic_DNA.
EMBL; AF533180; AAQ10720.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Martins C.R.F.;
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E16 HPV16
PRELIMINARY; PR
Q77E16;
Q77E16;
05-JUL-2004, integrated into Uni
05-JUL-2004, sequence version 1.
07-FEB-2006, entry version 11.
E6 oncoprotein (E6 protein).
ILT 46
108_9PAPI
Q89708_9PAPI
Q89708;
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Pfam, PF00518; E
Pfam, PF00518; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Viruses; dsDNA viruses, Alphapapillomavirus.
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Li; AJ388063; CAB45118.1; -; Genomic_DNA.
GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
GO:0003677; F:DNA binding; IEA.
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Pred. No. 3.5e-71;
2; Mismatches 4
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2; Mismatches
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RESULT 47

Q9MMP3 HPV16

ID Q5WMP3 H

AC Q9WMP3 T

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DE E6 prote

OS Human pa

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EMBL; U34117; AAA91664.1; -; Genomic DNA.
EMBL; U34118; AAA91665.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 151 AA; 18304 MW; OF312A8BDBA6
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Q9WMP3;
01-NOV-1999,
01-NOV-1999,
07-FEB-2006,
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01-NOV-1996,
07-FEB-2006,
                                         WEDLINE=20112892; PubMed=10644829; van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst Verheljen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; Walalysis of human papillomavirus type 16 E6 variants in relatip53 codon 72 polymorphism genotypes in cervical carcinogenesis. J. Gen. Virol. 81:317-325(2000).
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Human papillomavirus.
Viruses; dsDNA viruse
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Viruses; dsDNA viruses,
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36079021; PubMed=7494284;
wheeler C.M., Halpern A
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Pred. No. 3.5e-71;
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ID QUENNO_HPV16
AC QUENNO_
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DT 01-JUN-2002, 
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Query Match
Best Local Similarity
Matches 145; Conserv
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                                                                                                                                                                          EMBL; AF486314; AAL96619.1; -; Genomic_DNA.
EMBL; AF472509; AAO15705.1; -; Genomic_DNA.
EMBL; AF486324; AAL96629.1; -; Genomic_DNA.
EMBL; AY098918; AAM29166.1; -; Genomic_DNA.
GO; GO:0042025; C:host_cell_nucleus; IEA.
GO; GO:003677; F:DNA_binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Terai M., Ma Z., Burk R.D.;
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=B-350G, and Af2-a;
MEDLINE=22102962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., C
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2002, integrated into U
01-JUN-2002, sequence version
07-FEB-2006, entry version 13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Cerqueira D.M., Camara G.N.L., .R.F.;
                                                                                                                                                       IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                  under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                           by the UniProt Consortium, see http://www.uniprot.org/terms
  Conservative
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                                                                                                      19157 MW;
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                        96.9%;
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  Score 804; DB 2;
Pred. No. 3.7e-71;
2; Mismatches 4
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; Mismatches
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RESULT 50

Q919C4 HPVI6
ID 2919C4;
ID 2919C4;
AC Q919C4;
DT 01-DEC-2001, integrated into Uni
DT 01-DEC-2001, sequence version 1.
DT 07-FEB-2006, entry version 16.
DE E6 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dabNA viruses, no RNA s
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RM MEDLINE=21846229; PubMed=1185737
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Q9QDH5 HPV16
ID Q9QDH5 HPV16
AC Q9QDH5;
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Lee H.P., Song Y.S., Kim
Submitted (SEP-1999) to
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Viruses; dsDNA viruses,
Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF187868; AAF13396.1; -; Genomic DNA. GO; GO:0042025; C:host cell nucleus; IEA. GO; GO:0003677; F:DNA binding; IEA. InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted
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    NUCLEOTIDE SEQUENCE.
MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence version entry version 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                     19195 MW;
                                                                                                                                                                                                                                                                                                                                                                                               96.7%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                               Score 803; DB 2;
Pred. No. 4.7e-71;
                                                                                                                                   UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              UniProtKB/TrEMBL
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                                                                                                                                                             PRT;
                                                                   stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                     00564E1A8994CB0B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                             143
                                                                   Papillomaviridae;
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RESULT 51
Q91986_HPV16
ID Q91986;
AC Q91986;
DT 01-DEC-2001, a
DT 01-DEC-2001, a
DT 07-FEB-2006, e
DT 
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                                                                                                                                                                                                                Query Match
Best Local S
Matches 139
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Best Local S
Matches 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus.
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MEDLINE=21046229; PubMed=11857370; DOI=10.1002/ijc.10103;
MEDLINE=21046229; PubMed=11857370; DOI=10.1002/ijc.10103;
Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
Watte K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
"Sequence variation and physical state of human papilloma cervical cancer isolates from Australia and New Caledonia Int. J. Cancer 97:868-874(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E6 protein (Fragment)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L; AF404702; AAL01361.1; -; Genomic GO:0042025; C:host cell nucleus; Ii GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L; AF404698; AAL01353.1; -; Genomic_DN
GO:0042025; C:host_cell nucleus; IEA.
GO:0003677; F:DNA_binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121
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                                                                                                                                                                                                                                                                                                                                                                                                                                    PF00518; E6; 1.
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                                                                                                             PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLK
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   FYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNI
                                                                       PRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVCDKCLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                143
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                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      integrated into t
sequence version
entry version 16.
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                                                                                                                                                                                                                                                                                                                                                                ΑA;
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                                                                                                                                                                                                                                                                                                                                                                17272 MW;
                                                                                                                                                                                                                                                  93.3%;
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                                                                                                                                                                                                        Score 774; DB 2;
Pred. No. 3e-68;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleus; IEA.
ng; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 781; DB 2;
Pred. No. 6.2e-69;
1; Mismatches 2
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                                                                                                                                                                                                                                                                                                                                                                071F14EE3E6BE2AC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA.
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Attribution-NoDerivs License
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Caledonia.";
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Caledonia.";
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                                                                                                                                                                                                                                                                                    Length 143;
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RESULT 53
Q919C0 HPV16 PRELIMIN
ID Q919C0;
AC Q919C0;
DT 01-DEC-2001, integrated
DT 01-DEC-2001, sequence \( \)
DT 07-FEB-2006, entry vers
DE E6 procein (Fragment).
OS Human papillomavirus t)
OC Viruses; dsDNA viruses,
OC Alphapapillomavirus.
OX NCBI_TAXID=333760;
RN [1]
RP MCCLEOTIDE SEQUENCE.
RA Watts K.J., Thompson C.
RA Vatte K.J., Thompson C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9107 52
Q9102 H
AC Q919D2 H
AC Q919D2 P
DT Q1-DEC-2
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01-DEC-2001,
01-DEC-2001,
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  MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papilloma
                                                                                                                                                          Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                     Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA
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GO; GO:00042025; C:host cell nucleus; IE
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus cervical cancer isolates from Australia and New Caledonia.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
mr; PP00518; E6; 1.
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GG:0042055; C:host cell nucleus; IEA.
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erPro; IPR001334; E6.
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Pred. No. 3.6e-62;
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RESULT 56
Q919C8 HPV16
ID Q919C8;
AC Q919C8;
DT 01-DEC-2001, integrated into Unit of the control     RRT RAN OCC OCT DIT
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Q919B8 HPV16
Q919B8;
01-DEC-2001, i
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Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
MCBI_TaxID=333760;
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NUCLEOTIDE SEQUENCE.

MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;

MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103;

Matts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;

"Sequence variation and physical state of human papillomavirus type
"Sequence variation and physical state of human papillomavirus type
cervical cancer isolates from Australia and New Caledonia.";

Int. J. Cancer 97:868-874(2002).
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Viruses; dsDNA viruses, no RN
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98.4%;
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                                                                                                                                                                                                                                                                                                                                                   RNA stage; Papillomaviridae;
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nucleus; IEA.
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Pred. No. 1.1e-61;
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RESULT 57
Q91984 HPV16
ID Q91984;
DT 01-DEC-2001, 6
DT 01-DEC-2001, 6
DT 07-FEB-2006, e
DE & protein (Fr
OS Human papillom
OC Viruses; ds0NA
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Best Local S
Matches 126
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Best Local
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF404703; AAL01363.1; -; Genomic_DN
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003577; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer 97:868-874(2002).
                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                 TIHNIILECVYCKQQLLRKEVYDFAFRDLCIVYRDGNPYAVCDKCLKFYSKISEYRHYCY
                                                                           SVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCR
                                                                                                                                                                        TIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCY
  SSRTRRETQL
                                              SLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCR
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                                                                                                                                                                                                                                                                                                                                                   AA;
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96.9%;
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                                                                                                                                                                                                                                              Score 704; DB 2;
Pred. No. 2.2e-61;
2; Mismatches 2
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Pred. No. 1.1e-61;
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                                                                                                                                                                                                                                                                                                                                                   B6C2147D227EEDDC CRC64;
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RESULT 59
Q4TUF9_HPV
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Q919D0_HPV16
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01-DEC-2001, integ--
01-DEC-2001, sequence version
07-FEB-2006, entry version 1/
07-FEB-2006 (Fragment)
                                                                                                                                                                                                                                                                                                                                                        19-JUL-2005,
19-JUL-2005,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                     P9 HPV35
Q4TUF9 HPV35
Q4TUF9;
NUCLEOTIDE SEQUENCE.
STRAIN=NM1215, NM1301, NM2760, and NM3793;
PubMed=1627283; DOI=10.1128/JV1.79.21.13630-13640.2005;
PubMed=1627283; DOI=10.1128/JV1.79.21.13630-13640.2005;
Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allau Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T. Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M., Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
                                                                                                                                                                                               Human papillomavirus tyn
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
MCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus cervical cancer isolates from Australia and New Caledonia."; Int. J. Cancer 97:868-874(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF404695; AAL01347.1; -; Genomi GO; GO:0042025; C:host cell nucleus; GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                   E6 protein.
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NON_TER 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 702; DB 2; Length 130; Pred. No. 3.5e-61; l; Mismatches 3; Indels
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Best Local S
Matches 108
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98_9PAPI
Q84298_9PAPI
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01-NOV-1996, integrated into UniProtKB/TrEMBL.
01-NOV-1996, sequence version 1.
07-FEB-2006, entry version 26.
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type 16."
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EMBL; DQ057310; AAY58341.1; -; Genomic_DNA.
EMBL; DQ057311; AAY58342.1; -; Genomic_DNA.
EMBL; DQ057312; AAY58343.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
GO; GO:0003677; B:DNA binding; IEA.
SEQUENCE 149 AA; 18015 MW; 8354D5CFA293;
                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D10597; BAA01447.1; -; Genomic DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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J. Virol. 79:13630-13640(2005).
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NCE 149 AA; 1801
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                                                                                                                                                                                                                                                                         69.9%; Score 580; DB 2; Length 149; 71.5%; Pred. No. 4.4e-49; Live 13; Mismatches 28; Indels
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RESULT 62
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01-AUG-1992,
07-FEB-2006,
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                                                                                                                                                                                                                                                                           SEQUENCE
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-I- FUNCTION: Transcriptional transactivator. Binds double stran
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MEDLINE=94265501; PubMed=8205838;
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                                                                                                                                                                                                                                                                                                                               Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein; Oncogene; Transcription; Transcription regulation; Zinc; Zinc-finger. CHAIN 1 149 Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X74477; CAA52561.1; -; Genomic_DNA.
EMBL; M74117; AAA46966.1; -; Genomic_DNA.
PIR; E40824; WGWL35.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: This protein may be involved in the oncogenic potentia of this virus (associated with cancer of the uterine cervix).
-!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
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Pred. No. 6.9e-49;
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906 HPV16
Q91906;
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T 01-DEC-2001, sequence version 1.
JT 07-FEB-2006, entry version 16.
"" "rottein (Fragment)." RNA
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Q4TUF4;
19-JUL-2005,
19-JUL-2005,
07-FEB-2006,
                                                                                                                                         MEDLINE=21846229; PubMed=11857370; DOI=10.1002/ijc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physic:1 state of human papilloma cervical cancer isolates from Australia and New Caledonia Int. J. Cancer 97:868-874(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E6 protein (rraymemer).
Human papillomavirus type 16.
3-rww viruses, no RNA stage;
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J. Virol. 79:13630-13640(2005).
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Viruses; dsDNA viruses,
Alphapapillomavirus.
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EMBL; DQ057313; AAY58344.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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                                  by the UniProt Consortium, under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69.6%; llarity 71.5%; Conservative 1
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es, no RNA stage;
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Pred. No. 6.9e
13; Mismatches
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                                  see http://www.uniprot.org/terms
Attribution-NoDerivs License
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.9e-49;
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                                                                                                                                                                               papillomavirus Caledonia.";
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RESULT 65
Q4TUG1_HPV31
ID Q4TUG1;
AC Q4TUG1;
DT 19-JUL-2
DT 19-JUL-2
DT 07-FEB-2
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ID Q91912 H
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AC Q9192 H
DI 01-DEC-2
DI 07-FEB-2
DI 07-FEB
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Best Local S
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, GO:0003677; F:DNA binding; IEA
InterPro; IPR001334; E6.
R Pfam; pPF00518; E6; 1.
SEQUENCE 103
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local (
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Q919B2;
01-DEC-2001, integrate
01-DEC-2001, sequence
07-FEB-2006, entry ver
E6 protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NON TER
NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001334 Pfam; PF00518; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=2184629; PubMed=11857370; DOI=10.1002/jjc.10103; Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.; "Sequence variation and physical state of human papillomavirus cervical cancer isolates from Australia and New Caledonia.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/tu
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Int. J. Cancer 97:868-874(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GD: AF404704; AAL01365.1; -; Genomic
GO:0042025; C:host cell nucleus; II
GO:0003677; F:DNA binding; IEA.
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                                                                                                                                                                                                                                                                                             DIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVCDKCLKFYSKISEYRHYCYSLY
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Pred. No. 2.8e-47;
2; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                 Score 532; DB 2;
Pred. No. 1.6e-44;
L; Mismatches 2
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19-JUL-2005, 19-JUL-2005, 07-FEB-2006,

sequence entry ver

version rsion 5.

integrated into UniProtKB/TrEMBL

Q4TUG1_HPV31 Q4TUG1;

PRELIMINARY;

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SOR DESCRIPTION OF THE PROPERTY OF THE PROPERT
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NUCLEOTIDE SEQUENCE.
STRAIN=BR1213, BR1692, and MR9917;
STRAIN=BR1213, BR1692, and MR9917;
STRAIN=BR1213, DOI=10.1128/JVI.79.21.13630-13640.2005;
PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,
Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,
Chu T.Y., Cubie H.A., Cuschieri K., von Knabel-Doeberitz M.,
Chu T.Y., Cubie H.A., Cuschieri K., von Knabel-Doeberitz M.,
Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;
"Worldwide genomic diversity of the high-risk human papillomavirus
"Worldwide genomic diversity of the high-risk human papillomavi
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P17386;
01-AUG-1990,
01-AUG-1990,
07-FEB-2006,
Protein E6.
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EMBL;
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Viruses; dsDNA ....
                                                                                                                                                                                                                MEDLINE=89299478; PubMed=2545036; Goldsborough M.D., Disilvestre D., Temple G.F. "Nucleotide sequence of human papillomavirus neoplasia-associated virus.";
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Viruses; dsDNA viruses,
Alphapapillomavirus.
Du M., Fan X., Hong E., Chen J.J.;
"Interaction of oncogenic papillomavirus E6 proteins with fibulin-1.";
picchem. Riophys. Res. Commun. 296:962-969(2002).
                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses, Alphapapillomavirus.
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Name=E6;
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                                                                                         TRANSFORMATION.
MEDLINE=22188366; PubMed=12200142;
                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA]
                                                                                                                                              INTERACTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IL; DQ057307; AAY58338.1; -; Genomic_DNA.
IL; DQ057308; AAY58339.1; -; Genomic_DNA.
III; DQ057305; AAY58339.6.1; -; Genomic_DNA.
GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
QUENCE 149 AA; 17768 MW; 61C2A96EAC26
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ses, no RN
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Pred. No. 1.2e-43;
6; Mismatches 34
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                                                                                                                                           INHIBITION
                                                                                            DOI=10.1016/S0006-291X(02)02041-7;
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Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                     G.F.,
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                                                                                                                                                                                                                                             f., Lorincz A.T.;
type 31: a cervical
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RESULT
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Best Local
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Q4TUG5;
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19-JUL-2005,
07-FEB-2006,
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ZN_FING
MOTIF
SEQUENCE
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"Role of the PDZ domain-binding motif pathogenesis of human papillomavirus t J. Virol. 78:12366-12377(2004)
-!- FUNCTION: Transcriptional transact
NUCLEOTIDE SEQUENCE.
STRAIN=HK31B, HK31B, HK31C, and TL2069;
PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M.,
Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn
Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.
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PubMed=15507623; DOI=
Lee C., Laiming L.A.;
                                                                                                                       Human papillomavirus type
Viruses; dsDNA viruses. no
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PIR; A32444; W6WL31
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Distributed
                                                                                                          Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                            NCBI_TaxID=10585;
                                                                                                                                                     Name=E6;
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- SUBCELLULAR
- SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Transcriptional transactivator. Binds double stranded DNA. Has transforming activity. Inactivates, with E6-AP ubiquitin-
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149
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Transcription; Transcription regulation; Zinc; Zinc-
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Pred. No. 1.9e-43;
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Potential.
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61D2A86C362767D9 CRC64;
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Matches 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VE6 HPV33
P06427;
01-JAN-1988,
01-JAN-1988,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          type 16.";
J. Virol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Genome organization and nucleotide sequence of human papillomavirus type 33, which is associated with cervical cancer.";
J. Virol. 58:991-995(1986).
-i-FUNCTION: Transcriptional transactivator. Binds double stranded DNA (By similarity).
-i-FUNCTION: This protein may be involved in the oncogenic potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; DQ057303; AAY58334.1; -; Genomic_DNA.
EMBL; DQ057304; AAY58335.1; -; Genomic_DNA.
EMBL; DQ057306; AAY58333.1; -; Genomic_DNA.
EMBL; DQ057302; AAY58333.1; -; Genomic_DNA.
GQ; GQ:00042025; C:host cell nucleus; IEA.
GQ; GQ:0003677; F:DNA binding; IEA.
GQ; GQ:0003677; F:DNA binding; IEA.
SEQUENCE 149 AA; 17714 MW; 61D2A86C362767D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=86200464; PubMed=3009902;
Cole S.T., Streeck R.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus type 33.
Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
                                                                                                                                                                                                       EMBL; M12732; AAA46958.1; -; PIR; A03683; W6WL33.
                                                                                                                                                                                                                                                                                               Copyrighted
Distributed
      ZN_FING
                                                                                                                     Activator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.; "Worldwide genomic diversity of the high-risk human papillomavirus types 31, 35, 52, and 58, four close relatives of human papillomavirus
                                                                                                                                                    Pfam; PF00518; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=10586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                           of this virus (cervical neoplasia-associated virus).
SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
SIMILARITY: Belongs to the papillomaviruses E6 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KKKRFHNIGGRWTGRCIACWR--RPRTETQV 149
Transcription; Early protein; Metal-binding; Nuclear protein; Transcription; Transcription regulation; Zinc; Zinc-finger.

1 149 Protein E6.
/FTId=PRO 0000133353.
30 66 Potential.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79:13630-13640(2005).
                                                                                                                                                                               IPR001334; E6.
                                                                                                                                                                                                                                                                                         by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entry version
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Pred. No. 1.9e-43;
18; Mismatches 33
                                                                                                                                                                                                                                     Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papillomaviridae;
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RESULT 70
Q9IZG6_HPV58
ID Q9IZG6_HPV58
AC Q9IZG6;
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Best Local S
Matches 96
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Best Local
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01-JUN-2002,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E7_HPV58
Q8QSE7;
Q8QSE7;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAINE86/E7-HK-8;
MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan I
Cheung J.L.K., Cheng A.F.;
"Association of human papillomavirus type 58 variant with the r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF478157; AAL85402.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:DNA binding; IEA.
InterPro; IPR001134; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00518; E6; 1
SEQUENCE 149 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer.";
J. Natl. Cancer Inst. 94:1249-1253(2002).
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149
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17652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 503; DB z; -
Pred. No. 1.7e-41;
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Pred. No. 3.7e-43;
9; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UniProtKB/TrEMBL
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RESULT 71
O90723 HPV67
ID O90723 H
AC O90723 H
DT 01-NOV-1
DT 01-NOV-1
DT 07-FEB-2
DE ORF 86.
OS Human pa
OC Viruses;
OC Alphapas
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RN [1]
RN NUCLEOTI
RX MEDLINE-
RA Kirii Y.
RA WICLEOTI
RT Papillom
RL Virus Ge
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Best Local S
Matches 94
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EMBL; AP478152; AAL85397.1; -; Genomic_DNA.
EMBL; AP478153; AAL85408.1; -; Genomic_DNA.
EMBL; AP478154; AAL85399.1; -; Genomic_DNA.
EMBL; AP478154; AAL85399.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
SEQUENCE 149 AA; 17780 MW; 7CB6DCCC5D31B15
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MEDLINE=99073695; PubMed=9857984; DOI-
Kirii Y., Matsukura T.;
"Nucleotide sequence and phylogenetic
papillomavirus type 67.";
Virus Genes 17:117-121(1998).
                                                                                                                                                                                                                                                                                                                                                                                       090723_HPV67
090723;
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01-OCT-2000, sequence version 1.
07-FEB-2006, entry version 17.
                                                                                                                                                                                Alphapapillomavirus.
NCBI_TaxID=37120;
                                                                                                                                                                                                                                                                                                                                    01-NOV-1998, integrated into UniProtKB/TrEMBI 01-NOV-1998, sequence version 1.
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                                                                                                                                                                                                                              Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                         Human papillomavirus type 67
                                                                                                                                                                                                                                                                                                              07-FEB-2006,
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Pred. No. 2.2e-41
0; Mismatches 3
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                                                                                                     DOI=10.1023/A:1008002905588;
                                                                                                                                                                                                                                                                                                                                                                                                                    149
                                                     classification of
                                                                                                                                                                                                                                 Papillomaviridae
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types 31, o.
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19-JUL-2005,
07-FEB-2006,
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GO; GO:00
SEQUENCE
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Q4TUG8_I
                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                    PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005; Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B., Williamson A.L., Chung L.P., Colland J.C., Zuna R.E., Dunn S.T., Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M., Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.; "Worldwide genomic diversity of the high-risk human papillomavirus types 31, 35, 52, and 58, four close relatives of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10598;
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
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GO:0042025; C:host cell nucleus; IEA.
GO:003577; F:DNA binding; IEA.
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NCE 149 AA;
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AVCKVCLRLLSKISEYRHYNYSLYGETLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
                  AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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                                                                                                                                                                  149 AA;
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Pred. No. 5.4e-41;
(2; Mismatches 37;
                                                                                                                        Score 497; DB 2;
Pred. No. 6.8e-41;
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Best Local
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P26555;
01-AUG-1992;
01-AUG-1992;
07-FEB-2006;
                                 "Human papillomavirus type 58 DNA sequence.";
Virology 185:424-427(1991).
-!- FUNCTION: Transcriptional transactivator.
                                                                                                                                                                                                                                                                                                                     Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus.
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                                                                                                 MEDLINE=92024102; PubMed=1656594; Kirii Y., Iwamoto S., Matsukura T.; "Human papillomavirus type 58 DNA s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000,
                                                                                                                                                                                                                                                                                       NCBI_TaxID=10598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-E6HK3;
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                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein E6.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
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   (By
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry version 28
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AA; 17863 MW;
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                                                                                                                                                                                                                                                                                                                                    e 58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 497; DB 2;
Pred. No. 6.8e-41;
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                                                                                                                                                                                                                                                                                                                                                           stage;
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RESULT 75
Q547M1 HPV58
ID Q547M1 H
AC Q547
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                                                               types 31, 35,
type 16.";
J. Virol. 79:1
                                                                                                                          NUCLEOTIDE SEQUENCE.

STRAIN=ED1710, ED1767, ED6197, HK2178, and OK332;

PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;

PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;

PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;

Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Dunn S.T.,

Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,

Chu T.Y., Cubie H.A., Cuschier R.V., von Knebel-Doeberitz M.,

Wartins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;

"Worldwide genomic diversity of the high-risk human papillomavirus

"Worldwide genomic diversity of the high-risk human papillomavirus

"Expes 31, 35, 52, and 58, four close relatives of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE.

STRAIN=E6/E7-HK-1, E6/E7-HK-10, E6/E7-HK-11, E6/E7-HK-12, E6/E7
STRAIN=E6/E7-HK-15, E6/E7-HK-16, E6/E7-HK-2, E6/E7-HK-4, E6/E7-HK-6, E6/E7-HK-15, E6/E7-HK-6, E6/E7-HK-7, and E6/E7-HK-9;
E6/E7-HK-7, and E6/E7-HK-9;
MEDLIN=E22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
Chann P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chann Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Chenn C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Chenn C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung J.L.K., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung M.F., Cheung T.H., Li W.W.H., Lo K.W.K., Chann C.W., Cheung M.F., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung C.W., Cheung M.F., Cheung T.H., Li W.W.H., Lo K.W.K., Cheung C.W., Cheung M.F., Cheung C.W., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 5 Viruses; dsDNA viruses, no
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Q547M1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=E6;
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24-MAY-2005,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Association of human cervical cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2006,
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Pred. No. 8.5e-41;
Minmatches 36;
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HK-4, E6/E7-HK-6,
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RESULT 76
Q8QHQ3 HPW
ID Q9QH
AC Q8QH
DT 01-J
DT 07-P
DS Human
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OC Alp)
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Best Local S
Matches 93
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QBQHQ3_HPV58
QBQHQ3;
QBQHQ3;
Q1-JUN-2002, integrated into
Q1-JUN-2002, sequence versior
Q7-FEB-2006, entry version 1
                                                          NUCLEOTIDE SEQUENCE.

$TRAIN=E6/E7-HK-17, and E6/E7-HK-18;

$TRAIN=E6/E7-HK-17, and E6/E7-HK-18;

MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;

Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan Cheung J.L.K., Chang A.F.;

Cheung J.L.K., Chang A.F.;

"Association of human papillomavirus type 58 variant with the recervical cancer.";
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                                                                                                                                                                                                                                Human papillomavirus type 58.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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Distributed
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Chan P.K.S.,
    Copyrighted
                                          J. Natl. Cancer Inst. 94:1249-1253(2002).
                                                                                                                                                                                                            NCBI_TaxID=10598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0042025;
GO; GO:0003677;
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AF478156; AAL85401.1;
AF478158; AAL85403.1;
AF478159; AAL85404.1;
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AF478161; AAL85406.1;
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4; AALB5409.1; -; Genomic_DNA
5; AALB5410.1; -; Genomic_DNA
6; AAYSB327.1; -; Genomic_DNA
6; C:host cell nucleus; IEA.
7; F:DNA binding; IEA.
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AAY58328.1;
      the UniProt
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AAF60305.
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Pred. No. 8.5e-41;
0; Mismatches 36
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Attribution-NoDerivs License
    http://www.uniprot.org/terms
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07-FEB-2006, entry version 25.
E6 protein (Fragment).
Human papillomavirus.
Viruses; dsDNA viruses, no RNA unclassified Papillomaviridae.
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q80887_9PAPI
Q80887;
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EMBL; AF478167; AAL85412.1; -; Genomic_DN
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; U14516; AAB60570.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprobistributed under the Creative Commons Attribution-NoDerivs
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                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001334; E6. Pfam; PF00518; E6; 1.
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1 AA;
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Pred. No. 8.5e-41;
0; Mismatches 36;
                                                                                                                                                                                                                    Score 495;
Pred. No. 6.
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                                                                                                                                                                                                                                                                                                  22FDF3EA185ACBA7 CRC64;
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RESULT 78 Q4TUH6_HPV52 ID Q4TUH6_HPV52

PRELIMINARY;

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RESULT 79
VE6_HPV52
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Matches 88
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P36814;
O1-JUN-1994,
O1-JUN-1994,
O7-FEB-2006;
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19-JUL-2005,
07-FEB-2006,
                                                                                                                              Human papillomavirus type 52.
Viruses; dsDNA viruses, no RNA
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
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NUCLEOTIDE SEQUENCE [GENOMIC DNA] MEDLINE=94265501; PubMed=8205838; Delius H., Hofmann B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005; Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M., Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard F., "Worldwide genomic diversity of the high-risk human papillo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus type (Viruses; dsDNA viruses, no Alphapapillomavirus.
                                                                                                                                                                                                                                       Protein E6.
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GQ:0042025; C:hOst_cell nucleus; IEA.
GQ:0003677; F:DNA binding; IEA.
GQ:0003677; F:DNA binding; IEA.
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1. 79:13630-13640(2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
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                                                                                                                                                                                                                                                          sequence version entry version 27
                                                                                                                                                                                                                                                                                                                integrated into UniProtKB/Swiss-Prot
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Pred. No. 2.1e-40;
19; Mismatches 34
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                                                                                                                                                         stage;
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                                                                                                                                                                                                                                                                                                                                                                   148
                                                                                                                                                         Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papillomaviridae;
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papillomavirus
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S.T.,
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RESULT 80
Q4TUH4 HPV52
ID Q4TUH4;

AC Q4TUH4;

DT 19-JUL-2005, 8
DT 19-JUL-2006, 6
DE E6 protein.
GN Name=E6;
OS Human papillon
OC Viruses; dspNN/OC Alphapapillom
OX NCBI_TaxID=106
RN [1]
RP NUCLEOTIDE SER
RC Calleja-Macias
RA Calleja-Macias
RA Williamson A.1
RA Crypes 31, 35,
RT types 31, 35,
RT types 16.",
RL J. Virol. 79::
RA Martins C.R.,
RT types 16.",
RL J. Virol. 79::
RA MUCLEOTIDE SER
RA WILLIAMSON A.1
RA GCALLEJIAMSON A.1
RA GCALLAGA
RA GLA GLA GCA
RA GCALLAGA

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Matches 87
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ZN_FING
SEQUENCE
                                                                                                                                                                                                                                  STRAIN-HK1243, and HK2571;
PubMed=16227283; DOI=10.1128/JVI.79.21.13630-13640.2005;
Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B. Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T., Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M., Chu T.Y., Cubie H.A., Baschieri K., woncox N., Bernard H.U.;
Wartins C.R., Sanchez G.I., Bosch F.X., Muncox N., Bernard H.U.;
"Worldwide genomic diversity of the high-risk human papillomavirus types 31, 35, 52, and 58, four close relatives of human papillomavitype. 16.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus ty Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                 STRAIN=HK1243, and HK2571;
Callaja-Macias I.E., Kalantari M., Villa L.L., Prado J.C.,
Callaja-Macias I.E., Chung L.-P., Collins R.J., Zuna R.E., Du
Williamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Du
Chu T.-Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.V.
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                               Submitted (MAY-2005) to the EMBL/GenBank/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Copyrighted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Nuclear matrix-associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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E., Kalantari
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Pred. No. 6.6e-40;
9; Mismatches 35;
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/FTId=PRO_0000133369
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19-JUL-2005,
07-FEB-2006,
                                                                                                                               EMBL; DQ057291; AAY58322.1; -; Genomic_DNA.
EMBL; DQ057295; AAY58326.1; -; Genomic_DNA.
EMBL; DQ057299; AAY58321.1; -; Genomic_DNA.
GO; GO:0042025; C:host_cell_nucleus; IEA.
GO; GO:0003677; F:DNA_binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BR0258, ED123, and ED18604; Callaja-Macias I.E., Kalantari M., Villa L.L., Prado J.C., i Callaja-Macias I.E., Chung L.-P., Collins R.J., Zuna R.E., Dunu Milliamson A.-L., Chung L.-P., Collins R.J., Zuna R.E., Dunu Chu T.-Y., Cubie H.A., Cuschieri K., Knebel-Doeberitz M.V., Sanchez G.I., Bosch X., Bernard H.-U.; Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
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STRAIN-BR0258, ED123, and ED18604;

PubMed=16277283; DOI=10.1128/JVI.79.21.13630-13640.2005;

PubMed=16277283; DOI=10.1128/JVI.79.21.13630-13640.2005;

Calleja-Macias I.E., Villa L.L., Prado J.C., Kalantari M., Allan B.,

Williamson A.L., Chung L.P., Collins R.J., Zuna R.E., Dunn S.T.,

Chu T.Y., Cubie H.A., Cuschieri K., von Knebel-Doeberitz M.,

Martins C.R., Sanchez G.I., Bosch F.X., Munoz N., Bernard H.U.;

"Worldwide genomic diversity of the high-risk human papillomavirus

"Yorldwide genomic diversity of the high-risk human papillomavirus

"Yorldwide genomic diversity of the high-risk human papillomavirus

"Yorldwide genomic diversity of the high-risk human papillomavirus
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Viruses; dsDNA viruses,
Alphapapillomavirus.
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EMBL; DQ057293; AAY58324.1; -; Genomic_DNA.
GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
SEQUENCE 148 AA; 17926 MW; OCE9C7D7341A:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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ch 58.7%; S
l Similarity 61.7%; P
87; Conservative 19;
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                                                                                                                                                                                                                                                                                                               by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
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61.7%;
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Score 487; DB 2; 1
Pred. No. 6.6e-40;
9; Mismatches 35;
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Pred. No. 6.6e-40
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RESULT 82
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Best Local :
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01-JUN-1994,
07-FEB-2006,
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                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Viruses; dsDNA viruses,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X74476; CAA52555.1; PIR; S36515; S36515.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
-!- SIMILARITY: Belongs to the papillomaviruses B6 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-i- FUNCTION: Transcriptional transactivator. Binds double s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501; PubMed=8205838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Activator; DNA-binding; Early protein; Metal-binding; Nuclear Transcription; Transcription regulation; Zinc; Zinc-finger.
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123
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                          KQRFHNIRGRWTGRCMSCCRSSRT
                                                                                       VCQPCLLFYSKVRQYRRYNQSVYGRTLENLTNKQLCNILIRCGKCQKPLCPLEKQRHVDE 122
                                                                                                               FPNPEERPYKLPALCEEVNISIHEIBLDCVYCERQLYRCEVYDFIFRDLCVVYRKGKPLG
                                                                                                                                                                                                            FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
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NKRFHQIADQWTGRCTQCWRPSAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Consortium,
                                                                                                                                                                                                                                                                                               Score 484; DB 1;
Pred. No. 1.3e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                  Potential.
E2FCC6E62E4AF0DA CRC64;
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/FTId=PRO_0000133354.
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RESULT 83 Q82005_HPV73 ID Q82005_HPV73

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01-NOV-1996, ;
01-NOV-1996, ;
07-FEB-2006, ;
                                                                                                   88
                                                                                                                                                                                                                                                                                                                                     STRAIN-HPV16; TISSUE=Cervical tissue; Haegert D.G., Galutira D.F., Younghusband B.H.; Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Voelter C., He Y., Delius H., Roy Greenspan D., de Villiers E.-M.; "Novel HPV types present in oral with HIV infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus.
Viruses; dsDNA viruses, no RNA
unclassified Papillomaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996, integrated into U
01-NOV-1996, sequence version
07-FEB-2006, entry version 25
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DOI=10.1002/(SICI)1997-0215(19960516)66:4<453::AID-IJC7>3.0.CO;2-V;
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NCBI_TaxID=51033;
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GO:0003677; F:DNA binding; IEA
erPro; IPR001334; E6.
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:NNA binding; IEA.
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                                                                                                                                  U14512; AAB60566.1; -; Genomic_DNA.
O:0042025; C:host cell nucleus; IEA.
                                   PF00518; E6; 1.
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VCE 148 AA; 17630 MW;
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Pred. No. 1.6e-39;
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RESULT 86

Q80884 9PAPI
Q80884;
AC Q80884;
DT 01-NOV-1996, integrated into Uni
DT 01-NOV-1996, sequence version 1.
DT 07-FEB-2006, entry version 25.
DE E6 protein (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA 8
OC unclassified Papillomaviridae.
OX NCBI_TaxID-10566;
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RP NUCLEOTIDE SEQUENCE.
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SEQUENCE
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GO; GO:0042025; C:host cell nucleus; IEA.
GO; GO:0003677; F:DNA binding; IEA.
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Pred. No. 1.5e-39;
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Viruses; daDNA viruses, no
Alphapapillomavirus.
NCBI TaxID=45240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  I Conguet M., Beaudenon S., Orth G.,
"Two novel genital human papillomavirus (HPV)
related to the potentially oncogenic HPV39.",
J. Clin. Microbiol. 34:738-744(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-OCT-1996, sequence versi
07-FEB-2006, entry version
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                                                                                                                                                                                                                                                                                         EMBL; X67160; CAA47632.1; -; Genomic_DNA. InterPro; IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
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MEDLINE=97060129; PubMed=8904450;
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GO:0042025; C:host cell nucleus; IEA.
GO:0003677; F:NNA binding; IEA.
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o RNA stage; Papillomaviridae;
                                                              23;
                                                                                             Score 468.5; DB 1;
Pred. No. 4.7e-38;
                                                                                                                                                                                                                                 Potential. Potential.
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01-OCT-1996,
01-OCT-1996,
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"Two novel genital human papillomavirus (HPV) types,
related to the potentially oncogenic HPV39.";
J. Clin. Microbiol. 34:738-744(1996).
-!- FUNCTION: Transcriptional transactivator. Binds of
                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                DNA (By similarity).
-!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
-!- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
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NCBI_TaxID=39457;
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InterPro; IPR001334; E6.
Pfam; PF00518; E6; 1.
Activator; DNA-binding; Early protein; Metal-binding; Nuclear protein;
Activator; DNA-binding; Early protein; Zinc; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=97060129; PubMed=8904450;
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Viruses; dsDNA viruses,
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                                                                                                                                                                                            CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=E6;
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U22461; AAC54880.1;
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                                      VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLDK 121
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Genomic_DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stage; Papillomaviridae;
                                                                                                                               Mismatches
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                                                                                                                                         4.7e-38;
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                                                                                                                                                     DB 1;
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                                                                                                                                                                                  CRC64;
                                                                                                                                                     Length 158;
                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HPV68
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                                                                                                                               Gaps
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VE6_HPV
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Q2VJD5
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Best Local
                                                                                                                                                                                                                                                                                    HPV51
                                                                                                                                                                                                                    01-AUG-1992,
01-AUG-1992,
07-FEB-2006,
       MEDLINE-91303675; PubMed=1649326;
Lungu O., Crum C.P., Silverstein S.J.;
"Biologic properties and nucleotide sequence analysis of human papillomavirus type 51.";
J. Virol. 65:4216-4225(1991).
-1- FUNCTION: Transcriptional transactivator. Binds double stranded DNA (By similarity).
-1- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
-1- SIMILARITY: Belongs to the papillomaviruses B6 protein family.
                                                                                                                                                                                                                                                           VE6_HPV51
P26554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus type 68a.
Viruses; dsDNA viruses, no RNA
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2006, integrated into 10-JAN-2006, sequence version 07-FEB-2006, entry version 3.
                                                                                                                                                          Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=Plasmid 952;
PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
Narechania A., Chen Z., Desalle R., Burk R.D.;
"Phylogenetic Incongruence among Oncogenic Genital Alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QZVJDS_HPV68
QZVJD5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                 Human papillomavirus
                                                                                                                                                                                                              Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=338322;
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HPV68
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                                                                                                                                                 TaxID=10595;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DQ080079; AAZ39491.1; -; Genomic_DNA.
NCE 158 AA; 18796 MW; 46B37939CFBA6596 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                     TKRRLHKÍAGNFTGOCRHCWTSKREDRRRIROETOV 158
                                                                                                                                                                                                                                                                                                                                                            KKQRFHNIRGRWTGRCMSCCRSS----
                                                                                                                                                                                                                                                                                                                                                                                     AACOSCIKFYAKIRELRYYSESVYATTLETITNTKLYNLLIRCMSCLKPLCPAEKLRHLT
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                                                                                                                                                                                                                        sequence version entry version 28
                                                                                                                                                                                                                                               integrated into UniProtKB/Swiss-Prot.
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                                                                                                                                                                                                                       entry version
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                                                                                                                                                                       type s
                                                                                                                                                          e 51.
no RNA stage;
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Pred.
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                                                                                                                                                                       Papillomaviridae;
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Best Local :
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01-JUN-1994,
07-FEB-2006,
Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZN_FING
                                                                                                                                                                                                                                                                                   Pelius H., Hofmann B.;
Delius H., Hofmann B.;
"Primer-directed sequencing of human papillomavirus types.";
"Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VE6_HPV45
P21735;
                        InterPro, IPR001334, E6.
InterPro, IPR001334, E6.
Pfam; PF00518, E6; 1.
Activator; DNA-binding; Early protein; Metal-binding; Nuclear
Activator; DNA-binding; Early protein; regulation; Zinc; Zinc-
                                                                               EMBL; X74479; CAA52573.1;
EMBL; M38198; AAA46973.1;
PIR; S36561; S36561.
                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                              Submitted (AUG-1990) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501; PubMed=8205838;
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              Oncogene; Transcription; Transcription regulation; CHAIN 1 158 Protein E6.

    -!- FUNCTION: This protein has transforming activity in vitro.
    -!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarit)
    -!- SIMILARITY: Belongs to the papillomaviruses E6 protein family

                                                                                                                                                                                                                                                           Kaplan J.B.,
                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10593;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=E6;
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                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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                                                                                                                                                                                                                                FUNCTION: Transcriptional transactivator.
                                                                                                                                                                                                                   DNA (By similarity).
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103
151 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence version entry version 32.
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139
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Pred. No. 3.1e-37;
4; Mismatches 41
                                                                                           Genomic_DNA.
Genomic_DNA.
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Zinc-finger.
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RESULT 93

VE6 HPV18

ID VE6 HPV18

AC P06463;

DT 01-JAN-1988,

DT 01-JAN-1988,
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Best Local Similarity
Matches 82; Conserv
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Best Local
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182_9PAPI
Q80882_9PAPI
Q80882;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Haegert D.G., Galutira D.F., Younghusband B.H.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=HPV16; TISSUE=Cervical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA unclassified Papillomaviridae.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996, sequence version 07-FEB-2006, entry version 25.
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GG:004205; C:host cell nucleus;
GO:0003677; F:DNA binding; IEA.
erPro; IPR001334; E6.
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Pred. No. 3.3e-37;
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Human papillomavirus typviruses; dsDNA viruses; Alphapapillomavirus. NCBI_TaxID=333761;
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Name=E6;
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MEDLINE=87053870; PubMed=3023067;
Schneider-Gaedicke A., Schwarz B.;
"Different human cervical carcinoma cell lines show similar "Transcription patterns of human papillomavirus type 18 early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [MRNA].
MEDLINE=88188247; PubMed=2833614;
Tannokawa Y., Takebe
                                                                                                                               DOI=10.1128/JVI.74.20.9680-9693.2000;
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                                                                                                                                                                                                                                                 MEDLINE=94037097; PubMed=8221889; DOI=10.1016/0092-8674(93)90384-3; Scheffner M., Huibregtse J.M., Vierstra R.D., Howley P.M.; "The HPV-16 E6 and E6-AP complex functions as a ubiquitin-protein ligase in the ubiquitination of p53.";
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MEDLINE=87218459; PubMed=3034571;

Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;

Seedorf K., Oltersdorf proteins of the human papilloma viruses

"Identification of early proteins of the human papilloma viruses

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MEDLINE=87283882; PubMed=3039146;
MEDLINE=22188366; PubMed=12200142; DOI=10
Du M., Fan X., Hong E., Chen J.J.;
"Interaction of oncogenic papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sugimura T.;
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                                                                                                       oncoproteins."
                                                                                                                   adenovirus E4-ORF1 and high-risk
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MEDLINE=94037097; PubMed=8221889; DC
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                              DOI=10.1016/S0006-291X(02)02041-7;
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Best Local
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Q76Z97_HPV18
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10-MAY-2005,
07-FEB-2006,
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SEQUENCE
                                      Human papillomavirus type 18.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333761;
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ZN_FING
MOTIF
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EMBL; X05015; CAA28664.1; -; Genomic_DNA.
EMBL; M20325; AAA99514.1; -; mRNA.
EMBL; M26799; AAA46946.1; -; Genomic_DNA.
EMBL; X04773; CAA28466.1; -; Genomic_DNA.
EMBL; X04773; CAA02846.1; -; Unassigned_DNA.
EMBL; A06324; CAA00542.1; -; Unassigned_RNA.
EMBL; A06328; CAA00542.1; -; Unassigned_RNA.
EMBL; A06328; CAA00542.1; -; Unassigned_RNA.
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NUCLEOTIDE SEQUENCE
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Activator; DNA-binding; Early
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SUBUNIT: Forms a complex with E6-AP ubiquitin-protein ligase whi
interacts with human P53. Binds to human FBLN1 and MPDZ.
SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: Belongs to the papillomaviruses E6 protein family
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105
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156
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18872 MW;
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                                                                                                  RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein.
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Pred. No. 9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDZ-binding (By similarity).
TQV->DQA: Complete loss of binding
MPDZ protein.
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/FTId=PRO_0000133338.
Potential.
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scription regulation; Zinc; Zinc-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5BCF13CF43D157FA CRC64;
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Zinc-finger.
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Best Local
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01-AUG-1992,
01-AUG-1992,
07-FEB-2006,
             ZN_FING
                                                                                                                                                                                                                                                          Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen "Characterization of a novel human papillomavirus DNA carcinoma cell line ME180.";
J. Virol. 65:5564-5568 (1991).
                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses, no RNA unclassified Papillomaviridae. NCBI_TaxID=10602;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00518; E6; 1.
SEQUENCE 158 AA; 18872 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0042025;
GO; GO:0003677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Papillomaviruses.";
J. Virol. 79:15503-15510(2005).
                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By similarity-
-!- SIMILARITY: Belongs to the papillomaviruses E6 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VE6
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SEQUENCE
                                                                Activator; DNA-binding; Early protein; Metal-binding; Nuclear Transcription; Transcription regulation; Zinc; Zinc-finger.
                                                                                             InterPro; IPR001334; Pfam; PF00518; E6; 1
                                                                                                                      EMBL; M73258; -; NOT_ANNOTATED_CDS; PIR; C40509; W6WLPR.
                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC MEDLINE=91374616; PubMed=1716
                                                                                                                                                                                                                                                                                                                                                                                                      Human papillomavirus type ME180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Narechania A., Chen Z., Desalle 
"Phylogenetic Incongruence among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
                                                                                                                                                                                                                                                   -!- FUNCTION: Transcriptional transactivator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HPVME
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87; Conserv
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158 AA;
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Incongruence among Oncogenic Genital Alpha Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                     CE [GENOMIC DNA].
PubMed=1716694;
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Pred. No. 9e
                                                    regulation;
Protein E6.
              Potentia.
                                    Protein E6.
/FTId=PRO_0000133318
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2B1F406B563F05FC CRC64
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mavirus DNA in the cervical
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Matches 86
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Best Local S
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Q7KYK8;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-98090464; PubMed=9427755; DOI=10.1093/emboj/17.1.215; Reuter S., Bartelmann M., Vogt M., Geisen C., Napierski I., Kahn T. Delius H., Lichter P., Weitz S., Korn B., Schwarz E.; Delius H., Lichter P., Weitz S., Korn B., Schwarz E.; "APM-1, a novel human gene, identified by aberrant cotranscription with papillomavirus oncogenes in aa cervical carcinoma cell line, encodes a BTB/POZ-zinc finger protein with growth inhibitory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
MEDLINE=91374616; PubMed=1716694;
MEDLINE=91374616; PubMed=1716694;
Reuter S., Delius H., Kahn T., Hofmann B., Zur Hau
"Characterization of a novel human papillomavirus
"Characterization of a novel human papillomavirus
carcinoma cell line ME180.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 68.
Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-JUL-2004,
05-JUL-2004,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3L; Y14591; CAA74931.1; -; mRNA.
GO:0042025; C:host cell nucleus;
GO:0003677; F:DNA binding; IEA.
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                                                  KKQRFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                                               MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                             LFHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFGDLNVVYRDGVPL
SKRRFHKIAGNFTGQCRHCWTSKREDRRRTRQETQV
                                                                                                                                         AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                                        AACQSCIKFYAKIRELRYYSESVYATTLETITNTKLYDLSIRCMCCLKPLSPAEKLRHLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integrated into UniProtKB/TrEMBL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                         1.
18739 MW;
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                                                                                                                                                                                                                                                                                                                  54.4%; Score 451.5; DB 2; 55.1%; Pred. No. 2.2e-36; tive 21; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 451.5; DB 1;
Pred. No. 2.2e-36;
21; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                2B1F406B563F05FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       see http://www.uniprot.org/terms
Attribution-NoDerivs License
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mavirus DNA
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RESULT 98
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Best Local
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29_9PAPI
Q9UIZ9_9PAPI
                          type 39.";
Virology 181:419-423(1991).
-i- FUNCTION: Transcription
DNA (By similarity).

DNA representation of the protection
                                                                                                                                                                                                                                                       VE6_HPV39
P24835;
                                                                                                                                        Human papillomavirus tyr
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI TaxID=10588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.; "Characterization of a novel human papillomavirus DNA in the cervical carcinoma cell line ME180.", J. Virol. 65:5564-5568(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unclassified Papi
NCBI_TaxID=10566;
                                                                                           NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=91135017; PubMed=1847266;
Volpers C., Streeck R.E.;
                                                                                                                                                                                                                  01-MAR-1992,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000,
01-MAY-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9UIZ9
                                                                                                                                                                                                                                           01-MAR-1992, integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=91374616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human papillomavirus.

    -!- FUNCTION: This protein may be involved in the oncogenic
of this virus (cervical neoplasia-associated virus).
    -!- SUBCELLULAR LOCATION: Nuclear matrix-associated (By sim.

                                                                                                                                                                                                         Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                 "Genome organization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L; M73258; AAF14011.1; -; Genomic_DNA.
GO:0042025; C:host cell nucleus; IEA.
GO:003677; F:NNA binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF00518; E6; 1.
                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                        61
                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD
                                                                                                                                                                                                                                                                                                                                               KKQRFHNIRGRWTGRCMSCCRSS----RTRRETQL
                                                                                                                                                                                                                                                                                                                                                                                                                                LFHNPEERPYKLPDLCRTLDTTLHDVTIDCVYCRRQLQRTEVYEFAFGDLNVVYRDGVPL
                                                                                                                                                                                                                                                                                                                               SKRRFHKIAGNFTGOCRHCWTSKREDRRRTRQETQV
                                                                                                                                                                                                                                                                                                                                                                                AACOSCIKFYAKIRELRYYSESVYATTLETITNTKLYDLSIRCMCCLKPLSPAEKLRHLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NA viruses, no RNA
Papillomaviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             integrated into UniProtKB/TrEMBL
                                                                                                                                                                                                                   entry version 30.
                                               Transcriptional transactivator.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=1716694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19167 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54.48;
                                                                                                                                                                     es, no
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                                                                                                                                                            'e 39.
` RNA ⊁
                                                                                    nucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 451.5; DB 2
Pred. No. 2.3e-36;
1; Mismatches 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2E40C128FEF7902C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                stage; Papillomaviridae;
                                                                                                                                                                      stage;
                                                                                  sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162
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                                                                                                                                                                      Papillomaviridae;
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                                                                                    papillomavirus
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                                             Query Match
Best Local S
Matches 86
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QQQNP8_HPV18 PRELIMINARY;
QQQNP8;
01-MAY-2000, integrated into 01-MAY-2000, sequence version 07-FEB-2006, entry version 17
                                                                                                                                                             InterPro;
Pfam; PFOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZN_FING
ZN_FING
SEQUENCE
                                                                                                                                                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning of E6 and E7 Genes of Transformation Potential of E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, Alphapapillomavirus
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                        GO; GO:0042025; C:host cell nuc
GO; GO:0003677; F:DNA binding;
                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                        Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE
Veiko V.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
Laassri M., Gul'ko L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Activator; DNA-binding; Early protein; Metal-binding; Nuclear Oncogene; Transcription; Transcription regulation; Zinc; Zinc CHAIN 1 158 Protein E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kisseljev F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=333761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M62849; AAA47050.1; -; Genomic_DNA.
PIR; A38502; W6WL39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00518; E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -
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_HPV18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: Belongs to the papillomaviruses E6 protein family.
                                                                                                                                                                                                                              Y18491; CAB53096.1; -; Genomic_DNA.
O:0042025; C:host cell nucleus; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122
                                                                                                                                                             PF00518;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 62
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    N
                                                86;
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                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
  FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KRRFHKIAGSYTGOCRRCWTTKREDRRLTRRETOV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KORFHNIRGRWTGRCMSCCRSSR----TRRETOL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACQSCIKFYAKIRELRYYSDSVYATTLENITNTKLYNLLIRCMCCLKPLCPAEKLRHLNS 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FHNPAERPYKLPDLCTTLDTTLQDITIACVYCRRPLQQTEVYEFAFSDLYVVYRDGEPLA
                                                                                                                                                                                   IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR001334; E6.
                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32
105
158 AA;
                                                                                                                                       18; E6; 1.
158 AA; 18886 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182:139-149(1999).
                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integrated into UniProtKB/TrEMBL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18727 MW;
                                                                 54.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vinokurova
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             no RNA stage;
                                             21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                         Score 449.5; DB 2;
Pred. No. 3.5e-36;
1; Mismatches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 449.5;
Pred. No. 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gene a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                             IEA.
                                                                                                                                       5BCF13CF43D407AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1B5E9D55BC1B662E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 3.5e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Papilloma Virus Type 18 and and its Mutants.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cervical HPVs in Evolution; Genomic Sequence of IS39/AE2, of Oncogenic HPV 82 (W13B)."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
Narechania A., Chen Z., Desalle R., Burk R.D.;
"Phylogenetic Incongruence among Oncogenic Genital Alpha Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; dsDNA viruses, Alphapapillomavirus.
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Terai M., Burk R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papillomaviruses.";
J. Virol. 79:15503-15510(2005).
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129, A
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RESULT 1
US-10-530-253-3
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PRIOR FILING DATE: 2003-10-02
PRIOR PPLICATION NUMBER: US 60/415,929
- PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
                                           US-10-530-253-5
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                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 00630/100M137-US2
CURRENT FILING DATE: 205-04-04
PRIOR APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2003-10-03
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
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Query Match
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                                                                                                                        SEQ ID NO 5
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CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
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APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PARTILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
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                                                                             LENGTH: 24
TYPE: PRT
                                                                                                                                                SOFTWARE: PatentIn version 3.1
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                                                              ORGANISM: Human papillomavirus type 16
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No. US20060014926A1
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Pred. No. 6.5e-81;
    Score 828;
    DB
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US-10-484-063-27

Sequence 27, Application US/10484063

; Publication No. US20050048467A1

; GENERAL INFORMATION:
 GENERAL INFORMATION:
 APPLICANT: SASTRY, K. JAGANNADHA
 APPLICANT: TORTOLERO-LUNA, GUILLERMO
 APPLICANT: FOLIEN, MICHELE
 TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
 TITLE OF INVENTION: PRE-CEN-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
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; TYPE: PRT
; ORGANISM: Human papillomavirus
US-10-484-063-20
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Publication No. US20050048467A1
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Best Local Similarity
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APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: FOLLEN, MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED
TITLE OF INVENTION: PRE-CANCEROUS AND CANCEROUS GROWTHS, INCLUDING CIN
FILE REFERENCE: UTSC:560US
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CURRENT FILLING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/306,809
PRIOR PILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
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FILE REFERENCE: UTSC::560US
CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR FILING DATE: 2002-07-19

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Sequence 1, Application US/10530253 Publication No. US20060014926A1
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SEQ ID NO 27
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Best Local Similarity
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Someth, Larry
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER: OF SEQ ID NOS: 65
NUMBER: OF SEQ ID NOS: 65
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PRIOR FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 27
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TYPE: PRT
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TYPE: PRT
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Pred. No. 6e-81;
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; TYPE: PRT; ORGANISM: Human Papillomavirus US-10-858-384-2
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APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. SEQ ID NO 2
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Publication No. US20050033025A1
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Best Local Similarity
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TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR PILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
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nes 149; Conservative
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  61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
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                                                                    MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                                           MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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GUILLET, JEAN-GERARD
CONNAN, FRANCINE
                                                                                                                                  Conservative
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98.7%;
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Pred. No. 1.3e-80;
1; Mismatches 2
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Pred. No. 1.1e-80;
0; Mismatches 2;
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APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
ITITLE OF INVENTION: Complexes and Methods of Using Same
FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
INUMBER OF SEQ ID NOS: 198
SOFTWARE: CURASeqList version 0.1
SEQ ID NO 16
LENGTH: 158
TYPE: PAT
CORGANISM: Homo sapiens
US-10-367-057-16
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US-11-021-949-13
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US-10-367-057-16
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US-11-021-949-13
                                                                  TITLE OF INVENTION: ANTHODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION UMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 16, Application US/10367057 Publication No. US20050100554A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                APPLICANT: LU, PETER APPLICANT: GARMAN, JC APPLICANT: BELMARES, APPLICANT: DIAZ-SARM
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Best Local Similarity
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              ORGANISM: human papilloma virus (HPV)
                                                      ENGTH: 158
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DIAZ-SARMIENTO, CHAMORRO SOMOZA
                                                                                                                                                                                                                                                                    SCHWEIZER, JOHANNES
                                                                                                                                                                                                                                                                                                                      GARMAN, JONATHAN DAVID
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Pred. No. 1.3e-80;
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US-11-206-138-3
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SOFTWARE: Patentin version 3.3
SEQ ID NO 3
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Publication No. US20060039919A1
GENERAL INFORMATION:
APPLICANT: HealthBanks Biotech CO. LTD.
TITLE OF INVENTION: Fusion protein for int
FILE REFERENCE: P7819/0613
CURRENT APPLICATION NUMBER: US/11/206,138
CURRENT FILING DATE: 2005-08-18
                                                                                                                                                                                                            Sequence 2, Application US/10472724
Publication No. US20040171806A1
GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7
FILE REFERENCE: 4121-154
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Best Local Similarity
                                                  SOFTWARE: PatentIn version 3.2 SEQ ID NO 2
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                                                                                                  CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
                                                                                       NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Human papillomavirus type
                LENGTH: 171
TYPE: PRT
ORGANISM: Artificial Sequence
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98.0%;
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Pred. No. 1.3e-80;
l; Mismatches 2
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Pred. No. 1.3e-80;
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                                                                                                                                                                                                                                  genes and proteins useful for vaccination
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RESULT 13
US-10-530-253-11
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TYPE: PRT
; ORGANISM: Human papillomavirus type
US-10-530-253-9
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US-10-530-253-9
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                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
                                                                                                                     Sequence 11, Application US/10530253
Publication No. US20060014926A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10530253 Publication No. US20060014926A1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McBlhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REPERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOPTWARE: PatentIn version 3.1
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OTHER INFORMATION:
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98.0%; Pred. No. 1.5e-80;
tive 'l; Mismatches 2
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Pred. No. 2.2e-80;
0; Mismatches 2
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US-11-192-923A-2
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// ORGANISM: Human papillomavirus type 16
US-10-530-253-11

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Publication No. US20060018928A1
GENERAL INFORMATION:
APPLICANT: PANG, XIAOWU
TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS
TITLE OF INVENTION: RECOMBINANT REPLICON
FILE REFERENCE: 116620-003
CURRENT APPLICATION NUMBER: US/11/192,923A
CURRENT FILING DATE: 2003-01-29
PRIOR APPLICATION NUMBER: CN 03115272.4
PRIOR APPLICATION NUMBER: CN 03115273.2
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
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                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                      Query Match
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CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2003-01-30 NUMBER OF SEQ ID NOS: 45
                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                         LENGTH: 256
TYPE: PRT
ORGANISM: Human papillomavirus
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                                                                                                                                                     106 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 165
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226
                                                                          166 AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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                                                                                                           61 AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLD
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                                    KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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KKORFHNIRGRWTGRCMSCCRSSRTRRETQL 256
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Pred. No. 2.3e-80;
1; Mismatches 2;
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Pred. No. 2.2e-80;
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                                                                                                                                              NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
LENGTH: 273
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-4
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APPLICANT: MACEARLAN, RODERICK I. APPLICANT: MALLIAROS, JIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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LENGTH: 266
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                                                                                        Query Match
Best Local (
                                                                        Matches
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APPLICANT:
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TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOPTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Lombardo-Bencheikh, Angela TITLE OF INVENTION: Vaccine FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/AU98/00080 PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Bruck, Claudine
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ORGANISM: Human papillomavirus type 16
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                                                                                          Similarity
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MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 173
                     MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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                                                                        Conservative
                                                                                        99.2%;
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                                                                 Score 823; DB 4; Le
Pred. No. 2.5e-80;
Migmatches 2;
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Pred. No. 2.4e-80;
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                                                                                                          Length 273;
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PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 4
                                                                                                                                                            GENERAL INFORMATION:

APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
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                                                                                                                                                                                                                                                                                                            Sequence 10, Application US/10000903 Publication No. US20020182221A1
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CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
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CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
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TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
                                                                                                                  APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6 from Human papilloma virus type OTHER INFORMATION: 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 99.2%;
Local Similarity 98.0%;
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Pred. No. 2.5e-80;
1; Mismatches 2;
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US-10-899-771-10
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; ORGANISM: Homo sapien
US-10-000-903-10
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 10
LENGTH: 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOPTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEGION FOR STATE OF SEGION FOR STATE OF SEGION FOR                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 148;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus OTHER INFORMATION: 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRI
TYPE: PRI
ORGANISM: Artificial Sequence
PEATURE:
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253
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                                                                                                                                                                                                                                                                                                                                                                                                            148; Conservative
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                                   KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 283
                                                                                                                                    AVCDKCLKFYSKISEYRHYCYSLYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLD
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Pred. No. 2.7e-80;
1; Mismatches 2
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Pred. No. 2.7e-80;
1; Mismatches 2
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APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papi:
TITLE OF INVENTION: and Fusion Proteins Adjuvanted wit
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-24
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6
US-10-899-771-6
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US-10-899-771-6
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Publication No. US20050031638A1
GENERAL INFORMATION:
                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 28
SOPTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/10000903
Publication No. US20020182221A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILLING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Dalemans, Wilfried L.J. APPLICANT: Gerard, Catherine Mari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Vaccine FILE REFERENCE: B45107
                                                                                                                                          LENGTH: 37
TYPE: PRT
                 OTHER INFORMATION: Chimaeric protein (protein D
OTHER INFORMATION: influenzae B and E6E7 fusion
OTHER INFORMATION: virus type 16)
                                                                                          FEATURE:
                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 KKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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98.0%;
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Pred. No. 3.6e-80;
Pred. No. 3.6e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Papilloma Virus Proteins
juvanted with a CpG Oligonucleotide
                                               from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 371;
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                                          Haemophilius
Human papillo
                                             papilloma
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US-10-899-771-14
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US-10-000-903-14
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APPLICANT: Gerard, Catherine Marie Ghislair
APPLICANT: Lombardo-Benchelkh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                Sequence 14, Application US/10899771 Publication No. US20050031638A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 148; Conserv
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LENGTH: 390
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Best Local
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/10/899,771
FURING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
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ORGANISM: Homo sapien
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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Jo. US20020182221A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 823; DB 4; Length 390; Pred. No. 3.8e-80;
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Pred. No. 3.6e-80;
1; Mismatches 2
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; LENGTH: 248
; TYPE: PRT
; ORGANISM: Human papillomavirus type
US-10-530-253-7
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
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Best Local Similarity
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                                                                                                                                                                                                                                   Matches 148;
                                                                                                                                                                                                                                                                           Query Match
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PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus OTHER INFORMATION: pneumoniae and E6E7 fusion from Human papilloma OTHER INFORMATION: virus type 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                         Local Similarity
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                                                                   159
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KORFHNIRGRWTGRCMSCCRSSRTRRETOL
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                                                                   VCDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINCQKPLCPEEKQRHLDK
                                                                                                                                                  FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 158
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98.7%;
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Pred. No. 3.7e-80;
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Pred. No. 3.8e-80;
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KQRFHNIRGRWTGRCMSCCRSSRTRRETQL 248

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RESULT 26
US-11-072-288-1
                                                                       ; OTHER INFORMATION: Description of Artificial Sequence:Derivated from OTHER INFORMATION: human papillomavirus, strain HPV-16, E6 protein ; OTHER INFORMATION: fused F protein signals, clone E6*TMF. US-11-072-288-1
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; ORGANISM: Human papillomavirus type
US-10-177-390-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 25
US-10-177-390-6
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/072,288
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US/09/462,993
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: PR 97/09152
PRIOR FILING DATE: 1999-07-18
PRIOR APPLICATION NUMBER: PR 97/09152
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Publication No. USZ0050159386AI
GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
APPLICANT: BALLOUL, Jean-Marc
APPLICANT: BIZOUARNE, Nadine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/10177390 Publication No. US20030143743A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                           SEQ ID NO 1
LENGTH: 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 148;
Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear TITLE OF INVENTION: Polynucleotides by Electroporation FILE REPERENCE: 021505w0/JH/ml CURRENT APPLICATION NUMBER: US/10/177,390 CURRENT FILLING DATE: 2002-06-20 NUMBER OF SEQ ID NOS: 34 SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BALLOUL, Jean-Marc
APPLICANT: BIZOUARUS, Naddine
TITLE OP INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC
TITLE OP INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
FILE REFERENCE: 0.17753-122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Schuler, Gerold
APPLICANT: N.V. Antwerps Innovatiecentrum
                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Ver. 2.2
                                                                                                                                                                         FEATURE:
                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                         TYPE: PRT
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93.9%;
94.7%;
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Pred. No. 3.4e-80;
Score 779.5; DB 6; Pred. No. 1.1e-75;
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                       Length 243
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GENERAL INFORMATION:

APPLICANT: LU, PETER

APPLICANT: GARMAN, JONATHAN DAVID

APPLICANT: GARMAN, JONATHAN DAVID

APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: SCHWEIZER, JOHANNES

TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV

TITLE OF INVENTION: AND METHODS OF THEIR USE

FILE REFERENCE: VITA-012

CURRENT APPLICATION NUMBER: US/11/021,949

CURRENT FILING DATE: 2004-12-23

PRIOR APPLICATION NUMBER: 60/532,373
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US-10-530-253-18
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Publication No. US20060014926A1
                                                                                                                                                                                                                                                                              Sequence 14, Application US/11021949 Publication No. US20050142541A1
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Best Local Similarity
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APPLICANT: Jeffrey K. Pullen
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR PILING DATE: 2003-10-03
PRIOR PILING DATE: 2003-10-03
PRIOR FILING DATE: 2002-10-03
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71.5%;
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; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FASTSEQ for Windows Version 4.
; SEQ ID NO 14
; SEQ ID NO 14
; LENGTH: 149
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-14
                  RESULT 30
US-11-021-949-18
; Sequence 18, Application US/11021949
; Publication No. US20050142541A1
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US-10-530-253-16
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GENERAL INFORMATION:
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SEQ ID NO 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CASSECTI, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Susan P. McElhinen
TITLE OF INVENTION: HUMAN PAPILLOWAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SCOTTMANDE OF SEQ ID NOS: 65
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TYPE: PRT
ORGANISM: Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                          63.0%; Score 523; DB 5; Length 149;
64.9%; Pred. No. 3.2e-48;
tive 18; Mismatches 33; Indels
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SEQ ID NO 18

LENGTH: 149

TYPE: PRT

ORGANISM: human papilloma virus (HPV)

US-11-021-949-18
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                                                                                                                                                                                                                                                       ; TYPE: PRT ; ORGANISM: Human papillomavirus type US-10-530-253-17
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US-10-530-253-17
Sequence 17, Application US/10530253
Sequence 17, Application US/20060014926A1
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Best Local Similarity
                                                                                                                                                                       Matches
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                                                                                                                                                                                         Query Match 62.7%;
Best Local Similarity 63.6%;
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Strip K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100m137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR PILICATION NUMBER: PCT/US2003/031726
PRIOR PILICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LU, PETER APPLICANT: GARMAN,
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                                                                                                               1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                        AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
GICKLCLRFLSKISEYRHYNYSVYGNTLEQTVKKPLNEILIRCIICQRPLCPQEKKRHVD
                                                                                    MFQDTEEKPRTLHDLCQALETTIHNIELQCVECKKPLQRSEVYDFAFADLTVVYREGNPF
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BELMARES, MICHAEL P.
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                                                                                                                                                                       Score 520; DB 5;
Pred. No. 6.7e-48;
9; Mismatches 34
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; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-16
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                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 360, Applic Publication No. US20 GENERAL INFORMATION:
                                       PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 360
LENGTH: 149
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CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                          APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                                                                                                                                                                                                                                   APPLICANT: LU, PETER APPLICANT: GARMAN, CAPPLICANT: BELMARES,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
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APPLICANT: GARMAN, C
APPLICANT: BELMARES,
                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
                                                                                                                                                                                                                                                                                         APPLICANT:
ORGANISM: human papilloma virus (HPV)
                            TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/11021949
o. US20050142541A1
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                                                                                                                                                                                                                                                                                                                CHAMORRO SOMOZA
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: LU, PETER

APPLICANT: GARMAN, JONATHAN DAVID

APPLICANT: BELWARES, MICHABL P.

APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: SCHWEIZER, JOHANNES

TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS

TITLE OF INVENTION: AND METHODS OF THEIR USE

FILE REFERENCE: VITA-012

CURRENT APPLICATION NUMBER: US/11/021,949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 24
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Publication No. US20060014926A1
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Best Local Similarity
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUWAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/US2003/031726 PRIOR FILING DATE: 2003-10-02
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AVCKVCLRLLSKISEYRHYNYSLYGDTLEQTLKKCLNEILIRCIICQRPLCPQEKKRHVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 496; DB 5; L
Pred. No. 2.6e-45;
on. Mismatches 36;
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Pred. No. 1.6e-45;
22; Mismatches 37;
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CURRENT FILING DATE: 2004-12-23;
PRIOR APPLICATION NUMBER: 60/532,373;
PRIOR FILING DATE: 2003-12-23;
NUMBER OF SEQ ID NOS: 361;
SOFTWARE: FASTSEQ for Windows Version 4.0;
SEQ ID NO 15;
LENGTH: 149;
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
TYPE: PRT
                                  RESULT 37
US-11-021-949-17
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; Sequence 17, Application US/11021949
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; ORGANISM: Human papillomavirus type 52
US-10-530-253-22
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PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Seffrey K. Pullen
APPLICANT: Susan P. McElhiney
APPLICANT: Susan P.
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CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 59.8%; Score 496; DB 6; Local Similarity 61.6%; Pred. No. 2.6e-45;
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                                                                                                                                                                                        ANKRFHNIMGRWTGRCSECWR 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.7%; Score 487; DB 5; 61.7%; Pred. No. 2.4e-44;
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US-11-021-949-359
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GENERAL INFORMATION:
APPLICANT: LU, PETER
APPLICANT: GARWAN, JONATHAN DI
APPLICANT: BELMARES, MICHAEL I
APPLICANT: DIAZ-SARWIENTO, CH
                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 359
LENGTH: 148
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Publication No. US20050142541A1
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILLING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: LU, APPLICANT: GAF
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APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARM, ENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 148
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
                                                                                                                                             Local Similarity
les 87; Conserv
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                                                                               FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA
VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                    FPNPEBRPYKLPALCEEVNISIHEIELDCVYCERQLYRCEVYDFIFRDLCVVYRKGKPLG 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GARMAN,
                                                                                                                                             58.3%; Score 484; DB 6; Length 148; llarity 60.4%; Pred. No. 5.1e-44; Conservative 17; Mismatches 40; Indels
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RESULT 40
US-10-530-253-26
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; ORGANISM: human papilloma virus (HPV)
US-11-021-949-19
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 26, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
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                                                                 SEQ ID NO 26
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APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BILDARES, MICHAEL P.
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                          APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OGGOVING HUMAN PAPPLY
TITLE OGGOVING HUMAN PAPPLY
TITLE OGGOVING HUMAN PAPPLY
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PC/US2003/031726
PRIOR PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2003-10-03
                                                                                                                                                                                                                                                                                                       APPLICANT: Cassetti, Maria C. APPLICANT: Smith, Larry APPLICANT: Jeffrey K. Pullen APPLICANT: Susan P. McElhine:
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CURRENT FILING DATE: 2004-12-23
CRICK APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
                                                                                      NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
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SOFTWARE: FastSEQ for Windows Version 4.0
                        TYPE: PRT
ORGANISM: Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 148
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No. US20050142541A1
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1; Pred. No. 6.6e-44;
16; Mismatches 40; Indels
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                                                                                                                                              Sequence 21, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 361 LENGTH: 158
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Publication No. US20050142541A1
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APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: NTAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M37-US2
CURRENT APPLICATION NUMBER: US/10/530,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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CURRENT FILING DATE: 2004-12-23
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTONIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 15
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                               KORFHNIRGRWTGRCMSCCRSS----RTRRETQL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNPAERPYKLPDLCTALDTTLHDITIDCVYCKTQLQQTEVYEFAFSDLFIVYRNGEPYA
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION UMMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 24
LENGTH: 151
TYPE: PRT
ORGANISM: human papilloma virus (HPV)
US-11-021-949-24
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PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 21
LENGTH: 151
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; ORGANISM: Human papillomavirus type
US-10-530-253-21
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Best Local Similarity 57.0
86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV TITLE OF INVENTION: AND METHODS OF THEIR USE FILE REFERENCE: VITA-012
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APPLICANT: GARMAN, JONATHAN DAVID
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121
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                                                                                                                       AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEBKQRHLD 120
                                                                                                                                                                MFEDKRERPRTLHELCEALNVSMHNIQVVCVYCKKELCRADVYNVAFTEIKIVYRDNNPY
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EKKRFHEIAGRWTGQCANCWQRTRQRNETQV 151
                                                                                  AVCKQCLLFYSKIREYRRYSRSVYGTTLEAITKKSLYDLSIRCHRCQRPLGPEEKQKLVD
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DIAZ-SARMIENTO, CHAM
SCHWEIZER, JOHANNES
                                                                                                                                                                                                                                                55.4%; Score 460; DB 6; Length 151; 57.0%; Pred. No. 2.1e-41; tive 24; Mismatches 41; Indels
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RESULT 44

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; SEQ ID NO 29
LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-29
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US-11-021-949-29
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APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 20, Application US/10530253 Publication No. US20060014926A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: LU, PETER
APPLICANT: GARMAN, JC
APPLICANT: BELMARES,
APPLICANT: DIAZ-SARM
APPLICANT: SCHWEIZER,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 29, Application US/11021949
Publication No. US20050142541A1
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                                                                              Matches
                                                                                                                   Query Match
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APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
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les 87; Conserv
                                                                            Local Similarity es 87; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
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FDDPKQRPYKLPDLCTELNTSLQDVSIACVYCKATLERTEVYQFAFKDLCIVYRDCIAYA
                                  FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PDDPKQRPYKLPDLCTELNTSLQDVSIACVYCKATLERTEVYQFAFKDLCIVYRDCIAYA 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55.4%;
ilarity 56.1%;
Conservative 2
                                                                            55.4%;
ilarity 56.1%;
Conservative 2
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                                                                              22;
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Pred. No. 2.5e-41;
                                                                                              Score 459.5; DB 6
Pred. No. 2.5e-41;
                                                                                Mismatches
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      63
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APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR APPLICATION NUMBER: 50/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASEUSC for Windows Version 4.0
SEQ ID NO 28
LENGTH: 158
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US-10-530-253-15
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Best Local Similarity 56.1
Matches 87; Conservative
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SEQ ID NO 15
LENGTH: 158
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Publication No. US20050142541A1
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Publication No. US20060014926A1
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Someth, Larry
APPLICANT: Someth, Larry
APPLICANT: Someth, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
TILE REPERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2003-40-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
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; TYPE: PRT ; ORGANISM: human papilloma virus (HPV) US-11-021-949-28
RESULT 49
US-10-000-903-21
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PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOPTWARE: PatentIn version 3.2
SEQ ID NO 6
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Best Local Similarity
Matches 87; Conserv
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Best Local :
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                                                                                                                                                                                                                                                                                                                   Matches
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CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
PRIOR FILING DATE: 2002-03-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7
                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                               130
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                                                                                                                                                                                                                                                                                                                 l Similarity
87; Conserv
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                                                                                                                                                                                                                                    FEDPTRRPYKLPDLCTELNTSLQDIEITCVYCKTVLELTEVFEFAFKDLFVVYRDSIPHA
                                                                                                                                                                                                                                                            FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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                                                                               KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KRRFHNIAGHYRGQCHSCCNRARQERLQRRRETQV 158
                                                                                                                                                                                                                                                                                                             54.9%; Score 455.5; DB 4 ilarity 56.1%; Pred. No. 7.3e-41; Conservative 21; Mismatches 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes and proteins useful for vaccination
                                                                                                                                                                                                                                                                                                                                                      DB 4;
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                                                                                                                                                                                                                                                                                                                                                      Length 172;
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GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva,

APPLICANT: APPLICANT:

Cabezon Silva, Teresa Delisse, Anne-Marie Eva Fernande Gerard, Catherine Marie Ghislaine Lombardo-Bencheikh, Angela Sequence 21, Application US/10000903 Publication No. US20020182221A1

TITLE OF INVENTION: Vaccine

B45107

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US-10-899-771-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Rusion Proteins Adjuvanted with a CpG Oligonuclectide
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/9/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/ED98/08563
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version 3.0
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Best Local S
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LENGTH: 278
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                                                                                                                                                                                                                                                       OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6 from Human papilloma virus OTHER INFORMATION: 18)
                                                                                                                                                                                                                                                                                                                 LENGTH: 278
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKFLCPEEKQRHLDK
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                                                                VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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                                                                                                                                                                     54.9%; Score 455.5; DB 5; 56.1%; Pred. No. 1.3e-40;
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56.1%; Pred. No. 1.
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Query Match
Best Local Similarity
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US-10-899-771-23
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                                     CURRENT FILING DATE: 2004-07-27

CURRENT FILING DATE: 2004-07-27

PRIOR APPLICATION NUMBER: US/09/581,976

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 2000-06-20

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-18

PRIOR APPLICATION NUMBER: GB 9727262.9

PRIOR FILING DATE: 1997-12-24

NUMBER OF SEQ ID NOS: 28

SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Cabezor
APPLICANT: Delisse
APPLICANT: Gerard
APPLICANT: Lombar
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Dalemans,
APPLICANT: Gerard,
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LENGTH: 383
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Publication No. US20050031638A1
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Publication No. US20020182221A1
                       SEQ ID NO 23
                                                                                                                                                                                                                                                               APPLICANT: Dalemans, Wilfried L.J.

APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oli
FILE REFERENCE: B45124
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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383
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
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56.1%;
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Pred. No. 1.8e-40;
11; Mismatches 42
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Oligonucleotide
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; FEATURE:
; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius; OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma; OTHER INFORMATION: virus type 18)
US-10-899-771-23
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                                                                                                    US-10-800-023-27
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US-11-021-949-31
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US-11-021-949-31
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                                                                                                                              RESULT 54
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Matches
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                                         GENERAL INFORMATION:
                                                            Sequence 27, Application US/10800023 Publication No. US20040258688A1
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LENGTH: 162
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOPTWARE: PASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
APPLICANT: Steinman, Ralph APPLICANT: Nussenzweig, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                               1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 55.1
86; Conservative
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                                                                                                                                                                                                                                                                         AACQSCIKFYAKIRELRYYSESVYATTLETITNTKLYDLSIRCMCCLKPLSPAEKLRHLN
                                                                                                                                                                                                                                                                                                                                                        KRRPHNIAGHYRGQCHSCCNRARQERLQRRRETQV 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                        54.4%; Score 451.5; DB 6; 55.1%; Pred. No. 1.8e-40; tive 21; Mismatches 44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 455.5; DB 5; pred. No. 1.8e-40; 21; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 162;
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Smith, Larry

APPLICANT: Jeffrey K. Pullen

APPLICANT: Susan P. McSlhiney

TITLE OF INVENTION: HUWAN PAPILLOWAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS

FILE REFERENCE: 00630/100M137-US2

CURRENT APPLICATION NUMBER: US/10/530,253

CURRENT FILING DATE: 2005-04-04

PRIOR APPLICATION NUMBER: PCT/US2003/031726

PRIOR APPLICATION NUMBER: PCT/US2003/031726

PRIOR APPLICATION NUMBER: DCT/US2003/031726

PRIOR APPLICATION NUMBER: DCT/US2003/031726

PRIOR APPLICATION NUMBER: DCT/US2003/031726

PRIOR FILING DATE: 2003-10-02

NUMBER: DC SOOTMARE: PATENTARE: PATENTARE: PATENTING DATE: 2002-10-03

NUMBER: DS SOOTMARE: PATENTING DATE: PATENTING DA
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CURRENT APPLICATION NUMBER: US/10/800,023
CURRENT FILING DATE: 2004-03-14
PRIOR APPLICATION NUMBER: 09/925,284
PRIOR FILING DATE: 2001-08-09
PRIOR PPLICATION NUMBER: 09/586,704
PRIOR FILING DATE: 2000-06-05
PRIOR APPLICATION NUMBER: PCT/US96/01383
PRIOR APPLICATION NUMBER: 09/381,528
PRIOR APPLICATION NUMBER: 09/381,528
PRIOR FILING DATE: 1995-01-31
PRIOR FILING DATE: 1995-01-31
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SOFTWARE: FastSEQ for
SEQ ID NO 27
                                                                                                                                     Matches
                                                                                                                                                                        Best Local
                                                                                                                                                                                                   Query Match
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APPLICANT: Bonifaz, Laura
TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
TITLE OF INVENTION: of the Immune Response Therefrom
                                                                                                                                                                                                                                                                           TYPE: PRT ORGANISM: Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: human papilloma virus
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                                  FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KRRFHKIAGHYRGQCHSCCNRARQERLQRRRETQV 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KORFHNIRGRWTGRCMSCCRSSR----TRRETQL 151
   FHNPAERPYKLPDLCTTLDTTLQDITIACVYCRRPLQQTEVYEFAFSDLYVVYRDGEPLA
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                                                                                                                                                                 54.2%;
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Pred. No. 3e-40;
                                                                                                                              Score 449.5; DB
Pred. No. 3e-40;
9; Mismatches
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; SEQ ID NO 30
; LENGTH: 158
; TYPE: PRT
; ORGANISM: human papilloma virus (HPV)
US-11-021-949-30
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                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 57
            CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 30, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                            Sequence 25, Application US/11021949 Publication No. US20050142541A1
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APPLICANT:
APPLICANT:
                                                                                                                                                      APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                                                                                                                                                       APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/532,373
PRIOR PILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOPTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
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TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: LU,
APPLICANT: GAI
LENGTH: 151
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Similarity 55.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYA 61
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Vo. US20050142541A1
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Pred. No. 3e-40;
                                                                                                                                                                                                    STRAINS OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: human papilloma virus (HPV) US-11-021-949-27
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                                                                                                                                                                      US-10-530-253-23
                                                                                                                                                                                         RESULT 59
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Publication No. US20050142541A1
GENERAL INFORMATION:
                                                                                                               Sequence 23, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: LU, I
APPLICANT: GARN
APPLICANT: BELN
APPLICANT: DIA;
APPLICANT: SCHI
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Best Local
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CURRENT FILING DATE: 2004-12-23
RRIOR APPLICATION NUMBER: 60/532,373
RRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows Version 4.0
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElbinney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES
FILE REFERENCE: 00630/100M137-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: VITA-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 150
TYPE: PRT
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es 85; Conserv
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                                                                                                                                                                                                                                               121 EKRRFHEIAGQWKGLCTNCWR-PRRQTETQV 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83;
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                                                                                                                                                                                                                                                                                                                      AACKRCVIFYSKITEYRRYTCSVYGATLEALTKKSLCNLLIRCHRCQMPLGPEEKQRIVD
                                                                                                                                                                                                                                                                                                                                                                                         GARMAN, JONATHAN DAVID BELMARES, MICHAEL P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 436.5; DB 6;
Pred. No. 7.1e-39;
Wiematches 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 449; DB 6;
Pred. No. 3.2e-40;
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                            AND IMMUNOGENIC COMPOSITIONS
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APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTHRODIES FOR ONCOGENIC STRAINS OF
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR FILING DATE: 2003-12-23
PRIOR FILING DATE: 2003-12-23
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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; ORGANISM: human papilloma virus (HPV)
US-11-021-949-22
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US-10-530-253-23
                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                            Query Match
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LENGTH: 155
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR PILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
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Local Similarity 56.4%;
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                                                                                                                     62 VXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDK 121
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84; Conservative
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  KRRFHLIAHGWTGSCLGCWRQTSREPRES
                                       KORFHNIRGRWTGRCMSCCR-SSRTRRET 149
                                                                                 VCRVCLLFYSKVRKYRYYDYSVYGATLESITKKQLCDLLIRCYRCQSPLTPEEKQLHCDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VCRVCLLFYSKVRKYRYYDYSVYGATLESITKKQLCDLLIRCYRCQSPLTPEEKQLHCDR 124
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                                                                                                                                                                   FNNPQERPRSLHHLSEVLEIPLIDLRLSCVYCKKELTRAEVYNFACTELKLVYRDDFPYA
                                                                                                                                                                                                                                                       Conservative
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; Pred. No. 8.8e-38;
17; Mismatches 47;
                                                                                                                                                                                                                                                                         Score 426.5; DB 6; Pred. No. 8.8e-38;
                                                                                                                                                                                                                                                  Mismatches
153
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Best Local Similarity
Matches 81; Conserv
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Publication No. US20060014926A1
GENERAL INFORMATION:
                                                                                                                                     SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
LENGTH: 160
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Publication No. US20060014926A1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 39
LENGTH: 152
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                        Query Match
Best Local Similarity
                                                                    ORGANISM: Human papillomavirus type 59:-10-530-253-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
FITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR PILING DATE: 2002-10-03
                                                                                                                                                                                                                                                                               APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Someth, Larry
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR PILING DATE: 2003-10-02
                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
                                                                                                                      TYPE: PRT
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50.1%;
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Pred. No. 3.4e-37;
Score 415.5; DB 5;
Pred. No. 1.4e-36;
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                      Length 160;
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                   APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION UMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
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                                                                                                                                                                                                                                                                                                               RESULT 64
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US-11-021-949-32
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APPLICANT: LU, PETER
APPLICANT: GARMAN,
APPLICANT: BELMARES
                                                                                                                                                                                                                                               Sequence 26, Application US/11021949
Publication No. US20050142541A1
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Publication No.
                                                                                                                                                                                                                              GENERAL INFORMATION
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Best Local
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
CURRENT FILING DATE: 2004-12-23
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PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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TYPE: PRT
    APPLICATION NUMBER: 60/532,373
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vo. US20050142541A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50.1%; Score 415.5; DB 6; Length 160; 51.3%; Pred. No. 1.4e-36; tive 25; Mismatches 47; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
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RESULT 66
US-11-021-949-21
; Sequence 21, Application US/11021949
; Publication No. US20050142541A1
; GENERAL INFORMATION:
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APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STR
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/32,373
PRIOR FILING DATE: 2003-12-23
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SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 20
LENGTH: 153
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NUMBER OF SEQ ID NOS: 361
SOFTWARE: FastSEQ for Windows
SEQ ID NO 26
LENGTH: 151
TYPE: PRT
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Publication No. US20050142541A1
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50.0%; Pred. No. 2.3e-33;
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Pred. No. 1.5e-36;
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Indels Length 153;

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Gaps

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GENERAL INFORMATION:

APPLICANT: LU, PETER

APPLICANT: GARMAN, JONATHAN DAVID

APPLICANT: GARMAN, JONATHAN DAVID

APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA

APPLICANT: SCHWEIZER, JOHANNES

TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF

TITLE OF INVENTION: AND METHODS OF THEIR USE

FILE REFERENCE: VITA-012

CURRENT APPLICATION NUMBER: US/11/021,949

CURRENT PILING DATE: 2004-12-23

PRIOR APPLICATION NUMBER: 60/532,373

PRIOR APPLICATION NUMBER: 60/532,373

PRIOR PILING DATE: 2003-12-23

NUMBER OF SEG ID NOS: 361

SOFTWARE: FASTSEQ for Windows Version 4.0

SEG ID NO 23

LENGTH: 155

TYBE: PRT
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
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APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: SCHWEIZER, JOHANNES
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
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TYPE: PRT
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                                                                                                 4
                                                                                                                                            1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                          h 44.9%; Score 372.5; DB 6; Length 155; Similarity 50.7%; Pred. No. 6e-32; 76; Conservative 20; Mismatches 53; Indels 1
AVCRVCLLFYSKVRKYRYYKYSVYGATLESITKKQLSDLSIRCYRCQCPLTPEEKQLHCE
                                      AVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLD 120
                                                                                            IFSNTQERPRSLHHLSEVLQIPLLDLRLSCVYCKKELTSLELYRPACIELKLVYRNNWPY
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123
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APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICATION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CUURENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 1909-09-16
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
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US-10-751-845-157
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US-10-751-845-126
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                                                                                                                         PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 157, Applic Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
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                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING
FILE REFERENCE: 08191-013001
                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
FEATURE: OTHER INFORMATION: Artificial fusion sequence
                                                      ORGANISM: Artificial Sequence
                                                                                      TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Match 40.1%;
Local Similarity 65.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 HKRRFHYIAYAWTGSCLQCWRHT-SRQATE 152
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o. US20050100928A1
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Pred. No. 8e-28;
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CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 158
LENGTH: 237
TYDE: DET
              APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POI
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/99/664,225
PRIOR TILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-12-09
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                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                         Sequence 160, Appropriate Publication No.
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Best Local Similarity
Matches 66; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 08191-013001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Artificial fusion sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
APPLICATION NUMBER: US 60/154,665
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|------KISEYRHYCYSLYGTTLEQQYNKTLHEYML 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                       MFQDPQERPRKLPQLCTEL--------LLRREVYDFAFRDLCIVYRDGNPY
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                                                                                                                                                                                                                                                                            Application US/10751845
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                                                                                                                                                                                               Mary Lynne
Robert G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 333; DB 5;
Pred. No. 1.8e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 333; DB 5;
Pred. No. 1.8e-27;
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                                                                                                                                                          POLYEPITOPE POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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; FEATURE: ; OTHER INFORMATION: Artificial fusion sequence US-10-751-845-160
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                                                                                                                                                    , OTHER INFORMATION: HPV-16 L2/E6 fusion protein US-10-367-095-10
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US-10-367-095-10
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PRIOR FILLING DATE: 2002-02-14
PRIOR PELLOATION NUMBER: US 60/356,133
PRIOR FILLING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR FILLING DATE: 2002-02-14
PRIOR FILLING DATE: 2002-02-14
PRIOR FILLING DATE: 2002-02-14
                                                                                                                                                                                                                                                                   Remaining Prior Application data removed -
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 10, Applica Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 160
LENGTH: 261
                                                                            Query Match
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Best Local :
                                                                          Matches
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PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 44149-1US1
CURRENT APPLICATION NUMBER: US/10/367,095
CURRENT FILING DATE: 2003-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Robin A. Robinson
TITLE OF INVENTION: No. US20
                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/356,113 PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/356,123
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/356,154
                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                     LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 2002-02-14
APPLICATION NUMBER: US 60/356,135
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                  MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP 59
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                                                                                          38.9%; Score 323; DB 4; 1
100.0%; Pred. No. 5.5e-26;
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    Mismatches

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Pred. No. 2e-27;
                                                                          Mismatches
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MFQDFQERFRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP

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US-10-368-046-10
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                   FILE REFERENCE: 44149-2US1
CURRENT APPLICATION NUMBER: US/10/367,367
CURRENT FILING DATE: 2003-02-15
PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR PPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
PRIOR PILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR PILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR FILING DATE: 2002-02-14
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CURRENT FILING DATE: 2003-02-15
PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR PILING DATE: 2002-02-14
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SEQ ID NO 10
LENGTH: 536
TYPE: PRT
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Best Local
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PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,135
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                APPLICANT: Robin A. Robinson
TITLE OF INVENTION: Optimization of Gene Sequences of
TITLE OF INVENTION: Virus-Like Particles for Expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 13
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PRIOR FILING DATE: 2002-02-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Robin A. Robinson APPLICANT: Vittoria Cioce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE: OTHER INFORMATION: HPV-16 L2/E6 fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 60/356,113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          478 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP 536
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: 2002-02-14
NUMBER: US 60/356,157
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Pred. No. 5.5e-26;
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US-10-918-337-10
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                                                                                                                                                  ; OTHER INFORMATION: HPV-16 L2/E6 fusion protein US-10-918-337-10
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PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 536
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
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Best Local Similarity
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PRIOR FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: US 60/356,119
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CURRENT FILING DATE: 2004-08-13
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PRIOR APPLICATION NUMBER: US 60/356,161
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TITLE OF INVENTION: Optimization of Gene Sequences of
TITLE OF INVENTION: Chimeric Virus-Like Particles for
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/356,154 PRIOR FILING DATE: 2002-02-14
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                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                            LENGTH: 536
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APPLICATION NUMBER: US 60/356,133
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                     1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNP 59
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                                                                                          38.9%;
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Pred. No. 5.
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                                                                                                              DB 5;
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                                                                                                                            ) OTHER INFORMATION: Artificial fusion sequence US-10-751-845-159
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                                                              Query Match
Best Local Similarity
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SEQ ID NO 11
LENGTH: 150
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                                            Matches
                                                                                                                                                                                                                                                           SEQ ID NO 159
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                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NUCLEGIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR PILING DATE: 2000-08-18
PRIOR PILING DATE: 1909-12-09
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR PILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR PILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FASTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Homo sapiens
-10-367-057-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
TITLE OF INVENTION: Complexes and Methods of Using Same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hedley, APPLICANT: Urban, APPLICANT: Chicz,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                       FEATURE:
                                                                                                                                                                                      ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                   ENGTH: 119
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                                          48; Conservative
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RPRKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCL 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Urban, Robert G
Chicz, Roman M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jackson, Amanda;
Lewin, David A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/10751845
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                                   Score 189; DB 5; Lei
; Pred. No. 2.9e-12;
*** omatches 32;
                                          14; Mismatches
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                                                                                Length 119;
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                                        Indels 42;
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDIC!
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Dapillomavirus proteins and uses thereof
FITLE OF INVENTION: Dapillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAUGT-VILLADA, Isabelle
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SEQ ID NO 19
LENGTH: 33
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Best Local
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                    CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
                                                                                                                                                                                                                 APPLICANT: GUILLET, Jean-Gerard TITLE OF INVENTION: Mixture of peptides derived from E6 and/or TITLE OF INVENTION: papillomavirus proteins and uses thereof FILE REFERENCE: 45636-5071-US
                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
NUMBER OF SEQ ID NOS: 63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Pred. No. 1.3e-11;
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US-10-476-570-9
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                                                                                                                                                                                                                                                                                                                                                   RESULT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Mixture of peptides derived from E6 and/or TITLE OF INVENTION: papillomavirus proteins and uses thereof FILE REFERENCE: 45636-5071-US CURRENT APPLICATION NUMBER: US/10/476,570 CURRENT FILING DATE: 2003-11-04 PRIOR APPLICATION NUMBER: PCT/FR02/01533 PRIOR FILING DATE: 2002-05-03 PRIOR PILING DATE: 2002-05-03 PRIOR APPLICATION NUMBER: FR 01 05980 PRIOR FILING DATE: 2001-05-04 NUMBER OF SEQ ID NOS: 63 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 53
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LENGTH: 32
TYPE: PRT
ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10858384 Publication No. US20050033025A1
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Best Local Similarity
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Best Local Similarity
                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR E7 OF PPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET
APPLICANT: MAILLERE, Bernard
APPLICANT: BOUNGLUE MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
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100.0%; F±
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100.0%; Pred. No. 3.9e-10;
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APPLICANT: POUVELLE MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from 86 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION UNMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 55
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                                                                                                                                                                                                                                                               RESULT 83
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                                                        GENERAL INFORMATION:
APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, IS
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
APPLICANT: FERRIES,
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Best Local Similarity
Matches 30; Conserv
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NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 4
                                                                                                                                                                                               Sequence 8, Application US/10858384 Publication No. US20050033025A1
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                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE APPLICANT: INSTITUT NATIONAL DE LA SANTE ET APPLICANT: MAILLERE, Bernard BOURGAUUT-VULLADA, Isabelle APPLICANT: POUVELLE-MORATILLE, Sandra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: artificial sequence FEATURE:
OTHER INFORMATION: Description of the artificial sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 2
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                  73 ISEYRHYCYSVYGTTLEQQYNKPLCDLLI 101
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100.0%; Pred. No.
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      19.2%;
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Pred. No. 1e-09;
1; Mismatches
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FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR EILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 8
LENGTH: 29
LENGTH: 29
LENGTH: 29
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PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 29
TYPE: PRT
ORGANISM: artificial sequence
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDI
APPLICANT: MAILLERE, Bernard
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: BOUNGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
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                                                                                                       Sequence 5, Application US/11021949
Publication No. US20050142541A1
                                                                                       GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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APPLICANT: LU, PETER
APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment OTHER INFORMATION: for E6 of HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                  84 YGTTLEQQYNKPLCDLLIRCINXQKPLCP 112
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96.6%; Pred. No. 1e-09;
tive 1; Mismatches
    CHAMORRO SOMOZA
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APPLICANT: SCHWEIZER, JOHANNES
; TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
; TITLE OF INVENTION: AND METHODS OF THEIR USE
; FILE REFERENCE: VITA-012
; CURRENT APPLICATION NUMBER: US/11/021,949
; CURRENT FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR APPLICATION NUMBER: 60/532,373
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 361
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 24
                                                                                                                            RESULT 87
US-11-021-949-1
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US-11-021-949-5
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Best Local Similarity
Matches 37; Conserv
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Publication No. US20050100554A1
GENERAL INFORMATION:
APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
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Matches
                                                              GENERAL
                                                                                  Sequence 1, Application US/11021949 Publication No. US20050142541A1
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 23
GENERAL INFORMATION:
APPLICANT: LU, PETER
APPLICANT: GARMAN, JO
APPLICANT: BELMARES,
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PRIOR FILING DATE: 2002-02-14
NUMBER OF THE PRIOR FILING PATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Complexes and Methods of FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
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                                                                                                                                                                                                                 126 NRLKAKC-SLCR 136
                                                                                                                                                                                                                                                         130 GRWTGRCMSCCR 141
                                                                                                                                                                                                                                                                                                                                                                                                                           10 RKLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKF 69
                                                                                                                                                                                                                                                                                                   66 VSILEFVLYYQESYEVPEIEEILDRPLLQIELRCVTCIKKLSVAEKLEVVSNGERVHRVR 125
                                                                                                                                                                                                                                                                                                                                           70 YSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIR 129
                                                                                                                                                                                                                                                                                                                                                                                        6 RTVRQLSESLCIPYIDVLLPCNFCNYFLSNAEKLLFDHFDLHLVWRDNLVFGCCQGCART 65
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24; Conserv
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  BELMARES, MICHAEL P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.4%; Score 136.5; DB 5; ilarity 28.0%; Pred. No. 1.7e-06; Conservative 21; Mismatches 73;
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                      JONATHAN DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17.6%;
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Pred. No. 2.1e-08;
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APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerard
ITILE OF INVENTION: Mixture of peptides derived from E6 and/or E7
ITILE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: DCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
SPRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-03
PRIOR FILING DATE: 2001-05-04
NUMBER: OF SEQ ID NOS: 63
SOFTWARE: PatentIN Ver: 2.1
SEQ ID NO 40
LENGTH: 23
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US-10-476-570-40
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Sequence 44, Application US/10476570
Publication No. US20040170644A1
GENERAL INFORMATION:
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET
APPLICANT: MAILLERE, Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 40, Applica Publication No. US20 GENERAL INFORMATION:
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LENGTH: 25
TYPE: PRT
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Best Local S
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Best Local Similarity
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APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
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CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTSEQ for Windows Version 4.0
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APPLICANT: SCHWEIZER, JOHANNE;
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: human papilloma virus (HPV
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                                                                                                                                                                                                                                                                                                    Local 5.
                                                                                                                                                                                                                                                                    111 CPEEKORHLDKKORFHNIRGRWT 133
                                                                                                                                                                                                                       1 CPEEKQRHLDKKQRFHNIRGRWT 23
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                                                                                                                                                                                                                                                                                                                Similarity 100.
23; Conservative
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No. US20040170644A1
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                                                                                                                                                                                                                                                                                                         16.3%; Scc.
100.0%; Pr
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100.0%;
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                                                                                                                                                                                                                                                                                                                                     Score 135;
Pred. No.
                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                                                                                                                                                                                                                                                                                3e-07;
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                       B
                     LA RECHERCHE MEDICALE
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; Sequence 56, Application US/10476570; Publication No. US20040170644A1; GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 65
LENGTH: 24
TYPE: PRT
GRGANLSM: Human Papilloma virus
US-10-751-845-65
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                                                                                                            US-10-476-570-56
                                                                                                                                   RESULT 91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-751-845-65
                                                                                                                                                                                                                                                                                          Query Match 15.9%; Score 132; DB 5; Best Local Similarity 100.0%; Pred. No. 6.7e-07; Matches 24; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 65, Appropriate Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: POUVELLE WORATILLE, Sandra
APPLICANT: GUILLET, Jean-Gerack
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE APPLICANT: INSTITUT NATIONAL DE LA SANTE ET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/154,665 PRIOR FILING DATE: 1999-09-16
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NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: FR 01 05980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: artificial sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 IRGRWTGRCMSCCRSSRTRRETQL 151
                                                                                                                                                                                                                                  37 LLRREVYDFAFRDLCIVYRDGNPY 60
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No. US20050100928A1
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3.2e-07
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  RECHERCHE MEDICALE
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APPLICANT: COOPEIN, JEANNINE
APPLICANT: BOURGAULT VILLADA, ISABELLE
APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
CURRENT APPLICATION NUMBER: US/10/858,384
CURRENT APPLICATION NUMBER: US/20/4-06-02
PRIOR APPLICATION NUMBER: P3997012
PRIOR APPLICATION NUMBER: P3997012
PRIOR FILING DATE: 1999-06-03
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 10
LENGTH: 22
TYPE: PRT
DROANISM: Artificial Sequence
FEATURE
FEATURE:
COURSE THEORY AND THE PARTICULAR OF THE PARTICULAR OF SECTION OF THE PARTICULAR OF THE PARTIC
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APPLICANT: GUILLET, Jean-Gerard
APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: FR 01
PRIOR FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: FR 01
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
STOPE: PRT
ORGANISM: artificial sequence
FRATURE:
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Best Local Similarity
Wardhes 22; Conserva
; Sequence 152, Application US/10751845
                                    RESULT 93
US-10-751-845-152
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; OTHER INFORMATION: for E6 of HPV
US-10-858-384-10
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                111 CPEEKQRHLDKKQRFHNIRGRW 132
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                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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BOURGAULT-VILLADA, Isabelle
                                                                                                                                                                                                                                                                                                                                                 15.7%; Score 130; DB 5; ilarity 100.0%; Pred. No. 1e-06; Conservative 0; Mismatches
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APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR FILING DATE: 2000-08-18
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR PILING DATE: 1999-09-16
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US-10-751-845-66
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                                                                                                                                                                           ; ORGANISM: Human Papilloma virus US-10-751-845-66
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                                                                              Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 163
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 66
LENGTH: 23
TYPE: PRT
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 152
LENGTH: 42
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Publication No. US20050100928A1
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Best Local Similarity
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APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
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                    72 KISEYRHYCYSVYGTTLEQQYNK 94
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KISEYRHYCYSLYGTTLEQQYNK 23
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                                                                                       Conservative
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95.7%;
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                                                                                     1; Mismatches
                                                                                                        Score 126; DB 5;
Pred. No. 2.9e-06;
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Pred. No. 2.1e-06;
6; Mismatches 11
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US-10-858-384-6
US-10-858-384-6
; Sequence 6, Application US/10858384
; Publication No. US20050033025A1
; GENERAL INFORMATION:

APPLICANT: CHOPPIN, JEANNINE

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FILE REFERENCE: 0508-1037-1

CURRENT APPLICATION NUMBER: US/10/858,384

CURRENT FILING DATE: 2004-06-02

PRIOR APPLICATION NUMBER: FR 9907012

PRIOR FILING DATE: 1999-06-03

NUMBER OF SEQ ID NOS: 24

SOPTWARE: Patentin Ver. 3.2

SEQ ID NO 6

LENGTH: 22
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                                                                                            RESULT 97
US-10-476-570-27
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                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: human papilloma virus (HPV) US-11-021-949-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: LU, PETER
APPLICANT: GARMAN,
APPLICANT: BELMARES
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 361
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 23
TYPE: PRT
                                     Sequence 27, Application US/10476570 Publication No. US20040170644A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 22; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local (
APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/532,373
PRIOR FILING DATE: 2003-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/11/021,949
CURRENT FILING DATE: 2004-12-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: GARMAN, JONATHAN DAVID
APPLICANT: BELMARES, MICHAEL P.
APPLICANT: DIAZ-SARMIENTO, CHAMORRO SOMOZA
APPLICANT: SCHWEIZER, JOHANNES
TITLE OF INVENTION: ANTIBODIES FOR ONCOGENIC STRAINS OF HPV
TITLE OF INVENTION: AND METHODS OF THEIR USE
FILE REFERENCE: VITA-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FERRIES, ESTELLE.
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN TITLE OF INVENTION: OR E7 OF HPV, THEIR PRODUCTION AND THEIR USE TITLE OF INVENTION: PARTICULARLY IN VACCINATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-021-949-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of the Artificial Sequence: Peptide fragment OTHER INFORMATION: for E6 of HPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39 RREVYDFAFRDLCIVYRDGNPY 60
                                                                                                                                                                                                      99 LLIRCINXQKPLCPEEKQRHLDK 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                               1 LLIRCINCOKPLCPEEKORHLDK 23
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CONNAN, FRANCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BOURGAULT VILLADA,
                                                                                                                                                                                                                                                         Conservative
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95.7%;
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                                                                                                                                                                                                                                                                            Score 119; DB 6;
Pred. No. 1.6e-05;
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  LA RECHERCHE MEDICALE
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APPLICANT: GUILLET, Jean-Gerard
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: papillomavirus proteins and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT FILING DATE: 2003-11-04
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR FILING DATE: 2002-05-03
PRIOR FILING DATE: 2002-05-04
PRIOR FILING DATE: 2001-05-04
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 27
LENGTH: 23
TYPE: PRT
ORGANISM: artificial sequence
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US-10-476-570-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/938,249
CURRENT FILING DATE: 2004-09-10
PRIOR APPLICATION NUMBER: US/09/724,553
PRIOR FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 60/134,114
PRIOR FILING DATE: 1999-05-14
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR APPLICATION NUMBER: US 60/134,117
PRIOR APPLICATION NUMBER: US 60/134,118
                                                                Remaining Prior Application data removed - NUMBER OF SEQ ID NOS: 543
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 513, A Publication No.
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Best Local :
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APPLICANT:
APPLICANT:
                                                                                                                                                         PRIOR APPLICATION NUMBER: US 60/196,267 PRIOR FILING DATE: 2000-04-11
                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/176,195
PRIOR FILING DATE: 2000-01-14
PRIOR APPLICATION NUMBER: US 60/182,296
PRIOR FILING DATE: 2000-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Arbor Vita Corporation
TITLE OF INVENTION: Molecular Interactions in Hematopoietic
TITLE OF INVENTION: Cells
FILE REFERENCE: 020054-001130US
                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/170,453
                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/160,860
PRIOR FILING DATE: 1999-10-21
PRIOR APPLICATION NUMBER: US 60/162,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Schweizer, Johannes
                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-10-29
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1999-05-14
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Pred. No. 3.9e-05;
0; Mismatches (
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Sequence 4, Application US/10612818

Publication No. US20040110925A1

GENERAL INFORMATION:

APPLICANT: Impact Diagnostics

APPLICANT: Impact Diagnostics

ITITLE OF INVENTION: Peptides from the E2, E6 and E7 Proteins of Human Papillomaviruse

ITITLE OF INVENTION: 18 for Detecting and/or Diagnosing Cervical and Other Human Papi

ITITLE OF INVENTION: Associated Cancers

FILE REFERENCE: 3352-22

CURRENT FILING DATE: 2003-07-01

PRIOR APPLICATION NUMBER: US/10/612,818

CURRENT FILING DATE: 2003-07-02

PRIOR RILING DATE: 2003-07-02

PRIOR FILING DATE: 2003-07-02

PRIOR FILING DATE: 2003-07-02

PRIOR FILING DATE: 2001-04-05

NUMBER: OF SEQ ID NOS: 8

SOPTWARE: Patentin version 3.1

SEQ ID NO 4
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APPLICANT: COMMISSARIAT A L'ENERGIE ATOMIQUE
APPLICANT: INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
APPLICANT: MAILLERE, Bernard
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: BOURGAULT-VILLADA, Isabelle
APPLICANT: GUILLET, Jean-Gerard
APPLICANT: POUVELLE-MORATILLE, Sandra
APPLICANT: OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides derived from E6 and/or E7
TITLE OF INVENTION: Mixture of peptides and uses thereof
FILE REFERENCE: 45636-5071-US
CURRENT APPLICATION NUMBER: US/10/476,570
CURRENT APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: PCT/FR02/01533
PRIOR APPLICATION NUMBER: FR 01 05980
PRIOR FILING DATE: 2002-05-04
NUMBER OF SEO ID NOSE 63
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 41
LENGTH: 20
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
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Best Local S
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of the artificial sequence: peptide E6 121-140 \cdot 10-476-570-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match 13.9%; Score 115; DB 5; ]
Local Similarity 100.0%; Pred. No. 3.7e-05;
hes 20; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 20; Conserv
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Maximum Match 100%
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Perfect score:
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    Pred. No. is the nu
score greater than
and is derived by a
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Match
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1: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

3: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

5: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

6: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7: /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

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Sequence 6, Application US/10933854
Publication No. US20060105347A1
GENERAL INFORMATION:
APPLICANT: GTC Biotherapeutics, Inc.
APPLICANT: GTC Biotherapeutics, Inc.
APPLICANT: COx, Geoffrey F.
APPLICANT: NUMBER: US/10/933,854
CURRENT EILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/500,910
PRIOR FILING DATE: 2003-09-05
PRIOR FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 35
NUMBER OF SEQ ID NOS: 35
SEC IN NO. 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Human Alpha Fetoprotein
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/Accession No.
DATABASE ENTRY DATE: 1995-03-30
RELEVANT RESIDUES: (19)..(609)
US-10-933-854-4
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US-10-933-854-6
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; LENGTH: 591
; TYPE: PRT
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                     SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Cox, Geoffrey F.
TITLE OF INVENTION: Method for the Production of
TITLE OF INVENTION: Method for the Production of
TITLE OF INVENTION: MILK
ETLE OF INVENTION: MILK
ETLE OF SECULATION NUMBER: US/10/933,854
CURRENT FILING DATE: 2004-09-03
PRIOR APPLICATION NUMBER: 60/500,910
PRIOR FILING DATE: 2003-09-05
NUMBER OF SECULATIONS: 35
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Similarity 23.4%; Pred. No. 1.6;
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; DATABASE ACCESSION NUMBER: Genbank/Accession I; DATABASE ENTRY DATE: 1995-03-30; RELEVANT RESIDUES: (1)..(609)
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APPLICANT: Cox, Geoffrey F.
APPLICANT: Cox, Geoffrey F.
APPLICANT: Cox, Geoffrey F.
TITLE OF INVENTION: Method for the Production of Fusion Proteins in Transgenic Mammal
TITLE OF INVENTION: Milk
TILE REFERENCE: GTC-220 PCT
CURRENT APPLICATION NUMBER: US/10/933,854
CURRENT APPLICATION NUMBER: 60/500,910
PRIOR APPLICATION NUMBER: 60/500,910
PRIOR APPLICATION NUMBER: 60/500,910
PRIOR FILING DATE: 2003-09-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin version 3.2
SEQ ID NO 2
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Publication No. US20060105347A1
GENERAL INFORMATION:
APPLICANT: GTC Biotherapeutics, Inc
APPLICANT: Meade, Harry
APPLICANT: Cox, Geoffrey F.
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Best Local Similarity
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OTHER INFORMATION: Human Alpha Fetoprotein
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/Accession |
DATABASE ENTRY DATE: 1995-03-30
RELEVANT RESIDUES: (19)..(609)
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TYPE: PRT
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Pred. No. 1.6;
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RESULT 5
US-10-953-349-33870
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                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Zea mays subsp. mays
US-10-953-349-33870
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SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 33870
LENGTH: 809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 33870, Application US/10953349
Publication No. US20066107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 33871, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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Best Local (
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                                                                                                                                                                                                                                                                             Query Match 8.7%; Score 72.5;
Best Local Similarity 23.3%; Pred. No. 3.
Matches 34; Conservative 22; Mismatche
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TITLE OF INVENTION: SECOUNCE-DETERMINED DY
TITLE OF INVENTION: ENCOUNCE THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        517 ---NPVGGNEKCADVTIHIFFSKILKLAAIRIRNLCERVQCVEQTERVYNVFKQILEQQT 573
                                                                                                                                                                                   469 DDNADPRSPKRSCNESRNTVVERNLQTPPPKQSHMVSTSLKAKCHPLQSTFASPTVC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              574 TLFFNRHIDQLILCCLYGVAKVCQLE 599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  460 DDNADPRSPKRSCNESRNTVVERNLQTPPPKQSHMVSTSLKAKCHPLQSTFASPTVC---
                                                                                                                                     55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLEQQ-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   55 RDGNPYAVXDKCLK-----FYSKISE-----YRHYC-----YSVYGTTLEQQ-
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                                                                                                                                                                                                                             4 DPQERPRKLPQLCTELQTTIHDIILECVYCKQQ-----LLRREVY----DFAFRDLCIVY
TLFFNRHIDQLILCCLYGVAKVCQLE 608
                                                                                         ---NPVGGNEKCADVTIHIFFSKILKLAAIRIRNLCERVQCVEQTERVYNVFKQILEQQT 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---YNKPLCDLLIRCINXQKPLCPEE 114
                                           ---YNKPLCDLLIRCINXQKPLCPEE 114
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23.3%; Pred. No. 3.6;
ative 22; Mismatches 49; Indels 4
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                                                                                                                                                                                                                                                                                                                         DB 6;
                                                                                                                                                                                                                                                                             49; Indels
                                                                                                                                                                                                                                                                                                                         Length 809;
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NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2762
LENGTH: 531
Type:
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; ORGANISM: Zea mays subsp. mays
US-10-953-349-33869
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US-10-953-349-33869
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Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILLE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 33869
LENGTH: 867
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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Publication No. US20060105376A1
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
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271 DRNKETR 277
                                     144 RTRRETQ 150
                                                                                                                                                      175 LGCFKCKSCGKLLNAE------YISKDGLPYCEADYHAKFGIRCDSCEKY---ITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    641 TLFFNRHIDQLILCCLYGVAKVCQLE 666
                                                                                                               86 TTLE--QQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSS 143
                                                                                                                                                                                             28 LECVYCKO--QLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34; Conservative
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                                                                            RVLEAGEKHYHPSCALCVGC---
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23.3%; Pred. No. 3.9;
ative 22; Mismatches
                                                                                                                                                                                                                                  8.6%; Score 71; DB 22.0%; Pred. No. 3.3; ative 16; Mismatches
                                                                            -GQMFAEGEEMYLQGSSIWHPACRQAARTE
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US-10-953-349-6306
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US-10-953-349-17182
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO 6306
LENGTH: 419
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SOFTWARE: PatentIn version 3.3
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CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2
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CURRENT FILING DATE: 2004-09-30
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301
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                                                                              254 VCI----GNPGSLTDDQILEKSSLSRQRAARGMLRDSWIVGNSGFPLTDYL-
                                                                                                                 50 LCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94
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                                                                                                                                                                                                                                    37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLL--------RRE--
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Similarity 22.2%;
39; Conservative 2
                                                                                                                                                                                                                                                         Similarity
LVPYTRQNLTWTQHAFNESIGEIQGIATAAFERLKGRW-----ACLQKRTEVKLQ
                                     LCPEEKO----RHLDKKQ---
                                                                                                                                                          ESVHKI PNVVGSI YTTHI PI I APKVHVAAY FNKRH TERNQKTSYSI TVQGVVNADGI FTD
                                                                                                                                                                                             ERPRKLPQLCTELQTTIHDIILECVYCKQQLLRREV---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FNLIYDIGAHKDLITSYRDNNNHNI----LHLAGKLAPSEQLHV---VSGAALQMQRELL 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---VYDF-AFRDLCIVYRDGNPYAVXDKCLKFYSKI--SEYRHYCYSVYGTTLEQQYN--
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                         21.0%;
                                                                                                                                                                                                                                                       7.7%; Score 63.5;
21.0%; Pred. No. 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Score 65; DB 6; Length 369; Pred. No. 9.5; 24; Mismatches 59; Indels
                                                                                                                                                                                                                                    19; Mismatches
                                     ---RFHNIRGRWTGRCMSCCRSSRTRRETQ
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                                                                                                                                                                                                                                                                           DB 6;
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                                                                                                                                                                                                                                    69;
                                                                                                                                                                                                                                                                       Length 419;
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Sequence 6305, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579FUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40752
SOFTWARE: Patentin version 3.3
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                                                                                                                                                                                                                                                                                                                 ; LENGTH: 540
TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-6304
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6304
                                                                                                                                                                                                                                        Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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Best Local
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TYPE: PRT
422
                                                                                                                                                         315 ESVHKIPNVVGSIYTTHIPIIAPKVHVAAYFNKRHTERNQKTSYSITVQGVVNADGIFTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        397 LVPYTRQNLTWTQHAFNESIGEIQGIATAAFERLKGRW-----ACLQKRTEVKLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 VCI----GNPGSLTDDQILEKSSLSRQRAARGMLRDSWIVGNSGFPLTDYL--
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                                 110 LCPEEKQ-----RHLDKKQ------RFHNIRGRWTGRCMSCCRSSRTRRETQ 150
                                                                                                                  50 LCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKP 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        50 LCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKP 109
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LVPYTRONLTWTQHAFNESIGEIQGIATAAFERLKGRW-----
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                                                                          -GNPGSLTDDQILEKSSLSRQRAARGMLRDSWIVGNSGFPLTDYL
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21.0%;
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                                                                                                                                                                                                                                        19; Mismatches
                                                                                                                                                                                                                                                       Score 63.5;
Pred. No. 20;
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RESULT 14
US-10-953-349-32519
¡ Sequence 32519, Application US/10953349
¡ Publication No. US20060107345A1
¡ GENERAL INFORMATION:
¡ APPLICANT: ALEXANDROV, Nickolai et al.
¡ TITLE OF INVENTION: ENQUENCE-DETERMINED DNA
¡ TITLE OF INVENTION: ENCONDED THERBY
¡ FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: Patentin version 3.3 SEQ ID NO 32520 LENGTH: 276
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US-10-953-349-32520
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Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 32521
LENGTH: 247
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                                                                                                                                                                                                                                                                                            91 ---- QYNKPLCDLL 100
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Similarity 25.7%;
19; Conservative 1
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US/10/953,349
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1; Mismatches
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                                                               FRAGMENTS
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                                                               AND CORRESPONDING POLYPEPTIDES
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; TYPE: PRT ; ORGANISM: Triticum aestivum US-10-953-349-32519
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US-11-293-697-4876
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                                                                                                                                                                       Sequence 8, Application US/11106014 Publication No. US20060088846A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 4876
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publication No. US20066105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version
SEQ ID NO 32519
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              APPLICANT: Pagano, Michele
APPLICANT: Chiaur, Dah Sharim
APPLICANT: Latres, Esther
APPLICANT: Srivastava, Promod
APPLICANT: Srivastava, Promod
APPLICANT: Chandawarker, Rajiv
TITLE OF INVENTION: METHODS OIDENTIFY COMPOUNDS USEFUL FOR THE TREATMENT
TITLE OF INVENTION: OF PROLIFERATIVE AND DIFFERENTIATIVE DISORDERS
FILE REFERENCE: 5914-106-999
CURRENT APPLICATION NUMBER: US/11/106,014
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mes 33; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               59 AQNVQLYGTPKPCQY----CNIIAAFIGNKCQRCTNSEKKYGPPYSCEQCKQQCAFDRKD 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 CVYCKQQLLRREVYDFAF-----RDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYC---
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25.7%;
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Pred. No. 13;
18; Mismatches
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7;
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CURRENT FILING DATE:

2005-04-13

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RESULT 17
US-10-196-749-474
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-106-014-8
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                                                                                                                                                              PRIOR APPLICATION NUMBER: 10/052586
PRIOR FILING DATE: 2002-01-15
PRIOR APPLICATION NUMBER: 60/059263
PRIOR FILING DATE: 1997-09-18
PRIOR APPLICATION NUMBER: 60/059266
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR PPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/063120
PRIOR APPLICATION NUMBER: 60/063120
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT: Zhang, Zeni.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3430R1C340
                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/196,749
CURRENT FILING DATE: 2002-07-16
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PRIOR TILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: 09/385,219
PRIOR FILING DATE: 1999-08-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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OR FILING DATE: 1999-02-03
OR APPLICATION NUMBER: 60/098,355
OR FILING DATE: 1998-08-28
OR APPLICATION NUMBER: 60/124,449
OR FILING DATE: 1997-03-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                            APPLICATION NUMBER: 60/063486 FILING DATE: 1997-10-21
                                                                                                      APPLICATION NUMBER: 60/063121 FILING DATE: 1997-10-24
FILING DATE:
APPLICATION N
                                                                                                                                                 FILING DATE:
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                                          APPLICATION NUMBER: 60/063540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 FGPRLEQ-----LNTSLVLSLLSSEELCPTAGLPQRQID 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                122 QILKKPISEVSDGAFFDYMAVYLMCCPYTRRASKSSRPMYGAVTSFLHSLIIPNEPRFAL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84 YGTTLEQQYNKPLCDLLIRCINXQKPLCPEE--KQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36 QLLRR---EVYDFAFRDLCIVYRDGNPYA--VXDKCLKFYSKISEYRHYC-----YSV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Smith, Victoria Watanabe, Colin K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Godowski, Paul J. Gurney, Austin L.
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Goddard, Audrey
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  NUMBER: 60/063541
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                    1997-10-28
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; Pred. No. 22;
14; Mismatches
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APPLICANT: ALEXANDROV, NICKOlai et al.
APPLICANT: ALEXANDROV, NICKOLai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 18091
LENGTH: 176
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-18091
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-225
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Best Local Similarity
Matches 17; Conserv
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PRIOR FILING DATE: 1997-10-28
Prior Application data removed - Se
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 474
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SEQ ID NO 225
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  Best Local Similarity
                       Query Match
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CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ludwig Institute for Cancer Research et al. TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 41
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   713 TIKOTHSQELCKLMNLWTERFCALEEKCENIOKPLSSVQENIQQKSKDIVNKWTFHS 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            174 ICSALATVILLALLILCVIYCKROFMEKKP-SWSLRSQDIQY-NGSELSCFDR-----PQL 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 HEYAH 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         87 TLEQQYNKPLCDLL------IRCINXQKPLCP----EEKQRHLDKKQRFHN 127
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7.4%;
21.6%;
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Pred. No. 22;
  Score 61.5; D
Pred. No. 9.9;
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                                                                                                                                                                                                                                                                                    DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
                     DB
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US-10-953-349-18090
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US-10-953-349-18090
                                                                   ; ORGANISM: Glycine max US-10-953-349-18089
                                                                                                                                                                                                                                                                                                                                                          RESULT 21
                                                                                                             Sequence 18089, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN Version 3.3
SEQ ID NO 18089
LENGTH: 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18090, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Query Match 7.4%;
Best Local Similarity 21.6%;
Matches 27; Conservative 1
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CURRENT FILING DATE: 2004-09-30
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TYPE: PRT
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SOFTWARE: PatentIn version 3.3
                                                                                                      TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                            132 WTGRC 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                134 WVKKC 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 YGTTLEQQY -- NKPLCDLLIRCINXQKPLCPEEKQRHLDKKQ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75 VRTVLHQLYEMNPPKYTWFYNFVASNKPADGKRFIRSLGKEQQELAERVMVTRLH-LYGK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 YGTTLEQQY--NKPLCDLLIRCINXQKPLCPEEKQRHLDKKQ------RFHNIRGR 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 CKQQLLRREV-----YDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSV 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27;
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; Score 61.5; ; pred. No. 13; 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 61.5;
Pred. No. 12;
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                               DB 6;
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   44;
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                                 Length 220;
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   Indels
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 19918
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US-11-293-697-4346
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US-10-953-349-19918
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                                                                                                                                                                    ; ORGANISM: Glycine max US-10-953-349-19918
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4346
TEXTORIOR 1346
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Publication No. US20060107345A1
GENERAL INFORMATION:
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
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CURRENT FILING DATE: 2005-12-05
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                                                                                                                                                                                                              LENGTH: 2
                                                                                 Local Similarity
nes 29; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 XQKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRS 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             496 DLLIHKSIHTGEQPYKC-DECEKVFSRKSSLETH---KIGHTGEKPYKCKVCDKAFAC-- 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
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                                         18
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Similarity 24.7%; Pred. No. 44;
24; Conservative 13; Mismatches
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                                         BLQTTIHDIILE----
                                                                                   Conservative
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                                                                                 7.3%; Score 61; DB
20.9%; Pred. No. 17;
rative 23; Mismatches
                                         --CVYCKQQLLR---REVYDFAFRDLCIVYRDGNPYA
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                                                                                                                          Length 259;
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                                                                                   Gaps
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US-10-933-349-28497
US-10-933-349-28497
Sequence 28497, Application US/10953349
Sequence 21497, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ESQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILL REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 28497
LENGTH: 267
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US-10-953-349-19917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 19917
LENGTH: 355
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Publication No. US20060107345A1
GENERAL INFORMATION:
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                                                                                                                                                               TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                 Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167 ----CLEVSSKPQEAIAYCQK--ATSVCKARLHRLTDEVKSCSDLTSASELAQDLPACPK 220
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   40
                                     11 KLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFAF------RDLCIVYRDG 57
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   KFPSLPPVFQQTPNAV-----EELKLAREIYEQAVILSVKMEDQDAFERDFCQL----
                                                                               Conservative
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                                                                                             7.3%;
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20.9%; Pred. No. 24;
tive 23; Mismatches
                                                                               20;
                                                                           Score 60.5; D
Pred. No. 20;
20; Mismatches
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NUMBER OF SEQ ID NOS: 767
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 365
; LENGTH: 314
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-538-066-365
                                                                                                                                                                       FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3919
LENGTH: 706
TYPE: PRT
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US-11-293-697-3919
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US-11-293-697-3919
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                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3919, Application US/11293697 Publication No. US20060105376A1 GENERAL INFORMATION:
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APPLICANT: Epimmune Inc.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: HLA-A1, -A2, -A3, -A24, -B7
TITLE OF INVENTION: Peptides and Compositions
FILE REFERENCE: 2060.015PC06
CURRENT APPLICATION NUMBER: US/10/538,066
CURRENT FILING DATE: 2005-06-09
                                                                          Query Match
Best Local (
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Best Local (
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                                                          Matches
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                                                        Local Similarity
nes 43; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32;
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                5 POERPRK-----
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o. US20060094649A1
                                                          Conservative
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                                              7.3%; but
20.7%; Pred
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                                                        Score 60.5; DE Pred. No. 56; 22; Mismatches
---LPQ-LCTELQTTIHDIILECVYCK-----QQLLRREV-
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Pred. No. 23;
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                                                                                            DB 7;
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                                                                                          Length 706;
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                                                        Indels
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                                                          ; 68
                                                          Gaps
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                      42
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                                         US-10-505-928-175
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                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens
US-10-505-928-397
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                                                                                                                                                                                                                                                                Sequence 175, Application US/10505928

Publication No. US20060088532A1

GENERAL INFORMATION:

APPLICANT: Ludwig Institute for Cancer Research

TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 397, Applic Publication No. US20 GENERAL INFORMATION:
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SOPTWARE: PatentIn 3.2
SEQ ID NO 397
LENGTH: 971
  Query Match
                                                                                                                       SEQ ID NO 175
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                                                                                                                                 PKIUK FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
                                                                                                                                                                            CURRENT FILING DATE: 2004-08-27 PRIOR APPLICATION NUMBER: US 60/363,019 PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/505,928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ludwig Institute for Cancer Research TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
                                                                                                                                                                                                                                                            FILE REFERENCE: 28967/39178
                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
                                                                                                LENGTH: 1085
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           212 DSLYCCDRAEDH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152 CSYAGHHTNCREYCQAIFRTDSSPGPSQIKAVENYCASISPQLIHCVNNYTQSYPMRNPT 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      545 SRRAHLAEHQRAHT -- GNYKFRCAGCAK 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                487 DKLKRHMLIHEPFKKYKCPFSTHTGCSKEFNRP--DKLKAHILSHSGMKLHKCALCSKSF 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 THGSGGRFKCQV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            381 PQHSPKKDNAVYKCVKCVNKYSTPEALEHHLQTATHN--FPCPHCQKVFPCERYLRRHLP 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     104 CCELA----IALECRQACKQASSKNDISKVCRKEYENALFS--CISRNE-----MGSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67 LKFYSKISEYRHYCYSVYGTTLE------QQYNKPLCDLLIRCIN------X 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 CTELQTTIHDIILEC-VYCKQ-----QLLRREVYDFAFRDLCIVYRDGNPYAVXDKC 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OKPLCPEEKQRHLDKKQRFHNIRGRWTGRCMSCCRSSRTRRETQL 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -YDFAFRDLCIVYRDGNPYAVXDKCLKF----YSKISEYRH------YCYSVYG-- 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/10505928
o. US20060088532A1
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Pred. No. 79;
22; Mismatches
  Score 60.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CKKFFRREHYLKLHAHIHSGEKPYKCSVCESAFNRK 486
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  BG
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Length 1085;
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 13389
LENGTH: 233
                                                                                                                                                                                                                                                                                                                                                                          RESULT 31
US-10-953-349-13389
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                                                                                                  ; ORGANISM: Glycine max US-10-953-349-13389
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US-11-293-697-3034
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                          Query Match
Best Local Similarity
Matches 37; Conserv
                                                                                                                                                                                                                                                                                                                      Sequence 13389, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 3034, Application US/11293697 Publication No. US20060105376A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3034
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA FILE REFERENCE: H1-A0106
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                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 EEK---QRHLDKKQRFHNI 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     474 LPQLCTAMEQYKGD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   72
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KLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFA----FRDL-----CIVY 54
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                                   21; Mismatches
                                                   Score 59; DB
Pred. No. 24;
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4; Mismatches
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                                                                                                                                                                                                                                                                                          DNA FRAGMENTS
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                                   53;
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                                                                 Length 233;
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                                   Indels
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                                   44;
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                                   Gaps
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1032
LENGTH: 258
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-1032
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                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-1031
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US-10-953-349-1032
                                                                                                                                                                                                                                 FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VETSION 3.3
SEQ ID NO 1031
LENGTH: 369
                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1032, Application US/10953349 Publication No. US20060107345A1
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Best Local Similarity
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                                                                                                                      Matches
                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DN
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                     Local
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                                                    163 MAPDPPE-PQDLPEIC-----RDVMME--YSKQVMILGE---FLF-ELLSEALGLNPN
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61 AVXD-KCLKFYSKISEYRHYCYS---VYGTT 87 : | : | | : | : | : | : | : |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86
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                                                                                                                    l Similarity
27; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HLKDMECLKGLRMLCHYFPPCPEPDLTFGTS 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGRLESSPYSELLSPIHWEMTTEELARQFC----TLLGQSYENPLSVAVAAGVEGLPIL 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R---DGNPYAVXDKCLKFYSKISEY-RHYCYSVYGTTLEQQYNKPL---
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                                                                                  WEGDEGERERKLEGICTELGTTIHDIILECVYCKQQLLRREVYDEAFRDLCIVYRDGNEY 60
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29.7%;
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                                                                                                                    Score 59; DB of Pred. No. 40; No. 40; Pred. Mismatches
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                                                                                                                                                     DB 6;
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                                                                                                                                                    Length 369
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 RESULT 36
US-10-953-349-13387
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; ORGANISM: Arabidopsis thaliana US-10-953-349-1030
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                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Glycine US-10-953-349-13388
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn version 3.3
SEQ ID NO 1030
LENGTH: 376
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1030, Application US/10953349 Publication No. US20060107345A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13388, Application US/10953349
Publication No. US20060107345A1
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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les 27; Conservative
                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   170 MAPDPPE-PQDLPEIC-----RDVMME--YSKQVMILGE---FLF-ELLSEALGLNPN 215
                                                                                              236 AGRLESSPYSELLSPIHWEMTTEELARQFC----TLLGQSYENPLSVAVAAGVEGLPIL
                                                                                                                                                                                          178 KLVQIGSNLELKIH--TLQFVEVLQNGTRADALKYARTYLAPFASLNKGEFPKLMGCLLY 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       216 HLKDMECLKGLRMLCHÝFPPCPEPDLTFGTS 246
                                                                                                                                           55 R---DGNPYAVXDKCLKFYSKISEY-RHYCYSVYGTTLEQQYNKPL-----CDLL 100
                                                                                                                                                                                                                                       11 KLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFA-----FRDL------CIVY 54
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                                               IRCIN---XQKPLCPEEKQR----HLDKKQRFHNI 128
LKLANVMAAKKQEWQEMKQLPVPVELGKEFQFHSI 325
                                                                                                                                                                                                                                                                                       Conservative
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23.9%;
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Pred. No.
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Pred. No. 41;
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42;
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                             Sequence 25007, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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SEQ ID NO 25008
LENGTH: 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
-10-953-349-25008
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
PILE REFERENCE: 2750-1579PUS2
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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CURRENT FILING DATE: 2004-09-30
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ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                    CT-LKDTVKPVLIPCYDLVTRAAFVFSRADALEVDGYDFKMRDVC 214
                                                                                                                                                                                                                                                                                                                             CTELQTTIHDIILEC-----VYCKQQLLRREVYDFAFRDLC 51
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ilarity 28.9%;
Conservative
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                                                                                      CORRESPONDING POLYPEPTIDES
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US-10-953-349-25006
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US-10-953-349-37463
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Best Local Similarity 28.2
                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: Patentin version 3.3
SEQ ID NO 37463
LENGTH: 204
TYPE: PRT
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 25006
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANTI ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DI
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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Publication No. US20060107345A1
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SOFTWARE: PatentIn version
SEQ ID NO 25007
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                                                                      Matches
                                                                                   Query Match
Best Local Similarity
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nes 13; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            176 CT-LKDTVKPVLIPCYDLVTRAAFVFSRADALEVDGYDFKMRDVC 219
                                 121 KKORFHNIRGRWTGR--
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94 QRORGHH-RARGTSRRGWRRCSFASPRCSCSCLSCCRRCRRRR 135
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28.9%;
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                                                                                   7.0%;
                                                                 ; Score 58.5; D; Pred. No. 24; 4; Mismatches
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Pred. No. 48;
9; Mismatches
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                                 -CMSCCRSSRTRR 147
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                                                                                                      Length 204;
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                                                                      Indels
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; ORGANISM: Zea mays subsp. mays
US-10-953-349-38139
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US-10-953-349-38140
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                                                     Sequence 22153, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22153
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 38140
LENGTH: 251
TYPE: PRT
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Publication No. US200660107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: ALEXANDROY, Nickolai et al.
APPLICANT: ALEXANDROY, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 38139
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Best Local Similarity
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ORGANISM: Glycine max
                                          ENGTH: 421
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                                                                                                                                                                                                                                                                                                                                                                                                         170 QRORGHH-RARGTSRRGWRRCSFASPRCSCSCLSCCRRCRRRR 211
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Pred. No. 33;
4; Mismatches
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22151
LENGTH: 492
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APPLICANT: ALEXANDROV, Nickolai et al.

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FR.

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 22152
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-22152
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                                                                                                                                          ; ORGANISM: Glycine max US-10-953-349-22151
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US-10-953-349-22151
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Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                    Query Match
Best Local :
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Best Local :
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Best Local Similarity
                                                                                                                                                                                TYPE: PRT
                                                                     Local Similarity
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                               45 FAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYC-YSVYGTTLEQQYNKPLCDLLIRC 103
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                                                                                    7.0%;
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22.9%; Pred. No. 59;
tive 11; Mismatches
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                                                                   Score 58.5; D
Pred. No. 61;
11; Mismatches
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Pred. No. 52;
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                                                                                                       DB 6;
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HYCTKTCHALENQLOGSOPCEDCYLSC 249
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                                                                       Indels
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US-11-170-482-16
; Sequence 16, Application US/11170482
; Publication No. US20060094037A1
; GENERAL INFORMATION:
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US-10-953-349-24130
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                                                                                                                                                                                                                                                                                                              Sequence 24130, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579FUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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SEQ ID NO 24130
LENGTH: 152
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                                                                                                                                       Query Match
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PRIOR PILING DATE: 2001-08-11
PRIOR APPLICATION NUMBER: US/09/945,258
PRIOR PILING DATE: 2001-08-11
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PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FastSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2005-06-28
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APPLICANT: Fraser, Paul E.
APPLICANT: University of Toronto
TITLE OF INVENTION: PROTEINS RELATED TO SCHIZOPHRENIA AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 1034/1H570
                                                                                                                                                                                                     ORGANISM: Glycine max
                                                                                                                                                                                                                                  TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                         7.0%; Score 58; DB 6; Length 152; Local Similarity 26.8%; Pred. No. 20; hes 19; Conservative 15; Mismatchen 20. 7-3 %
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            105 NXOKPLCPEEKORHLDKKORFHN--IRGRW----TGRCMSCCRSS 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          529 NNSWFQSILKHDLRSY-LDDRPLQHYIAVS-----SPTNTTYVVQY--ALANLTGKAT 578
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  469 WQSPEEDLNFVTDTAKALANVATVLARALYELAGGTNFSSSIQADPQTVTRLLYGFLVRA
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  62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35;
                                          88 LEQQYNKPLCDLLIRCINXQKPLCPE----EKQRHLDKKQRFHNIRGRWTGRC---MSCC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FQDPQE-----RPRKLPQLCTELQTTIHDI----ILECVYCKQQLLRREVYDFAFRD 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     708
LNEEMNKGLLTMLSEELNLQKIVANETMEHTKQLIMDARKTFSHYQ-KEAEKCNIGVETC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLTREQCQDPSKVPNESKDLYEYSWVQGPWNSNRTERLPQCVRST 623
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21.2%; Pred. No. 9:
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RESULT 50
US-10-953-349-22948
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; ORGANISM: Glycine max
US-10-953-349-22949
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-24129
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Publication No. US20060107345A1

GENERAL INFORMATION: US20060107345A1

GENERAL INFORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: ENCONDED THERBY

FILE OF INVENTION UNDEER: US/10/953,349

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: PatentIn version 3.3

SEQ ID NO 24129

LENCYPUL 177
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22949
LENGTH: 264
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publication No. US20066107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
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Best Local Similarity
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Best Local (
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                                                                                                                                                           39 QYKNTTLPQ--TTLKTSVKELDLEAALAERELHVKLRKEAAD----
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                                                                                                                   63 XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKFLCDLLIRCINXQKPL-CP-EEKQRHLD 120
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                                                                               --KITKLRRNV-EMDEYDYMHWRRSFEER----EALTRDISCRKALGLPLEEPGRYMD
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26.7%; Pred. No. 40;
ative 20; Mismatches
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Pred. No. 23;
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22948, Application US/10953349

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RESULT 52
US-10-953-349-22947
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US-10-953-349-22312
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Sequence 22947, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VETBION 3.3
SEQ ID NO 22312
LENGTH: 390
TYPE: DET
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GENERAL INFORMATION:
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les 32; Conserv
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                                                                                                                                                                                                                                                125 -- FHNIRGRW 132
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                                                                                                                                                                                                                                                                                        SYRTMLEKMIRDSMHQSVIYKEQVRLNQAASNALMARLEAQREICDAAEKDLHKKYKQRD 125
                                                                                                                                                                                                                                                                                                                                 EYRHYCYSVYGTTLEQ-----QYNKPLCDLLIRCINXQKPLC-PEEKQRHLDKKQR- 124
                                                                                                                                                                                                                                                                                                                                                                         TKMQAEIQKIDDE----VNEMKLKNEEEKLAIQDLEMALIKRRKK----AEKCRRLAEAQS 65
                                                                                                                                                                                                                                                                                                                                                                                                                TELOTTIHDIILECVYCKQQLLRREVYDFAFRDL--CIVYRDGNPYAVXDKCLKFYSKIS 74
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22947
LENGTH: 393
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-22947
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22311
LENGTH: 423
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US-10-953-349-21322
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                                                                                                                                                                Sequence 21322, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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Best Local 9
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             APPLICANT: ALEXANDROV, Nick-clai et al.
TITLE OF INVENTION: SEQUENCE TERRINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FAPILICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn
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nes 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               XDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPL-CP-EEKQRHLD 120
                                                                                                                                                                                                                                                                                                                                                                                                         SYRTMLEKMIRDSMHOSVIYKEQVRLNQAASNALMARLEAQREICDAAEKDLHKKYKQRD 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                 EYRHYCYSVYGTTLEQ------QYNKPLCDLLIRCINXQKPLC-PEEKQRHLDKKQR- 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TKMQAEIQKIDDE----VNEMKLKNEEEKLAIQDLEMALIKRRKK----AEKCRRLAEAQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELOTTIHDIILECVYCKQQLLRREVYDFAFRDL--CIVYRDGNPYAVXDKCLKFYSKIS
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23.1%; Pred. No. 66;
ative 19; Mismatches
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; Sequence 22310, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRJ
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
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US-10-953-349-22310
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US-10-953-349-21321
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; ORGANISM: Glycine max
US-10-953-349-21322
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATCHTIN Version 3.3
SEQ ID NO 21321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 21321, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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 SEQ ID
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 22310
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                           226 ----RDQARKKLAEIFASIITSRKSASKSEEDMLQCFIDSKYKDGRSTTEAEVTGLLIA 280
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Similarity 22.6%;
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Pred. No. 67;
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                                                                                                                              FRAGMENTS
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                                                                                                                              AND CORRESPONDING POLYPEPTIDES
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Sequence 12540, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 12540
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US-10-953-349-12540
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US-10-953-349-21320
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US-10-953-349-21320
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 21320
LENGTH: 518
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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Best Local Similarity
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TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                  ALFAGOHTSSITSTWIG 328
                                                                                                                                                                                                                                                                                                                                                        ----QRFHNIRGRWTG 134
                                                                                                                                                                                                                                                                                                                                                                                            ----RDQARKKLAEIFASIITSRKSASKSEEDMLQCFIDSKYKDGRSTTEAEVTGLLIA 311
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Pred. No. 79;
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Pred. No. 82;
                                                                                                                                            DNA FRAGMENTS
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                                                                                                                                            AND CORRESPONDING POLYPEPTIDES
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Sequence 3341, Application US/11293697
Publication No. US20066105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILLNG DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3341
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                                                                                     US-11-293-697-3341
                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-11-293-697-3341
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; ORGANISM: Homo mapienm
US-11-318-156-6
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US-11-318-156-6
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  Best Local Sig
Matches 29;
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Best Local Similarity 26.7%;
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                                           Query Match
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PRIOR FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: US 09/290,333
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR FILING DATE: 1997-03-03
NUMBER OF SEO ID NOS: 11
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APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
FILE REFERENCE: 44158/254623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/11/318,156
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/10/293,816
PRIOR FILING DATE: 2002-11-12
                                                                                                                            LENGTH: 185
TYPE: PRT
                                                                                                       ORGANISM: Homo sapiens
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h 6.8%; Score 56.5; I Similarity 23.8%; Pred. No. 35; 29; Conservative 17; Mismatches
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Similarity 35.8%;
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Pred. No. 31;
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Pred. No. 55;
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                                         DB 7;
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                                         Length 185;
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Indels
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; LENGTH: 293
; TYPE: PRT
; ORGANISM: Homo &
US-11-318-156-2
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APPLICANT: Von Bulow, Gotz
TITLE OF INVENTION: A LYMPHOCYTE SURFACE RECEPTOR THAT BINDS
TITLE OF INVENTION: CAML AND METHODS OF USE THEREOF
FILE REFERENCE: 44158/254623
CURRENT APPLICATION NUMBER: US/11/318,156
CURRENT FILING DATE: 2005-12-23
PRIOR APPLICATION NUMBER: US/10/293,816
PRIOR APPLICATION NUMBER: US/10/293,816
PRIOR FILING DATE: 2002-11-12
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 2001-02-14
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 09/290,333
PRIOR FILING DATE: 1999-04-12
PRIOR APPLICATION NUMBER: US 08/810,572
PRIOR PILING DATE: 1999-03-03
PRIOR FILING DATE: 1997-03-03
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 3991
TENEMONIA SECTION 15.5
                                                                                                                                                                                                                                                                                Sequence 3991, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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                                             Query Match
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  Best Local Similarity Matches 19; Conserv
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                 LENGTH: 51
TYPE: PRT
                                                                                                             ORGANISM: Arabidopsis thaliana
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  Conservative
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6.8%; Score 56.5; DB 27.5%; Pred. No. 1e+02; tive 10; Mismatches
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Pred. No. 57;
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                                           DB 6;
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                                             Length 516;
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  19;
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  Gaps
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-3990
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US-10-953-349-3990
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Best Local S
Matches 19
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 3989
LENGTH: 547
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Publication No. US20060107345A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3990
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: ENCOUDED THERBY
FILE OF INVENTION: ENCOUDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                  TYPE: PRT
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6.8%; Score 56.5; DB 6;
Local Similarity 27.5%; Pred. No. 1.1e+02;
hes 19; Conservative 10; Mismatches 21;
                                                                                                                                                                   Local Similarity
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                                     136 CMSCCRSSR 144
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                                                                                                          78 HYCYSVYGTTLEQQ--YNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQRFHNIRGRWTGR 135
                                                                                                                                                   19;
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SQSCVSSSR 469
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                                                                         HYVYNNHGYSSEEETMYSAETAE----
                                                                                                                                                   Conservative
                                                                                                                                                6.8%; Score 56.5; DB 6;
27.5%; Pred. No. 1.1e+02;
vative 10; Mismatches 21;
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                                                                         ---SRNYPTPP-----RKSEFHHER----VGR
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RESULT 65
US-11-293-697-3121
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US-11-293-697-3838
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US-11-293-697-3121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3838
LENGTH: 968
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Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3121
LENGTH: 840
TYPE: PRT
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Matches
                                                                                                                     Sequence 19251, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 6.8%; Score 56.5; DB 7; Best Local Similarity 21.7%; Pred. No. 2.le+02; Matches 25; Conservative 17; Mismatches 42;
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TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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CURRENT FILING DATE: 2005-12-05
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                                                                                                                                                                                                                                                                                                                                                                                               181 RKVROMFQEADTDENOGTLTFEEFCVFYKMMSLRRDLY----LLLLSYSDKKDHLTVEE 235
                                                                                                                                                                                                                                                                                                   236 LAQFL-KVEQKMNNVTTDYCLDIIKKFEVSEENKVKNVLGIEGFTNFMRSPACDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84 YGTTLEQQYNKPLCDLLI------RCINXQKPLCPEEKQRHLDKKQRFHNI 128
                                                                                                                                                                                                                                                                                                                                               66 CLKFYSKISEYRH-----YCYSVYGTTLEQQYNK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                             10 RKLPQLCTELQTTIHDIILE----CVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDK 65
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14; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.8%; Score 56.5; DB 7;
26.4%; Pred. No. 1.8e+02;
ative 12; Mismatches 18
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US-11-259-950-95
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; ORGANISM: Glycine max
US-10-953-349-19251
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19251
LENGTH: 233
                                                                                                                                                                       Matches
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 95
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                                                                                                                                                                                                                                                        OTHER INFORMATION: Recombinant Tissue Factor with truncated cytoplasmic domain -11-259-950-95
                                                                                                                                                                                                                                                                                                 LENGTH: 279
TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/11/259,950
CURRENT FILING DATE: 2005-10-27
PRIOR APPLICATION NUMBER: US 60/622,737
PRIOR FILING DATE: 2004-10-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/252,233
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 11/033,489
PRIOR FILING DATE: 2005-01-11
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PRIOR FILING DATE: 2004-01-13
PRIOR APPLICATION NUMBER: US 10/465,789
PRIOR FILING DATE: 2003-06-18
PRIOR APPLICATION NUMBER: US 09/990,087
PRIOR FILING DATE: 2001-11-20
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APPLICANT: Pureza, Vincent
APPLICANT: Sligar, Stephen G.
TITLE OF INVENTION: Tissue Factor Compositions
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                                                                                                                                                                                         Match 6.7%; Score 56; DB Local Similarity 18.1%; Pred. No. 61;
                                                                                   153
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                                                                                                                          14 QLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLC---IVY-----RDGNPYAVX 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 KLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFA-----FRDL------CIVY
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TNTNEFLIDVDKGENYCFSVQAVIPSRTVNRKSTDSPVECMGQEK 249
                                      DKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQK 108
                                                                                   OVGTKVNVTVED----
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; TYPE: PRT
; ORGANISM: Glycine
US-10-953-349-19821
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US-10-953-349-19821
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19821
LENGTH: 303
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Publication No. US/20060107345A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PAtentIn version 3.3
SEQ ID NO 19822
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Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
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TYPE: PRT
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Local Similarity 22.6%; Pr
les 28; Conservative 23;
  116
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                                    147 RETQ 150
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                                                                          64
                                                                                                                                                    14 KHITEKDVYNLLSNEEHILGEESS-QSSNDK-----KINDLRERGYMKYGC---QHYRR
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QEVQ 119
                                                                          RCRIRAPCCDEIFDCRH--
                                                                                                              ----PLCDLLIRCINXQKPLCPEEKQR--HLDKKQRFHNIRGRWTGRCMSCCRSSRTR 146
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                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                            6.7%; Score 56; DB 22.6%; Pred. No. 66; ative 23; Mismatches
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Pred. No. 64;
23; Mismatches
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                                                                            CHNEAKUNINIDOKHR-HDIPRHOVKOVI--CSLCETE
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RESULT

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US-10-953-349-6767
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US-10-953-349-19820
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RESULT 73
US-10-953-349-19250
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Matches
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 6767
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Best Local Similarity 22.6%;
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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TYPE: PRT
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                                                                         138 E 138
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                                                                                                                                                                                  40 REVYDFAFRDLCIV-----YRDGNPYAVXDKCLKF--YSKISEYRHYCYSVYGTTLE 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 KHITEKDYYNLLSNEEHILGEESS-QSSNDK-----KINDLRERGYMKYGC---QHYRR 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35 QQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNK 94
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Pred. No. 79;
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Pred. No. 68;
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                                                                                                                                                                                                                                                            -----CVYCKQQLLR
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RESULT 74
US-10-953-349-19249
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US-10-953-349-19249
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 19249
LENGTH: 410
TYPE: PRT
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Publication No. US20060107345A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 19250
LENGTH: 385
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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CURRENT FILING DATE: 2004-09-30
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                                      101 IRCIN---XQKPLCPEEKQR----HLDKKQRFHNI 128
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37; Conserva
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37; Conserv
                                                                                                                                                                                                KLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFA-----FRDL------CIVY 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KLPQLCTELQTTIHDIILECVYCKQQLLRREVYDFA-----FRDL------CIVY 54
                                                                               AGRLESSPYSELLSPIHWEMTTEELTROFC----TLLGOSYENPLSVAVAAGVEGLPTL 315
                                                                                                                       R---DGNPYAVXDKCLKFYSKISEY-RHYCYSVYGTTLEQQYNKPL--
                                                                                                                                                            KLVQIGSNLELKIH--TLQFVEVLQNGTRADALKYARTYLAPFASLNKGEFPKLMGCLLY 260
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LKLANVMAAKKQEWQEMKQLPVPVELGKEFQFHSI
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RESULT 75 US-10-953-349-8916 ; Sequence 8916, Ap

Application US/10953349

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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 8916
LENGTH: 170
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                                                                                                                  US-10-953-349-34189
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US-10-953-349-34190
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US-10-953-349-34190
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US-10-953-349-8916
Sequence 34189, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
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LENGTH: 274
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SOFTWARE: PatentIn version 3.3
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                            36 QLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFY----
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23.5%;
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Pred. No. 67;
8; Mismatches
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CURRENT APPLICATION NUMBER: US/10/953,349;
CURRENT FILING DATE: 2004-09-30;
NUMBER OF SEQ ID NOS: 40252;
SOFTWARE: PatentIn version 3.3;
SEQ ID NO 34189;
LENGTH: 278;
TYPE: PRT;
ORGANISM: Zea mays subsp. mays
US-10-953-349-34189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 34188, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: SICCONDED THERBY
FILE REFERENCE: 2750-1579BUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: Patentin version 3.3
SEQ ID NO 34188
LENGTH: 280
                                                 APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DN
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 938
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US-10-953-349-938
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Best Local
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Best Local Similarity 23.5%;
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LENGTH: 403
TYPE: PRT
ORGANISM: Arabidopsis thaliana
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nes 16; Conserv
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ilarity 23.5%;
Conservative
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Pred. No. 69;
8; Mismatches
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Pred. No. 68;
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                                                                                                                                                                                      DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 937
LENGTH: 436
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-10-953-349-937
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                                                                       RESULT 82
US-10-953-349-936
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US-10-953-349-937
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APPLICANT: ALEXAUROV, Nickolai et al.
APPLICANT: ALEXAUROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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Publication No. US20066107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
               Sequence 936, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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LENGTH: 436
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SOFTWARE: PatentIn version 3.3
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APPLICANT: ALEXANDROV, Nickolai et al
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Pred. No. 1.1e+02;
3; Mismatches 15
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                                                                                                                                                                                                                                                                DB 6;
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US-10-953-349-9967
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-9968
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US-10-953-349-9968
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TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-10-953-349-936
                                                                                 ; ORGANISM: Arabidopsis thaliana US-10-953-349-9967
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                                                                                                                     CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 42052
SOFTWARE: PatentIn version 3.3
SEQ ID NO 9967
LENGTH: 538
TYPE: PRT
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APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PatentIn version 3.3
SEQ ID NO 9968
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Best Local
  Matches
                                        Query Match
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Local Similarity es 12; Conserv
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Local Similarity 36.4%;
es 12; Conservarina
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  Conservative
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36.4%;
                     36.4%;
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                     Score 55.5; DB 6;
Pred. No. 1.4e+02;
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Pred. No. 1.3e+02;
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Pred. No. 1.3e+02;
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  Mismatches
  1.4e+02;
ches 15;
                                      Length 538;
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CVYCKQQLLRREVYDFAFRDLCIVYRD---GNP

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US-10-505-928-94
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-4398
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-505-928-94
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US-11-293-697-4398
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Publication No. US20060088532A1
GENERAL INFORMATION:
APPLICANT: Ludwig Institute for Cancer Research.
TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES
FILE REFERENCE: 28967/39178
CURRENT APPLICATION NUMBER: US/10/505,928
CURRENT FILING DATE: 2004-08-27
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                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
SOFTWARE: Patentin 3.2
SEQ ID NO 94
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LENGTH: 764
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Best Local Similarity
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
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                                        135 RCMSCCRSSR 144
                                                                                                                  89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68 KFYSKISEYRH------YCYSVYGTTLEQQYNK-----PLCDLLIRCINXQK 108
                                                                                                                                                                                        29 ECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSKISEYRHYCYSVYGTTL
                                                                                                                                                                                                                                  33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.7%;
Similarity 21.3%;
                                                                                                                EQQYNKPLCDLLIRCINXQK------PLCPE----EKQRHLDKKQRFHNIRGRWTG 134
                                                                                                                                                      KCTVCK-----EGFSLA-RGSCI--PDCEPGTYFDSEL---IRCGECHHTCGTCVGPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PMESRNLWREVTRYLRLGDIDAATEQKRHLEEKQRVEERKRENLRTPW 742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KVHRVTAEVKHSPTNTIVCKAHGEWNGTLEFTYNNGETKVIDTTTLPVYPKKIRPLEKQG
  NCLSCAGSSR 913
                                                                            EE------HKVCRRCDE 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                  6.7%;
25.4%;
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                                                                                                                                                                                                                                  9
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Pred. No. 2e+02;
                                                                                                                                                                                                                              Score 55.5; DB 6; Length 969;
Pred. No. 2.6e+02;
9; Mismatches 45; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -CPEEKORHLDKKORF-----HNIRGRW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . 2e+02;
29;
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                                                                                                                                                                                                                                43;
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APPLICANT: ALEXANDROV, Nickolai et al.
FITILE OF INVENTION: SEQUENCE-DETERMINED DNA FR.
FITILE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9684
LENGTH: 433
LENGTH: 433
TYPE: PRT
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US-10-953-349-9685
                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Arabidopsis thaliana US-10-953-349-9684
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Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROY, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
FULE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         131 KFPGRKYKEHPFWKEKYCPFHEVDG--TPKCCSCER
                                         117 RHLDKKQR------FHNIRGRWTGRCMSCCR 141
                                                                                        106 -KPIAMHE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 RHLDKKOR------FHNIRGRWTGRCMSCCR 141
138 KFPGRKYKEHPFWKEKYCPFHEVDG--TPKCCSCER 171
                                                                                                                               57 GNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQ 116
                                                                                                                                                                              80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         57 GNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQL-LRREVYDFAF----RDLCIVYRD 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -KPIAMHE----FSNTKGRCH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FKDPVEEDGNLPRVDLNVNHP-HSI---CDGCKSAIEYGRSVHALGVNWHPECFCCRYCD 98
                                                                                                                                                                                                                     FQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQL-LRREVYDFAF----RDLCIVYRD 56
                                                                                                                                                                           FKDPVEEDGNLPRVDLNVNHP-HSI---CDGCKSAIEYGRSVHALGVNWHPECFCCRYCD 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                 6.6%; Score 55; DB 6; Le larity 21.8%; Pred. No. 1.2e+02; Conservative 16; Mismatches 56;
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21.8%;
                                                                                        -FSNTKGRCH
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Pred. No. 1.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164
                                                                                                                                                                                                                                                                                                             Length 433;
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                                                                                          ITCYERSHPNCHVCKK 137
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RESULT 90
US-11-293-697-3790
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US-11-293-697-3101
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US-11-293-697-3101
                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3790
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Matches
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 3101
LENGTH: 541
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens -11-293-697-3790
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                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                       ENGTH: 541
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  495
                                    116 QRHLDKKQRFHNIRGRWTGRCMSC 139
                                                                                                                                                       398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 NSHLAVHQRLHSREG--PSRCPQC 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            439 IAGLIRHQ----RTHTGEKPYECNQCGKAFRDSSCLTKHQRIHTKETPYQCPECGKSFKQ 494
                                                                                                                                                                                          13 POLCTELOTTIHDIILECVYCKOQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSK 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13 PQLCTELQTTIHDIILECVYCKQQLLRREVYDFAFRDLCIVYRDGNPYAVXDKCLKFYSK 72
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NSHLAVHORLHSREG--PSRCPQC 516
                                                                                                                                                     PYECKECGKT----FIESAY----LIRHQ-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISE-YRHYCYSVYGTTLEQQYNKPLCDLLIR---CINXQKPL-----CPE----EK 115
                                                                                                                ISE-YRHYCYSVYGTTLEQQYNKPLCDLLIR---CINXQKPL------CPE-----EK 115
                                                                         IAGLIRHQ----RTHTGEKPYECNOCGKAFRDSSCLTKHQRIHTKETPYQCPECGKSFKQ 494
                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                   6.6%;
                                                                                                                                                                                                                                  16;
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; Pred. No. 1.6e+02;
16; Mismatches 53
                                                                                                                                                                                                                              Score 55; DB 7;
Pred. No. 1.6e+02
16; Mismatches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 7;
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                                                                                                                                                     ----RIHTGEKPYGC-NQCQKLFRN 438
                                                                                                                                                                                                                                                                   Length 541
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RESULT 93
US-11-293-697-3380
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; ORGANISM: Glycine max
US-10-953-349-21080
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                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 21080
LENGTH: 167
TYPE: PRT
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS A
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 9683
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Publication No. US20060107345A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                 Query Match
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: ENCONDED THERBY
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                                                                                                                                                                                                                                                                                 / Match
Local Similarity 20.2%; Pred. No. 50
Local Similarity 20.2%; Pred. No. 50
Local Similarity 20.2%; Mismatche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 21.8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 233 -KPIAMHE----FSNTKGRCH------ITCYERSHPNCHVCKK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      177 FKDPVEEDGNLPRVDLNVNHP-HSI----CDGCKSAIEYGRSVHALGVNWHPECFCCRYCD 232
                                                                                                                                                                                                   47
                                                                                                              97
                                                                                                                                                     66 CLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQRHLDKKQR 124
                                                                                                                                                                                                                                          14 QLCTELQTTIHDIILECVYCKQQLLR-----REVYDFAFRDLCIVYRDGNPYAVXDK 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 GNPYAVXDKCLKFYSKISEYRHYCYSVYGTTLEQQYNKPLCDLLIRCINXQKPLCPEEKQ 116
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                                                                                                              LVKEKERVLEKYNHLFTETGPTKRHKRNS-----FEAKKHVHPTKEKRHQKQSRK 146
                                                                                                                                                                                                   QLC-----H--LMISVYYRNNMLQDLVKLFKGLEAFDRKPRDKSIIQKVANAYEVLG- 96
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Pred. No. 1.6e+02;
L6; Mismatches 56;
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                                                                                                                                                                                                                                                                                        Mismatches
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Application US/11293697

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; Sequence 21078, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: ALEXANDROV, Nickolai et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRANCISCO THERBY FILE REFERENCE: 2750-1579PUS2; CURRENT APPLICATION UNMBER: US/10/953,349; CURRENT FILING DATE: 2004-09-30
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; LENGTH: 281
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-293-697-3380
                                                                                                                                                                                                   US-10-953-349-21078
                                                                                                                                                                                                                        RESULT 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; ORGANISM: Glycine max US-10-953-349-21079
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 21079
LENGTH: 300
TYPE: PRT
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Matches
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Publication No. US20060107345A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: ALEXANDROY, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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Local Similarity 21.2%;
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                                                                                                                                                                                                                                                                                          230 LVKEKERVLEKYNHLFTETGPTKRHKRNS-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AHLAEHQRAHT--GNYKFRCAGCAK 145
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20.2%; Pred. No. 94;
tive 24; Mismatches
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Pred. No. 88;
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                                                                                        FRAGMENTS AND CORRESPONDING POLYPEPTIDES
                                                                                                                                                                                                                                                                                       ----FEAKKHVHPTKEKRHQKQSRK 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44;
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                                          US-10-953-349-33222
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                                                                                                              GEMERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-99-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 33222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 33223, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 21078
LENGTH: 308
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Best Local Similarity
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Best Local Similarity
  Query Match
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILTATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                       TYPE: PRT
ORGANISM: Zea mays
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                                                                                                 LENGTH: 358
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                                                         subsp. mays
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  6.68;
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Pred. No. 1.1e+02;
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Pred. No. 97;
  Score 54.5;
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Length
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US-10-953-349-33221
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PACENTIN VERSION 3.3
SEQ ID NO 36844
LENGTH: 393
TYPE: PRT
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 33221
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                              TYPE: PRT
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46 AFRDLCIVYRDGNPYAVXDKCLKFYSKI 73
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Publication No. US20060107345A1
GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 30935
LENGTH: 80
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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E7 protein - human papillomavirus type 35
(;Species: human papillomavirus type 35)
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: F40824; S35522
C;Accession: F40824; S35522
R;Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.
Virology 186, 770-776, 1992
A;Title: The phylogenetic relationship and complete nucleotide sequence of h
A;Title: The phylogenetic relationship and complete nucleotide sequence of h
A;Reference number: A40824; MUID:92124753; PMID:1310198
A;Recession: F40824
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A;Accession: Canal Complete nucleotide sequence of h
A;Residues: translation not shown
A;Residues: 1-99 cMAR
A;Residues: 1-99 cMAR
A;Cross-references: UNIPROT:P27230; UNIPARC:UPI000000035E; GB:M74117; NID:g3
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J. Virol. 65, 2093-2097, 1991
A; Title: A negative element in the human poapillomavirus
A; Reference number: Z17014; MUID:91162763; PMID:1848319
A; Accession: T10428
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A;Title: The region of the HPV E7 oncoprotein homologous to adenovirus Ela and SV40 larg A;Reference number: S12367; MUID:90107938; PMID:2153075
A;Accession: S12367
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A;Molecule type: protein
A;Residues: 1-98 <BAR>
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Virology 145, 181-185, 1985
A;Title: Human papillomavirus type 16 DNA sequence.
A;Reference number: A22355; MUID:85246220; PMID:2990099
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A; Residues: 1-98 < KEN>
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A; Residues: 1-98 < SEE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Superfamily: papillomavirus E7 protein; Keywords: DNA binding; early protein; transcription regulation; 58-94/Region: zinc finger CCCC motif
                                                                           Cross-references: UNIPROT:P27230; UNIPARC:UPI000000035E; GB:M74117; NID:g333050;
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                         H.; Hofmann, B.
to the EMBL Data Library,
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B7 protein - human papillomavirus type 33 C;Species: human papillomavirus type 33 C;Date: 30-Jun-1987 #sequence_revision 30-C;Pate: 30-Jun-1987 #sequence_revision 30-C;Pate: 30-Jun-1987 #secoksion: A01689; S23881; S23827 R;Cole, S.T.; Streeck, R.E. J. Virol. 58, 991-995, 1986

30-Jun-1987

#text_change 09-Jul-2004

J. Virol. 58, 991-995, 1986 A; Title: Genome organization

A; Molecule type: DNA A; Residues: 1-97 < COL>

A; Accession: A03689

A; Reference number:

A93020;

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A;Cross-references: UNIPROT:P06429; UNIPARC:UPI000013840C; R;Snijders, P.J.F.; van den Brule, A.J.C.; Schrijnemakers,

GB:M12732; NID:g333049; PIDN: H.F.J.; Raaphorst, P.M.C.; Mei

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A;Molecule type: DNA
A;Residues: 1-98 <GOL>
A;Cross-references: UNIPROT:P17387; UNIPARC:UPI000013840A; GB:J04353; NID:g
A;Cross-references: UNIPROT:P17387; UNIPARC:UPI000013840A; GB:J04353; NID:g
C;Comment: This protein may be involved in the oncogenic potential of this
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc fing
C;Keywords: DNA binding; early protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                R;Goldsborough, M.D.; Disilvestre, D.; Temple, G.F.; Lorincz, Virology 171, 306-311, 1989
A;Title: Nucleotide sequence of human papillomavirus type 31: A;Reference number: A94398; MUID:89299478; PMID:2545036
A;Accession: B32444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C;Accession: B32444
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A;Accession: S36522
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-99 <DEL>
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                        CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
CKSTLRLCVQSTQVDIRILQELLMGSFGIVCPNCSTR
                                                                                 WRGETPTLODYVLDLOPEATDLHCYEQLPDSSDEEDVIDSPAGQAEPDTSNYNIVTFCCQ
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73.5%;
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71.1%;
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Pred. No. 2.2e-35;
Magmatches 14;
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Pred. No. 2.
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submitted to the EMBL Data L
A;Description: HPV type 33 i
A;Reference number: $19906
A;Accession: $23831
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-97 <$NI>
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836574
836574
836574
C:Species: human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Species: human papillomavirus type 52
C:Colate: 08-May-1995 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Colate: 08-May-1995 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C:Colate: 08-May-1995 #sequence revision 26-Jul-1996 #text_change 09-Jul-2004
C:Colate: 08-May-1995 #sequence revision papillomavirus types.
A;Reference number: $36469
A;Reference number: $36469
A;Recession: $36574
A;Residues: 1-99 < DEL>
A;Cross-references: UNIPROT:P36831; UNIPARC:UDI000013841C; EMBL:X74481; NID:g397038; C;Superfamily: papillomavirus E7 protein
C;Superfamily: papillomavirus E7 protein; transcription regulation
                                                                                                                                          B7 protein - human papillomavirus type 58
c; Species: human papillomavirus type 58
h; Note: host Homo sapiens (man)
C; Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
c; Accession: F36779
R; Kirii, Y; Iwamoto, S.; Matsukura, T.
virology 185, 424-427, 1991
N; Title: Human papillomavirus type 58 DNA sequence.
h; Title: Human papillomavirus type 58 DNA sequence.
h; Reference number: A36779; MUID:92024102; PMID:1656594
h; Accession: F36779
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A;Cross-references: UNIPROT:P26557; UNIPARC:UPI00000034BB; GB:D90400; NID:g222386; C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
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A; Residues: 1-98 < KIR>
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Pred. No. 1
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Pred. No. 9.4e-26;
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A;Cross-references: UNIPROT:P04020; UNIPARC:UPI00001383F7; GB:M14119; NID:g333026; PIDN: C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding; early protein; transcription regulation; zinc finger F;58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virology 151, 124-130, 1986

Wirology 151, 124-130, 1986

A,Title: The nucleotide sequence and genome organization
A,Title: The nucleotide sequence and genome organization
A,Title: The nucleotide sequence and genome organization
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A;Residues: 1-98 <SCH3
A;Residues: 1-98 <SCH3
A;Cross-references: UNIPROT:P06464; UNIPARC:UPI0000138429; GB:X00203; NID:g60955;
A;Cross-references: UNIPROT:P06464; UNIPARC:UPI0000138429; GB:X00203; NID:g60955;
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger
F;58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                        A; reference number: A90975; MUID:84131949; PMID:6321162 A; Recession: D20558
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C;Species: human papillomavirus type 6b
C;Date: 30-Sep_1987 #sequence_revision 30
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A; Residues: 1-98 < DAR>
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;Species: human papillomavirus type 11
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2341-2348, 1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQ-PETTDLYXXXQLNDSSEEE-DEIDGPAGQAEPDRAHYNIVTFC 58
MHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCDSNVRLVVECTDGDIRQLQDLLLGTLNIVCPICAPKP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WHGRLVTLKDIVLDLQPPDPVGLHCYEQLEDSSEDEVDKVD--KQDAQPLTQHYQILTCC
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1986
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                                                                                            47.0%;
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                                                                                                                                                                                                                                                                                                                                          Demankowski, C.; Lattermann, O.; Zech, R.; Wolfsperger,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
                                                                            15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 245; DB 1; ]
Pred. No. 3.5e-20;
4; Mismatches 29;
                                                                                              Score 243;
Pred. No. 5.
                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                30-Sep-1987 #text_change 09-Jul-2004
                                                                                              DB 1;
.9e-20;
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                                                                                28;
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CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97

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E7 protein - human papillomavirus type 45 C;Species: human papillomavirus type 45 C;Date: 20-Feb-1995 #sequence_revision 20-C;Accession: S36562 R;Delius, H.; Hofmann, B.
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(;Species: rhesus papillomavirus
(;Species: rhesus papillomavirus
(;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
(;Accession: B38503
R;Ostrow, R.S.; LaBresh, K.V.; Faras, A.J.
Virology 181, 424-429, 1991
A;Title: Characterization of the complete RhPV 1 genomic sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence and an interpretable complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhPV 1 sequence complete RhP
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R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 19
A;Description: Primer-directed sequencing of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E7 protein - human papillomavirus type 34 (;Species: human papillomavirus type 34 (;Species: human papillomavirus type 34 (;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 (;Date: 20-Feb-1997 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004 (;Date: 20-Feb-1997 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revision 20-Feb-1995 #sequence_revisi
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A; Residues: 1-97 < DEL>
          submitted to the
                                                                                                                                                                                                                                                                                                                                                          RESULT 11
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;Cross-references: UNIPROT:P22161; UNIPARC:UPI000013842F; EMBL:M37717;Cross-references: UNIPROT:P22161; UNIPARC:UPI000013842F; EMBL:M37717;Superfamily: papillomavirus E7 protein
;Keywords: DNA binding; early protein; transcription regulation
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;Superfamily: papillomavirus E7 protein; transcription regulation
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H.; Hofmann, B.
to the EMBL Data
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49.0%;
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43.8%; Pred. No. 3.7
Library, August 1993
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Pred. No. 1.1e-17;
18; Mismatches 29;
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of human papillomavirus
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3.7e-17;
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A;Accession: 336562
A;Accession: 336562
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                 R;Delius, H.; Hofmann, B. submitted to the EMBL Data Library, August A;Description: Primer-directed sequencing of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control of the control 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:P36826; UNIPARC:UPI0000138409; EMBL:X74474; NID:g396973; PID:C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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A;RCsobs-references: UNIPROT:P21736; UNIPARC:UPI0000138416; EMBL:X74479; NID:g397022; PID:C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-105 < DEL>
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A; Accession: S36504
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                                                                                                    ;Cross-references: UNIPROT:P36832; UNIPARC:UPI000013841D; EMBL:X74482; NID:g397046; PID
;Superfamily: papillomavirus E7 protein
;Keywords: DNA binding; early protein; transcription regulation
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40.3%;
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Score 208.5; DB 2
Pred. No. 4.5e-16;
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Pred. No. 3.5
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Pred. No. 1.4e-16;
5; Mismatches 32;
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ches 33;
                                  DB 2;
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                                  Length 105;
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45;

Conservative

Mismatches

Indels

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Gaps

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E7 protein - human papillomavirus type 13
C.Species: human papillomavirus type 13
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
C;Accession: 842955
C;Accession: 842955
R;van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; (Virology 190, 587-596, 1992
                                                                                                                                                            A; Nolecule type: DNA
A; Rolecule type: DNA
A; Residues: 1-105 < COL>
A; Cross-references: UNIPARC: UPI0000000DB5; GB: X05015; NID: g60975;
C; Superfamily: papillomavirus E7 protein
C; Keywords: DNA binding; early protein; transcription regulation
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A;Accession: B42955
A;Molecule type: DNA
A;Residues: 1-101 <VAN>
A;Residues: 1-101 <VAN>
A;Cross-references: UNIFROT:002271; UNIPARC:UPI00001383F9; EMBL:X62843; NID:g60295; PIDN C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger F;61-97/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                      R;Cole, S.T.; Danos, O.
J. Mol. 193, 593-608, 1987
J. Mol. Biol. 193, 593-608, 1987
A;Title: Nucleotide sequence and comparative analysis of the human papillomavirus
A;Reference number: A92937; MUID:87283882; PMID:3039146
A;Reference H26251
                                                                                                                                                                                                                                                                                                                                                                                                                           A;Title: Identification of early proteins of the human papilloma viruses type 16 (A;Reference number: A91068; MUID:87218459; PMID:3034571
A;Reference number: B26165
A;Molecule type: DNA
A;Residues: 1-105 <SEE>
A;Cross-references: UNIPROT:P06788; UNIPARC:UPI0000000DB5; GB:X04773; NID:g60876;
A;Cross-references: UNIPROT:P06788; UNIPARC:UPI000000DB5; GB:X04773; NID:g60876;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7 protein - human papillomavirus type 18
C;Species: human papillomavirus type 18
C;Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text
C;Accession: B26165; H26251
R;Seedorf, K.; Oltersdorf, T.; Kraemmer, G.; Roewekamp,
EMBO J. 6, 139-144, 1987
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Matches 46
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                                               MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LTSCSKCCSNVRLVVECTGPDIHDLHDLLLGTLNIVCPLCAPK 100
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  MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
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                                                                                                                  38.8%; Score 200.5;
39.6%; Pred. No. 3.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 200.5; DB 1; Pred. No. 3.3e-15; 13; Mismatches 35;
                                                                                            20;
                                                                                            Pred. No. 3.5e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-Sep-1987 #text_change
                                                                                                                                           DB 1;
                                                                                                                                           Length 105;
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                                                                                            11;
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                                                                                                                                                                                                                                          PIDN: CAA28665.1;
                                                                                            Gaps
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B44890
E7 protein
C;Species:
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E7 protein - pygmy chimpanzee papillomavirus (type 1)
E7 protein - pygmy chimpanzee papillomavirus
C;Species: pygmy chimpanzee papillomavirus
C;Species: pygmy chimpanzee papillomavirus
C;Accession: B36818
C;Accession: B36818
R;van Ranst, M.; Fuse, A.; Fiten, P.; Beuken, E.; Pfister, H.; Burk, R.D.; Opdenakker, G
Virology 190, 587-596, 1992
A;Title: Human papillomavirus type 13 and pygmy chimpanzee papillomavirus type 1: Comparz
A;Reference number: A42955; MUID:92391075; PMID:1325697
A;Accession: B36818
A;Residues: 1-98 <VAN>
A;Residues: 1-98 <VAN>
A;Residues: 1-98 <VAN>
A;Residues: 1-98 <VANS
A;Coss--references: UNIPARC:UPI000013842E; EMBL:X62844; NID:g61010; PIDN:CAA44656.1; PID
C;Reywords: DNA binding; early protein; transcription regulation; transforming protein; F;58-94/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                         A;Cross-references: UNIPROT:P27231; UNIPARC:UPI0000138414; GB:M73236
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Human papillomavirus type 42: new sequence, conserved A;Reference number: A39451; MUID:92087479; PMID:1309278 A;Accession: F39451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E7 protein - human papillomavirus type 42
C;Species: human papillomavirus type 42
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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A; Residues: 1-93 < PHI>
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                                                                                            Ľ
                                                                                                                                                                                    44;
                                                                                                                                1 MHGDTPTLHEYMLDLQP--ET-TDLYXYXQLNDSSEEEBBBIDGPAGQAEPDRAHYNIVTF 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHGDTPTLHEYMLDLQPETTDLYXXYXQLNDSSEEEDEIDGPAGQAEPD--RAHYNIVTFC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MHGKYTTLKDIVLDLSPDPVGLHCNEQLD--SSEEDEVDEQATQATQATFTQHYQIVTCC
CTOCYKSVKLVVQCTEADIRNLOOMLLGTLDIVCPLCAR
                                           CCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
                                                                                          MRGETPTLKDIVLFDIPTCETPIDLYCYEQL-DSSDEDD
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                                                                                                                                                                                                       35.5%;
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                                                                                                                                                                                    17;
                                                                                                                                                                                    Score 183.5;
Pred. No. 2.4e
17; Mismatches
                                                                                                                                                                                    2.4e-13;
ches 27;
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    91
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18

- human papillomavirus type of human papillomavirus type 66

66

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C;Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-20 (C;Accession: B44890 R;Tawheed, A.R.; Beaudenon, S.; Favre, M.; Orth, G. J. Clin. Microbiol. 29, 2656-2660, 1991 A;Title: Characterization of human papillomavirus type 66 from an invasive A;Reference number: A44890; MUID:92129556; PMID:1663515 A;Accession: B44890 A;Molecule type: DNA A;Residues: 1-105 cTAW A;References: UNIPROT:Q80956; UNIPARC:UPI0000138426 A;Cross-references: UNIPROT:Q80956; UNIPROT:UPI0000138426 A;Cross-references: UNIPROT:UPI0000138426 A;Cross-references:UPI0000138426 A;Cross-references:UPI0000138426 A;Cross-references:UPI0000138426 A;Cross-references:UPI0000138426 A;Cross-references:UPI0000138426 A;Cross-references:UPI0000138426 A;Cross-references:UPI0000138426 A;Cro
R; Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August
A; Description: Primer-directed sequencing o
A; Reference number: $36469
A; Accession: $36580
A; Molecule type: DNA
A; Residues: 1-105 < DEL>
A; Cross-references: UNIPROT: P36833; UNIPARC
                                                                                                                                                                                                                                       E7 protein - human papillomavirus type 56 C;Species: human papillomavirus type 56 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: $36580 R;Delius, H.; Hofmann, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: A comparative sequence analysis of two human papillomavirus (HPV) types 2a and A;Reference number: S15614; MUID:91188699; PMID:1964523
A;Accession: S15622
A;Molecule type: DNA
A;Residues: 1-92 <HIR>
A;Residues: 1-92 <HIR>
A;Cross-references: UNIDROT:P22160; UNIPARC:UPI0000138421; EMBL:X55965; NID:g60882; PIDN C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc finger F;55-91/Region: zinc finger CCCC motif
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$15622
E7 protein - human papillomavirus type 57
C/Species: human papillomavirus type 57
C/Species: human papillomavirus type 57
A/Note: host Homo sapiens (man)
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: $15622
R/Hirsch-Behnam, A.; Delius, H.; de Villiers, E.M.
Virus Res. 18, 81-98, 1990
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S36580
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           h 34.5%; Score 178.5; DB 1; Similarity 43.3%; Pred. No. 8.6e-13; 42; Conservative 15; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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Pred. No. 2.7e-13;
       UNIPARC: UPI0000138420;
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of human
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                                                                                                                                                                             papillomavirus
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   EMBL:X74483; NID:g397053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92;
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C;Accession: F40415

R;Lungu, O.; Crum, C.P.; Silverstein, S.J.
J. Virol. 65, 4216-4225, 1991

A;Title: Biologic properties and nucleotide sequence analysis A;Reference number: A40415; MUID:91303675; PMID:1649326

A;Accession: F40415
                                                                                                                                                                                                                                                                                                                                                                              A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992
C;Accession: F40415
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C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                    A;Cross-references: UNIPROT:P26558; UNIPARC:UPI000013841B; GB:M62877 C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-101 < LUN>
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R;Delius, H.; Hofmann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              submitted to the EMBL Data Library, August 1993 A;Description: Primer-directed sequencing of hu
                                                                                                                                                                                                                                                         A; Status: translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  W7WL51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                    7 protein - human papillomavirus type 51 Species: human papillomavirus type 51
                                                                                              Query Match
Best Local (
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/Species: human papillomavirus type 7
/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
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                                   MHGDTPTLHEYMLDLQPET-TDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH----YNIV 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QDLQVNLQSFKIVTHCVFCHCLVRLVVHCTATDIRQVHQLLMGTLNIVCPNCA
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MRGNVPQLKDVVLHLTPQTEIDLQCYEQF-DSSEEEDEVDNMRDQLPERRAGQATCYRIE 59
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                                                                         Score 178; DB 1; Pred. No. 1.1e-12; 6; Mismatches 37;
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Pred. No. 1e-12;
2; Mismatches
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Pred. No. 9.9
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RESULT 25
S36480
E7 protein -
C;Species: hu
C;Date: 20-Fe
C;Accession:
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C;Species: human papillomavirus type 2a
A;Note: host Homo sapiens (man)
C;Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C;Accession: S15615
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A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-92 <AIR>
A),Cross-references: UNIPROT:P25485; UNIPARC:UPI0000138408; EMBL:X55964
A;Cross-references: UNIPROT:P25485; UNIPARC:UPI0000138408; EMBL:X55964
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation; zinc:F;55-91/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                       A;Accession: S36533
A;Molecule type: DNA
A;Residues: 1-86 <DEL>
A;Cross-references: UNIPROT:B36818; UNIPARC:UPI00001383F6; EMBL:X74465; NID:g396901; PID
C;Superfamily: papillomavirus E7 protein; transcription regulation
C;Keywords: DNA binding; early protein; transcription regulation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Delius,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E7 protein - human papillomavirus type 10 C;Species: human papillomavirus type 10 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: $36533
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                 ein - human papillomavirus type 17
es: human papillomavirus type 17
20-Feb-1995 #sequence_revision 20
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18, 81-98, 1990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42;
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                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                        CSLPLRLVVECSHADIRALEQLLLGTLKLVCPRC
                                                                                                                                                                                         CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC 94
                                                                                                                                                                                                                               WHGPHPTVKDIELSLAPEDIPV-----CNVQLDEEDYTDA----VEPAQQAYRVVTECTK
                                                                                                                                                                                                                                                            WHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.9%; Score 175.5; DB 1
43.3%; Pred. No. 1.8e-12;
tive 13; Mismatches 35
                                                                                                                                                                                                                                                                                                                        33.6%; Score 173.5;
42.6%; Pred. No. 2.9
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                     20-Feb-1995
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ches 35;
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                   #text_change
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R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: S36480
A;Accession: S36480
A;Molecule type: DNA
A;Mosidues: 1-95 < DEL>
A;Cross references: UNIPROT:P36821; UNIPARC:UPI00001383FB; EMBL:X74469; NID:g396932; C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Volpers, C.; Streeck, R.E. Virology 181, 419-423, 1991
A;Title: Genome organization and nucleotide sequence of A;Reference number: A38502; MUID:91135017; PMID:1847266
A;Accession: B38502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E7 protein - human papillomavirus type 39
C;Species: human papillomavirus type 39
A;Note: host Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: B38502
A;Molecule type: DNA
A;Residues: 1-104 <DEL>
A;Residues: 1-104 <DEL>
A;Cross-references: UNIPROT:P36827; UNIPARC:UPI000013840B; EMBL:X74475;
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                       E7 protein - human papillomavirus type 32 (;Species: human papillomavirus type 32 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 C;Accession: S36510 R;Delius, H.; Hofmann, B.
                                                                                                                                                                                                                                                                                                                                                 RESULT
S36510
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                                                                                                                            A; Reference number: A; Accession: S36510
                                                                                                                                                                       submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-109 < VOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: translation not shown
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Best Local Similarity
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHGDTPTLHEYMLDLQP----ETTDLYXYXQLNDSSEEEDEIDGP------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43;
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                                                                                                                                                     S36469
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39.1%;
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Pred. No. 9.1e
16; Mismatches
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).1e-12;
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                                                       NID: g396981;
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PID

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E7 protein - human papillomavirus type ME180 (provirus)
C;Species: human papillomavirus type ME180
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C;Accession: D40509
C;Accession: D40509
C;Reuter, S.; Dellus, H.; Kahn, T.; Hofmann, B.; zur Hausen, H.; Schwarz, E.
J. Virol. 65, 5564-5568, 1991
A;Title: Characterization of a novel human papillomavirus DNA in the cervica A;Reference number: A40509; MUID:91374616; PMID:1716694
A;Accession: D40509
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A; Residues: 1-92 < DEL>
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;Superfamily: papillomavirus E7 protein; transcription regulation
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Best Local
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61
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                                                                                                                                                                                              Similarity
                                                                                                                            MHGDTPTLHEYMLDLQP----ETTDLYXYXQLNDSSEEEDEIDGPAGQAE-----PDR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQ--PETTDLYXYXQLNDSSEEED--EIDGPAGQAEPDRAHYNIVT
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QRHTIQCTCCKCNNLLQLVVEASRENLRNVELLFMDSLNFVCPWCA
                                        AHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                                                                    MHGPKPTVQEIVLELCPCNEIEPVDLVCHEQLGDSDDEIDEPDHAVNHHQHQLLARRDEQ 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHGTRPSLADITLILEEIPEIIDLHCDEQF-DSSEEENNHQLTEPAVQA---
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                                                                                                                                                                          Conservative
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39.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32.2%; Score 166.5; 43.4%; Pred. No. 1.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17; Mismatches
                                                                                                                                                                                            Score 157.5; DB 1; Pred. No. 2.3e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 169; DB 2; Length 104; Pred. No. 1.1e-11;
                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.9e-11;
ches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34,
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                                                                                                                                                                          Indels
                                                                                                                                                                                                                Length 110;
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                                           95
                                                                                                                                                                          11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12;
                                                                                                                                                                                                                                                                                                                                                                                                                                        the cervical
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                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                       NID:g184383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56
                                                                                                                                 49
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C;Accession: $36545
C;Accession: $36545
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
submitted to the EMBL Data Library, August 1993
                                                                                                                              E7 protein - human papillomavirus type C;Species: human papillomavirus type 26 C;Date: 20-Feb-1995 #sequence_revision
                                                                                                                                                                                                         RESULT
S36545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-93 <DEL>
A;Residues: 1-93 <DEL>
A;Cross-references: UNIPROT:P36820; UNIPARC:UPI00001383FA; EMBL:X74468; NID:g396924;
C;Superfamily: papillomavirus E7 protein; transcription regulation
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Accession: S36474
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
submitted to the Library accused accused as a second control of hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
S36474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E7 protein - human papillomavirus type 15
C;Species: human papillomavirus type 15
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E7 protein - human papillomavirus type (;Species: human papillomavirus type 40 C;Date: 20-Feb-1995 #sequence_revision C;Accession: S36556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
S36556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:P36829; UNIPARC:UPI0000138412; EMBL:X74478; NID:g397014; PID:C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                     A; Reference number: S36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: S36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Description: Primer-directed sequencing of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-111 <DEL>
A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: S36474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Accession: S36556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: S36469
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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nes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40;
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MHGDTPTLHEYMLDLOP--ETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 WHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAH------
S36545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                      CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDLQVNLQSFKVVTRCVFCQCLVRLAVHCSITDITQFQQLLMGTLHIVCPNCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                                                                                                                                                                                                                                                                                        CFCDSKLRLIVVATPFGIRSQQDLLLEEVKLVCPGCREK
                                                                                                                                                                                                                                                                                                                                                                                                  MIGKEATIPDIVLELQELVQPTDLHCYEEL --- SEEETE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    40.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 148; DB 2;
Pred. No. 2.2e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                          20-Feb-1995
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                                              of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                     #text_change 09-Jul-2004
                                              papillomavirus types.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                        89
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E7 protein - human papillomavirus type la
C;Species: human papillomavirus type la
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C;Accession: C17475
R;Danos, O.; Katinka, M.; Yaniv, M.
EMBO J. 1, 231-236, 1982
A;Title: Human papillomavirus la complete DNA sequence: a novel type of genome organizat
A;Reference number: A90970; MUID:84182467; PMID:6325156
A;Accession: C17475
A;Accession: C17475
A;Residues: 1-93 -CDAN
A;Residues: 1-93 -CDAN
A;Cross-references: UNIPROT:P06465; UNIPARC:UPI00001383FD; GB:V01116; GB:X03321; NID:g60
R;Danos, O.; Engel, L.W.; Chen, E.Y.; Yaniv, M.; Howley, P.M.
J. Virol. 46, 557-566, 1983
A;Title: Comparative analysis of the human type la and bovine type 1 papillomavirus gend
A;Reference number: A92993; MUID:83189357; PMID:6302319
C;Superfamily: papillomavirus E7 protein
C;Superfamily: papillomavirus E7 protein
                                                                                                                                   R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August
A;Description: Primer-directed sequencing c
A;Reference number: S36469
A;Accession: S36591
A;Molecule type: DNA
A;Residues: 1-93 <DEL>
                                                                                                                                                                                                                                                                            B7 protein - human papillomavirus type 9
(;Species: human papillomavirus type 9
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36591
R;Dellus, H.; Hofmann, B.
                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 34
S36591
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A;Residues: 1-104 <DEL>
A;Residues: 1-104 <DEL>
A;Crose-references: UNITROT:p36824; UNIPARC:UPI0000138404; EMBL:X74472; NID:g396956;
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                             A;Cross-references: UNIPROT:P36817; UNIPARC:UPI00001383F5; EMBL:X74464; NID:g397068; C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 CKCDSTLRLCVQSTHVDIRTLBDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPET--TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MHGDTPTLHEYMLDLQPB-TTDLYXYXQLN----DSSEEEDBIDG------PAGQAEPD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         h 26.7%; Score 138; DB 1; Similarity 33.0%; Pred. No. 2.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27.2%;
Similarity 36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AYCEKLVRLTVLADHSAIRQLEELLLRSLNIVCPLCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MVGEMPALKDLVLQLEPSVLDLDLYCYEEVPPDDIEEELVS-----
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23.6%;
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Score 122; DB 2;
Pred. No. 1.7e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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of human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37; Indels
                                                                                                                                                                                                                                                                                                                           #text_change 09-Jul-2004
                                                                                                                                                                                                                                   papillomavirus
                     Length 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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E7 protein - human papillomavirus type 12
C;Species: human papillomavirus type 12
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36539
                                                                                                                                                                                                                              A;Cross-references: UNIPROT:P36819; UNIPARC:UPI00001383F8; EMBL:
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: UNIPROT:P36823; UNIPARC:UPI0000138403; EMBL:X74471; NID:g396948; PID:C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
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R;Dellus, H:; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus
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336492
E7 protein - human papillomavirus type 25
C;Species: human papillomavirus type 25
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995
C;Accession: S36492
                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-103 <DEL>
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A; Residues: 1-102 < DEL>
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35; Conservative
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                                                                                                                 1 MHGDTPTLHEYML---DLQPET--TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIV 55
                                                                                                                                                          34;
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                                                                                                                                                                          Similarity
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                                  T--FCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC
                                                                             MIGKEVTVQDFTLELSELQPEVLPVDLLCEEELPNEQETEEESD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVAPCGCCEVKLRIFVKATDFGIRTLQNLLIEELQLLCPEC
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  APCGCSSCEVNLRIFVNATDTGIRTLQDLLISDLQLLCPEC
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                                                                                                                                                      Conservative
                                                                                                                                                                      23.0%;
33.7%;
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                                                                                                                                                        16;
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                                                                                                                                                      Score 119; DB 2;
Pred. No. 4.1e-06;
6; Mismatches 37
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ches 34;
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                                                                             IDRTVFKII
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RESULT S36486

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E7 protein - human papillomavirus type 5 (Species: human papillomavirus type 5 (Species: human papillomavirus type 5 (C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change C;Accession: G26277 R;Zachow, K.R.; Ostrow, R.S.; Faras, A.J. Virology 158, 251-254, 1987 A;Title: Nucleotide sequence and genome organization of human pa A;Reference number: A94360; MUID:87207670; PMID:3033892 A;Accession: G26277 A;Molecule type: DNA A;Residues: 1-103 <ZAC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Nolecule type: DNA
A; Residues: 1-103 < KIY>
A; Residues: 1-103 < KIY>
A; Cross-references: UNIPROT: P22423; UNIPARC: UPI0000138417; GB: M32305; NID: g333062; C; Superfamily: papillomavirus E7 protein
C; Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Residues: 1-102 <DEL>
A;Cross-references: UNIPROT:P36822; UNIPARC:UPI00001383FC; EMBL:X74470; NID:g396940; C;Superfamily: papillomavirus E7 protein C;Keywords: DNA binding: Aarly received.
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(;Species: human papillomavirus type 19
(;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
(;Accession: $36486
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A,;Description: Primer-directed sequencing of human papillomavirus types.
A,Reference number: $36469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kiyono, T.; Adachi, A.; Ishibashi, M. Virology 177, 401-405, 1990
A;Title: Genome organization and taxonomic A;Reference number: A35324; MUID:90281611; A;Accession: B35324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: host Homo sapiens (man)
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
C;Accession: B35324
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Best Local S
Matches 33
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Best Local
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                                                                                                                                                                                                                                                                                                                                                            TFC-CK-CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC 94
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                                                                                                                                                                                                                                                                                                                                     APCGCSCCEVKLRIFVNATNRGIRTFQELLTGDLQLLCPEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDL---QPET--TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIV 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 113; DB 1; Length 103; Pred. No. 1.9e-05;
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PMID:2162112
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ches 35;
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                                                                                        papillomavirus
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R;Fuchs, P.G.; Iftner, T.; Weninger, J.; Pfister, H.
J. Virol. 58, 626-634, 1986
A;Title: Epidermodysplasia verruciformis-associated human papillomavirus
A;Reference number: A93019; MUID:86200410; PMID:3009874
A;Accession: A03691
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R;Yabe, Y.; Sakai, A.; Hitsumoto, T.; Kato, H.; Ogura, H.
Virology 183, 793-798, 1991
A;Title: A subtype of human papillomavirus 5 (HPV-5b) and its
A;Reference number: A40480; MUID:91306467; PMID:1649510
A;Accession: F40480
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A;Cross-references: UNIPROT:P26559; UNIPARC:UPI00000006C7; GB:D90252;
A;Cross-references: UNIPROT:P26559; UNIPARC:UPI00000006C7; GB:D90252;
C;Superfamily: papillomavirus E7 protein; transcription regulation
C;Keywords: DNA binding; early protein; transcription regulation
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                                                                                                                                                                                            A;Cross-references: UNIPROT:P06430; UNIPARC:UPI00001383F4; A;Note: this ORF is not annotated in GenBank entry PPH8CG
                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-103 < FUC>
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C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
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                                                                                                                                                   ;Superfamily: papillomavirus E7 protein;Keywords: DNA binding; early protein; t
                                                                                                                                                                                                                                                                                                                                                                                                            7 protein - human papillomavirus type 8
;Species: human papillomavirus type 8
;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
                                                                                     Query Match
Best Local
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1 MHGDTPTLHEYML---DLQPET--TDLYXXXQLNDSSEEBBEIDGPAGQAEPDRAHYNIV
                                                                   l Similarity
33; Conserv
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32; Conservative
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                                                                     Conservative
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                                                                                                                                                      early protein; transcription regulation
                                                                                     20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21.1%; Score 109; DB 1; L
31.7%; Pred. No. 5.4e-05;
31.7%; Mismatches 37;
                                                                   17;
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Pred. No. 2.5e-05;
8; Mismatches 37;
                                                                 Score 105; DB 1; I
Pred. No. 0.00015;
7; Mismatches 37;
                                                                                                       Length 103
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                                                                     Indels 14;
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E/ protein - cottontail rabbit papillomavirus
C:Species: cottontail rabbit papillomavirus
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 16-Feb-1997
C;Accession: A03692
R;Giri, I; Danos, O.; Yaniv "
RESULT 44
$19907
$E7-C protein - human papillomavirus type 33
$C;Species: human papillomavirus type 33
$C;Date: 30-Jun-1992 #sequence_revision 30-Ju
$C;Accession: $19907
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Proc. Natl. Acad. Sci. U.S.A. 82, 1580-1584, 1985
A;Title: Genomic structure of the cottontail rabbit (Shope) papil
A;Reference number: A94027; MUID:85166175; PMID:2984661
A;Accession: A03692
A;Accession: A03692
A;Molecule type: DNA
A;Residues: 1-94 <GIR>
A;Cross-references: UNIPARC:UPI000000954
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Carcinog. 4, 382-387, 1991
A;Title: The B subgroup bovine papillomaviruses lack an A;Reference number: A61399; MUID:92000191; PMID:1654923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 early protein E7 - bovine papillomavirus type 4 C;Species: bovine papillomavirus type 4 C;Date: 09-Sep-1994 #sequence_revision 09-Sep-19C;Accession: B61399
                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: UNIPROT:Q7LZV7; UNIPARC:UPI000002F8BF; GB:X59063C;Superfamily: bovine papillomavirus type 4 E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-98 < JAC>
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A;Status: preliminary
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Best Local 9
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                                                                                                                                                                                                                CCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEBB----DEIDGPAGQABPDRAHYNIVTF 57
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                                                                                                                                                                        CYACEQVEREAVVTSTEGIHQEQQLEFDNEFLECAACSKQ
                                                                                                                                                                                                                                                             MKGQNVTLQDIAIELED-----TISPINLHCEEBIETEEVDTP-
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                                                                                                                                                                                                                                                                                                                                                Conservative
                    #sequence_revision 30-Jun-1992 #text_change
                                                                                                                                                                                                                                                                                                                                                             16.2%; Score 83.5; DB 2; 27.0%; Pred. No. 0.036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.8%; Score 87; 32.6%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                16;
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                        09-Jul-2004
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A;Molecule type: DNA
A;Residues: 1-102 <GRO>
A;Cross-references: UNIPARC:UPI000017495D
C;Superfamily: papillomavirus B7 protein
C;Keywords: DNA binding; early protein; t:
                                                                                                                                                                     C;Accession: A03693
R;Groff, D.B.; Lancaster, W.D.
J. Virol. 56, 85-91, 1985
A;Title: Molecular cloning and nucleotide sequence of deer A;Reference number: A93013; MUID:85293253; PMID:2993669
A;Accession: A03693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: DNA
A;Residues: 1-98 <JAC>
A;Cross-references: UNIPROT:Q8BDD8; UNIPARC:UPI00000FA386; GB:X59062
C;Superfamily: bovine papillomavirus type 4 E6 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    early protein E7 - bovine papillomavirus type 3
C;Species: bovine papillomavirus type 3
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: A61399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:Q81886; UNIPARC:UPI00000F593F; EMBL:X64086; NID:g60282; C;Superfamily: papillomavirus E7 protein C;Keywords: early protein
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A;Description: HPV type 33 in a tonsillar carcinoma generates its putative E7 mRNA via A;Reference number: S19906
                                                                                                                                                                                                                                                                                    C;Species: deer papillomavirus
C;Date: 28-May-1986 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Jackson, M.E.; Pennie, W.D.; McCaffery, R.E.; Smith, K.T.; Grindlay, G.J.; Campo, M.S. Mol. Carcinog. 4, 382-387, 1991
A;Title: The B subgroup bovine papillomaviruses lack an identifiable E6 open reading franchers and the companies. A61399; MUID:92000191; PMID:1654923
A;Accession: A61399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
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                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              YVCENPLRLALVSSPDGTHQLHQLLLDCTSLLCANCSRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSE--EEDEIDGPAGQAEPDRAHYNIVTFC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MKGQDVTLKNVAVELEDVVSPI----ILDCEEEIETEEVDCP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STASDLRTIQQLLMGTVNIVCPTCAQQ 55
15.0%;
llarity 32.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                        early protein; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15.4%;
25.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
Score 77.5; D
Pred. No. 0.17
8; Mismatches
  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 79.5; DB Pred. No. 0.099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 80; DB 2;
Pred. No. 0.047;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                      28-May-1986 #text_change 16-Feb-1997
                    .17,
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                                    DB 1;
  31,
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                                                                          regulation
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                                      Length 102;
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  Indels
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                                                                                                                                                                                                            papillomavirus
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Gaps
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38

IDGPAGQAEP--DRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS

95

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RESULT 48
$36568
S7 protein - human papillomavirus type 49
E7 protein - human papillomavirus type 49
C; Species: human papillomavirus type 49
C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #t.
C; Accession: $36568
R; Delius, H; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A, Description: Primer-directed sequencing of human papars A; Reference number: $36469
A; Accession: $36568
A; Molecule type: DNA
RESULT 49
W7WLEP
E7 proteir
                                                                                                                                            S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: UNIPROT:P27556; UNIPARC:UPI0000138413; EMBL:X56147; NID:960942; C;Superfamily: papillomavirus E7 protesin
C;Keywords: DNA binding; early protesin; transcription regulation; transforming prote E;Keywords: DNA binding; early protein; transcription regulation; transforming prote E;Ke2-99/Region: zinc finger CCCC motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Nucleotide sequence of A;Reference number: A43550 A;Accession: B43550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E7 protein - human papillomavirus type 41
C;Species: human papillomavirus type 41
A;Note: host Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 09-Jul-2004
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A; Residues: 1-114 <HIR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Hirt, L.; Hirsch-Behnam, A.; De Villiers, E.M. Virus Res. 18, 179-190, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                         Residues: 1-103 <DEL>
;Cross-references: UNIPROT:P36830; UNIPARC:UPI0000138419; EMBL:X74480; NID:g397030; PID;Superfamily: papillomavirus E7 protein
;Superfamily: papillomavirus E7 protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Accession:
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protein
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European
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                                                                                                                                                                                                                                MHGDTPTLHEYMLDLQ-PETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH---YNIVT 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FCCKCDSTLRLCVQSTHVDIRTLEDLLMGT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQ---PETTDLYXYXQLNDSSEEEDEIDGPAGQA-EPDRAHYNIVT 56
                                                                                                                                              FC-CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                         MIGKEVTIPDIILQEEFGQPIDLQCYENLTAEAPAEQEL----EAEEELIQGIPYKVIA 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AK 100
                                                                                                       TCGGGCGARLRVFVLATDAAIRSFQELLLEELQFLCPQCREE
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                                                                                                                                                                                                                                                                        Conservative
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    e1k
                                                                                                                                                                                                                                                                                          14.5%;
  papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.7%; Score 76; DB 1;
26.7%; Pred. No. 0.29;
cive 17; Mismatches 49
                                                                                                                                                                                                                                                                      21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human
                                                                                                                                                                                                                                                                      Score 75; DB 2; Length 103; Pred. No. 0.33; Indels 21; Mismatches 45; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    papillomavirus
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: C96767
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Accession: C96767
A,Accession: C96767
A,Accession: C96767
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
C96767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: DNA
A;Residues: 1-102 <PET>
A;Cross-references: UNIPARC:UPI000013842D; GB:M15953; NID:g333025; PIDN:AAA66850.1; PID:g
C;Superfamily: papillomavirus E7 protein
C;Keywords: DNA binding; early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Pettersson, U.
submitted to GenBank, August 1987
A;Reference number: A94506
A;Accession: G94506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A94457
A; Accession: G94457
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A; Residues: 1-102 <AHO>
                                                                                                                                                                                                                                                                                                                         A; Map position:
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A;Cross-references: UNIPARC:UPI000013842D; GB:M15953; NID:g333025; PIDN:AAA66850.1; PID:S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Species: European elk papillomavirus
;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
;Accession: B29499; G94457; G94506
;Ahola, H.; Bergman, P.; Stroem, A.C.; Moreno-Lopez, J.; Pettersson, U.
                                                                                                                                                                                                                                                                                                                                                                                Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                         1-1273 <STO>
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                                                                                                                                                                                                                                  Similarity
--NIVTFCCKCDSTLRLCVQSTHVDIRTLED
                                                                                          LHAENLGIESVLVDGEPTVFEYYPHHÓNSETESNWNSVSDPÁSAÁDAAAMEYVGVLKRED 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PPSQKGHKKGHKKVYSVTVPCNGCDKNLEFCARTSSATILTLQNLLLKDLDFLCSTC 97
                                                                                                                                             WHGDTFTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHY------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAGQAEPDRAH --- YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPIC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                              UNIPROT:Q9C9B7; UNIPARC:UPI00000A4ABB; GB:AE005173; NID:g7109476;
                                                                                                                                                                                                                                  13.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cited by GenBank
                                                                                                                                                                                                                                  Score 70.5;
Pred. No. 16;
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Pred. No. 0.48;
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                                                                                                                                                                                                          39;
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                                                                                                                                                                                                                                                                Length 1273;
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Marziali,
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N; Contains:
C; Species:
C; Date: 06-
C; Accession
R; Chan, W.
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C;Species: Mina
                                                                                                                                                                           submitted to the EMBL Data Library, September 1993
A;Reference number: S37431
A;Accession: S37431
A;Accession: S37431
A;Accession: S37431
A;Accession: S37431
A;Accession: S37431
A;Accession: Agreement Saration of CDNAs encoding human brain ankyrins reveal a A;Reference number: A39643; MUID:91302466; PMID:1830053
A;Status: preliminary
A;Status: preliminary
A;Status: preliminary
A;Molecule to the EMBL Data Library
A;Reference number: A39643
A;Status: preliminary
A;Status: preliminary
A;Molecule tree: MBL Data Library
A;Molecule tree: MBL Data Library
A;Molecule to the EMBL Data Library
A;Molecule to t
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N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid
N;Contains: ankyrin 2, short form
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569
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S37431
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A; Residues: 1-622 < BLA>
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submitted to the EMBL Data Library,
A; Description: The murine rck gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q04859; UNIPARC:UPI000002747F; EMBL:X66983; NID:g53913; PIDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-622 < RES>
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R;Bladt, F.; Birchmeier, C.
Differentiation 53, 115-122, 1993
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                                                                   A;Molecule type: mRNA
A;Residues: 1-2077 <OT1>
A;Cross-references: UNIPARC:UPI0000177547; GB:X56957
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Best Local S
Matches 20
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Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Oct-2004
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protein kinase ATP-binding mo
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ilarity 32.3%;
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Pred. No. 14;
8; Mismatches 1
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                                                                           submitted to the EMBL Data A; Reference number: Z21774 A; Accession: T38157
                                                                                                                                                                                                                              short-chain dehydrogenase/reductase (BC 1.-.-.) SPAC22A12.17c [similarity] -
C;Species: Schizosaccharomyces pombe
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 05-Oct-2004
C;Accession: T38157
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A; Molecule type: DNA
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A;Title: 440-kD ankyrinB: structure of the major developmentally regulated A;Reference number: A49462; MUID:94075409; PMID:8253844
A;Accession: A49462
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-3924 <RES>
A;Cross-references: UNIPARC:UPI0000125B19; EMBL:Z26634; NID:g406287; PIDN:C:C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GDB:127607; OMIM:106410
A;Map position: 4q25-4q27
C;Superfamily: ankyrin; ankyrin repeat homology
C;Keywords: alternative splicing
F;2-3924/Product: ankyrin 2, long form #status;
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A;Molecule type: DNA
A;Residues: 463-474,'PB',477-495 <TSB>
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Genomics 10, 858-866, 19
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F;232-264/Domain:
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15; Conserv
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Pred. No. 1e+0
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                                                                                                  Length 3924;
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                                                                    Gaps
 2560
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Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, ne EMBL Data Library, September 1997

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Library, September

Data

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E6 protein - bovine papillomavirus type 4
C; Species: bovine papillomavirus type 4
C; Species: bovine papillomavirus type 4
C; Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #to
C; Accession: B27129
R; Patel, K.R.; Smith, K.T.; Campo, M.S.
J. Gen. Virol. 68, 2117-2128, 1987
J. Gen. Virol. 68, 2117-2128, 1987
A; Title: The nucleotide sequence and genome organizati
A; Reference number: A92795; MUID:87282264; PMID:303904
A; Recession: B27129
A; Molecule type: DNA
A; Residues: 1-99 < PAT>
A; Residues: 1-99 < PAT>
A; Residues: 1-99 < PAT>
A; Roserences: UNIPROT: P08350; UNIPARC:UPI0000138
A; Cross-references: UNIPROT: P08350; UNIPARC:UPI0000138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se A;Reference number: ABO502; MUID:21534947; PMID:11677608
A;Accession: AD0782
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable L-serine ammonia-lyase (EC 4.3.1.17) [imported] - Salmonella enter C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002 C;Accession: AD0782
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C;Superfamily: microbial L-serine dehydratase
C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaoxa, P.
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C;Superfamily: short-chain dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: oxidoreductase
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                                                                                                                                                                                                                                                                                                                                                                                                                             В
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A; Residues: 1-455 < PAR>
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HVVDTALYLGLLGCQPENVDLRSHMAVIKRAENENKIELPLSDAGGITIKVKIIANHQAH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAGQAEPDRAHYN-IVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXP---ICSQ 96
                                                                                                                                                                                                                                                                                                                                                                                                                          P--GHPYAMTFCARDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PGEKAAKEIAQANGVKTYTCKCDVTIPKEVEHAFAEIQKVFD----TIDIVVPNNGICTG 111
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Pred. No. 1
     UNIPARC:UPI00001383AE;
s type 4 E6 protein
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PMID:3039043
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hypothetical protein ydbD [imported] - Escherichia coli (strain O157:H7, substrain C;Species: Escherichia coli
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: H85738
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPROT:QBX9S0; UNIPARC:UPI00000D07B3; GB:BA000007; A;Experimental source: strain O157:H7, substrain RIMD 0509952 C;Genetics: A;Gene: ECs2009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia
                                                                                                A;Cross-references: UNIPROT:Q8X9S0; UNIPARC:UPI00000D07B3; A;Experimental source: strain 0157:H7, substrain EDL933
                                                                                                                            A; Molecule type: DNA
A; Residues: 1-770 <STO>
                                                                                                                                                                                              A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7 A;Reference number: A85480; MUID:21074935; PMID:11206551
                                                                                                                                                                                                                           iller, L.; Grotbeck, E.J.
Nature 409, 529-533, 2001
                                                                                                                                                                                                                                           R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.;
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Matches
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Best Local
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N.; Yasunaga, T.; Kuhara, S.;
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 Similarity
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17; Conserv
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Score 65; DB:
Pred. No. 38;
11; Mismatches
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Pred. No.
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Pred. No. 4.1;
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Shiba, T.;
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; Hattori, M.; Shinagawa,
 20;
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   16;
                                                                                                                                                                                                                                                            J.D.; Rose,
                                                                                                                                                                                                                                             Potamousis,
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Gaps
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K.; Ag
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HEYMLDLQPETTD----LYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVT------

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C;Accession: D86342
C;Accession: D86342
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Chin, C.W.; Chung, M.K.; Luzar, L.

Rature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A;Accession: D86342
A;Accession: D86341; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status preliminary
A;Molecule type: DNA
A;Residues: 1-100 <JAC>
A;Cross-references: UNIPROT:Q7LZV6; UNIPARC:UPI0000178418; GB:X59064
A;Cross-references: UNIPROT:Q7LZV6; UNIPARC:UPI0000178418; GB:X59064
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C;Species: bovine papillomavirus type 6
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
C;Accession: C61399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              S
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C; Superfamily: 1
                                                                                                                                                                                                                                                                                                       A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
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A;Title: The B subgroup bovine papillomaviruses lack an A;Reference number: A61399; MUID:92000191; PMID:1654923
A;Accession: C61399
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A; Residues: 1-614 <STO:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                             Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
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                                                                                                                                                                               Similarity
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VTFCCKCDSTLRLCVQSTHV--DIRTLEDLLMGTLGIVXPICSQ 96
                                                  PAIHPAMVDLKGKAYDL-----LRQNAQKFLMEDLYRNPGPLQYDGPGADAK----
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                                                                                                  PTLHEYMLDLQPETTDLYXYXQLNDSSEE---ED----EIDGPAGQAEPDRAHYNI
                                                                                                                                                                                                                                                       pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructok
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                  UNIPARC: UPI000004829A; GB: AE005172; NID: g4836893; PIDN: AAD30596.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CK-CDSTLRLCVQSTHVDIRTLEDLLM-GTLGIVXPICSQK 97
                                                                                                                                                                             12.5%; Score 64.5;
25.0%; Pred. No. 34;
                                                                                                                                                       15;
                                                                                                                                                       Mismatches
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Mismatches
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                                                                                                                                                     28; Indels
                                                                                                                                                                                                  Length 614;
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                                                                                                                                                  35;
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                                                                                                                                                     Gaps
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C; Superfamily: Phospholipase A2
C; Superfamily: Phospholipase A2
C; Keywords: calcium; heterodimer; metalloprotein; pyroglutamic acid; venom
F;1-16/Domain: signal sequence #status predicted <STG>
F;17-38/Domain: propeptide #status predicted <PRO>
F;17-38/Domain: propeptide #status predicted <PRO>
F;39-76,84-118,125-138/Product: crotcoxin acidic subunit status experimental <CHA>
F;39-76/Domain: crotoxin acidic subunit chain B #status experimental <CHB>
F;18-118/Domain: crotoxin acidic subunit chain C #status experimental <CHC>
F;125-138/Domain: crotoxin acidic subunit chain C #status experimental <CHC>
F;42-131,44-60,59-111,65-138,66-104,73-97,91-102/Disulfide bonds: #status predicted
F;44/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental chain C #status predicted
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A;Residues: 39-73; 'N',75-76; 'XXXXXXXXXX,',95-102,'G',104-118;125-138 <AIR1>
A;Residues: 39-73; 'N',75-76; 'XXXXXXXXXXX,',95-102,'G',104-118;125-138 <AIR1>
A;Residues: 39-73; 'N',75-76; 'XXXXXXXXXXX,',95-102,'G',104-118;125-138 <AIR1>
A;Raind, S.D.; Yates III, J.R.; Martino, P.A.; Shabanowitz, J.; Hunt, D.F.; Kaiser, I.I.
Biochim. Biophys. Acta 1040, 217-224, 1990
A;Title: The anino acid sequence of the acidic subunit B-chain of crotoxin.
A;Reference number: S11382; MUID:90381276; PMID:2400773
A;Accession: S11382
                                                                                                                                                                                                                                                                                                              SIEPIL protein precursor - beet
C;Species: Beta vulgaris (beet)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 31-Dec-2004
C;Accession: T14580
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Biochemistry 24, 7054-7058, 1985
A;Title: Rattlesnake presynaptic neurotoxins: primary structure and evolutionary origin A;Reference number: A90500; MUID:86104201; PMID:4084559
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A;Title: Cloning and sequencing of cDNAs encoding the two subunits of crotoxin.
A;Reference number: S01392; MUID:89016587; PMID:3174444
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                                                                                                                                                                                     R;Alexandrova, R.; Barkla, B.; Blumwald, submitted to the EMBL Data Library, June A;Reference number: Z18149
A;Accession: T14580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Molecule type: protein
A;Residues: 'Z',85-118 <AIR2>
A;Cross-references: UNIPARC:UPI000017277A
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A; Residues: 1-138 <BOU>
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                                                                                                                 A; Molecule type: mRNA
                                                                                                                                             A;Status: preliminary; translated
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A;Cross-references: UNIPROT:Q39436;
A;Experimental source: storage tissu
                                                                            A;Residues: 1-391 <ALE>
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTDLYXYXQLNDSSEEEDEI----DGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQST 72
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                                                                                                                                                         from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                          June
                                            UNIPARC: UPI00000AD016;
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                                            EMBL: X87931; NID: g1107525
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A;Title: Studies of the sequence of Mojave toxin: the acidic subunit.

A;Reference number: A38106

A;Accession: A38106

A;Accession: A38106

A;Reference number: A38106

A;Accession: A38106

A;Residues: 41-80;84-91,'Q',94-102,'G',104-116,'D',118;127-138 <BI2>
A;Cross-references: UNIPARC:UPI000017277B; UNIPARC:UPI000017277D; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI0000017277B; UNIPARC:UPI0000017277B; UNIPARC:UPI000017277B; UNIPARC:UPI0000017277B;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: protein
A;Residues: 41-80;84-119;127-138 <BIE>
A;Residues: 41-80;84-119;127-138 <BIE>
A;Residues: UNIPARC:UPI000017277B; UNIPARC:UPI000017277C; UNIPARC:UPI000017277D
A;Cross-references: UNIPARC:UPI000017277B; UNIPARC:UPI000017277C; UNIPARC:UPI000017277D
A;Bieber, A.L.; Becker, R.R.; McParland, R.; Hunt, D.F.; Shabanowitz, J.; Yates III, J.F.
Toxicon 27, 31, 1989
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A;Title: Genomic sequences encoding the acidic and basic A;Reference number: I51380; MUID:94156205; PMID:8112610 A;Accession: I51380
A;Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: UNIPROT:P18998; UNIPARC:UP10000131109; EMBL:U01026; NID:g451315; R;Bieber, A.L.; Becker, R.R.; McParland, R.; Hunt, D.F.; Shabanowitz, J.; Yates III, submitted to the Protein Sequence Database, November 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Crotalus scutulatus scutulatus (Mojave rattlesnake)
C;Date: 13-Sep-1996 #sequence_revision 14-Feb-1997 #text_change 16-Aug-2004
C;Accession: I51380; A33006; A38106
R;John, T.R.; Smith, L.A.; Kaiser, I.I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: siep11
C;Superfamily: S-locus glycoprotein; S-locus-specific glycoprotein homology
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-391/Product: SIEP1L protein #status predicted <MAT>
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A; Accession: A33006
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A; Residues: 1-138 < JOH>
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   19 TTDLYXYXQLNDSSEEEDEI----DGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIVTFCCK--CDSTLRLCVQSTHVD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NSTLSILRLGIDGNLRVFTYSDKVD
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29.3%;
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31.8%;
<del>..</del>
                                                                                                      6
                                                                                                      Score 63; DB 1; Length 138; Pred. No. 9.9; 6; Mismatches 13; Indels
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Pred. No. 27;
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C;Keywords: ATP
F;501-835/Domain
F;509-517/Region
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T40062
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A; Accession: T40062
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                                                                                                                                                                     Matches
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;509-517/Region: protein
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nes 13; Conserv
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A; MOLECULE - 125.0 <LYN>
A; Residues: 1-125.0 <LYN>
A; Cross-references: UNIPROT: 094385; UNIPARC: UPI000006C88E;
A; Cross-references: Strain 972h-; cosmid c29A10
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N;Alternate names: protein J0531; protein YJL16
C;Species: Saccharomyco
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R;Lyne, M.; Rajandream, M.A.; Barrell, submitted to the EMBL Data Library, De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable nuclear envelope pore membrane protein - fission yeast (Schizosacc C; Species: Schizosaccharomyces pombe C; Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Dec-2004
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A;Residues: 1-586,'KCFKNHST',595,'TCLQC',601,'KHFEN',607-855 <KRO>
A;Cross-references: UNIPARC:UPI00001689F1; EMBL:U15300; NID:g557483; PIDN:AAA50395.1;
                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated
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A;Residues: 1-855 <OBE>
A;Cross-references: UNIPROT:P38970;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: SGD:S0003701; MIPS:YJL165c
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IHNSSRILGOYTLOVLPEGTAKINPLHENYCLNSLRKDQ-
                                      MHGDTPTLHEYMLDLQPETT----DLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVT 56
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                                                                                                          Score 63; DB 2;
Pred. No. 1.1e+02;
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Pred. No. 71;
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December 1998
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C;Access
R;Gray,
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hypothetical protein F8F16.240 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 09-Jul-2004 C;Accession: T04509 R;Bevan, M.; Brandt, P.; Dose, S.; Jarke, D.; Scharfe, M.; Schon, O.; Hoheis submitted to the Protein Sequence Database, April 1998
                                                                                                                                        RESULT
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A;Gene: vp80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Jin, T.; Qi, B.; Qi, Y.
submitted to the EMBL Data Library, December 1997
A;Description: Leucania separata multiple nuclear polyhedrosis virus genome DNA 5118bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Date: 23-A;
C; Accession:
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A;Map position: 1
A;Introns: 225/3; 321/2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, November 1996
A;Reference number: Z19285
A;Reccession: T20513
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-1490 <WIL>
A;Cross-references: UNIPROT:001319; UNIPARC:UPI000007CA61; EMBL:Z81494; PIDN:CAB04052.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F02E9.4 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
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A;Molecule type: DNA
A;Residues: 1-675 <JIN>
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A; Accession: T00198
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;Species: Leucania separata nuclear polyhedrosis virus
;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
;Accession: T00198
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                  1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                    12.0%; Score 62; DB 25.6%; Pred. No. 71;
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                                            hypothetical protein F19B2.6 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T21104 R;Mortimore, B. submitted to the EMBL Data Library, January 1998 A;Reference number: Z19374
                       A; Reference number: A; Accession: T21104
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  A;Status: preliminary; translated
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RyTheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 815-820, 2000

A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W. A; Title: Sequence and analysis of ChM.; Venter, J.C.; Davis, R.W. A; Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F86458
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A;Introns: 14/1; 57/3; 246/3; 303/2; 394/3
A;Note: F8F16.240
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A;Accession: T04509
A;Molecule type: DNA
A;Residues: 1-433 <BEV>
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A; Residues: 1-508 <STO>
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Best Local (
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261 VHYCCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stein, 73879-71181 [imported] - Arabidopsis thaliana
Arabidopsis thaliana (mouse-ear cress)
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                                           64 TLRLCV 69
                                                                                                                                                                                15;
                                                                                                                                    6 PTLHEYMLDLQPETTDLYXYXQLNDSSEE--EDEIDGPAGQAEPDRAHYNIVTFCCKCDS 63
                                                                                                                                                                                                        Similarity
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                                                                                      PVVNHRGVSSQPESQPV---NHINDGHEQQCDQDVEGFKEMEEDERNNIGTSSACCSCRT
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                                                                                                                                                                                                        11.9%;
22.7%;
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Pred.
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Pred. No. 50;
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                                                                                                                                                                                                                              Length 508;
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from GB/EMBL/DDBJ

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endo-1,3(4)-beta-glucanase (EC 3.2.1.6) 1, Osg1 - rice
N;Alternate names: endo-1,3(4)-beta-glucanase; endo-1,3-beta-glucanase; Osg1 p
C;Species: Oryza sativa (rice)
C;Date: 09-Dec-2002 #sequence_revision 09-Dec-2002 #text_change 09-Jul-2004
C;Accession: JC7867
R;Yamaguchi, T.; Nakayama, K.; Hayashi, T.; Tanaka, Y.; Koike, S.
Biosci. Biotechnol. Biochem. 66, 1403-1406, 2002
A;Title: Molecular cloning and characterization of a novel beta-1,3-glucanase A;Reference number: JC7867; MUID:22152203; PMID:12162569
A;Accession: JC7867
A;Molecule type: DNA
A,Residues: 1-338 <7AM>
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C;Species: Xenopus laevis (African clawed frog)
C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004
C;Accession: A59282
R;Bhati.Dey, N; Taira, M.; Conti, M.A.; Nooruddin, H.; Adelstein, R.S.
Mech. Dev, 78, 33-36, 1998
A;Title: Differential expression of non-muscle myosin heavy chain genes duri A;Reference number: A59282; MUID:99077683; PMID:9858676
A;Accession: A59282
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A;Residues: 1-823 <WIL>
A;Cross-references: UNIPROT:Q9XXS6; UNIPARC:UPI0000060FA9; EMBL;AL021447; NID:e1519050;
A;Experimental source: clone F19B2
C;Genetics:
                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q8LP99; UNIPARC:UPI00000A0FDD; DDBJ:AB070742
C;Comment: This enzyme, a hydrolytic enzyme, which belongs to monocotyledonous endo-beta
glucans, synergistically acts with chitinase to inhibit fungal growth in vitro. It is al
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A;Residues: 1-1964 <BHA>
A;Cross-references: UNIPROT:093522; UNIPARC:UPI00000FB8F7; GB:AF055895; NID:g3660671; PI
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A59282
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C;Superfamily: myosin heavy chain; myosin motor domain
F;84-764/Domain: myosin motor domain homology <MMO>
                                             A; Introns: 2
C; Keywords:
                                                                                                                  C;Genetics:
A;Gene: osgl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 밁
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1053 LEGDSTDLHDQIAELQAQIAEL--KLQL---AKKEEELQAALARAEEEAAQKNL 1101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         174 -- AQQHAQMEIPTMSHQLIGT 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       176/3; 369/3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                             glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNI 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          σ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTL 65
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                                             hydrolase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11.9%; Score 61.5; DB 2; 27.8%; Pred. No. 2.5e+02; tive 15; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.9%; Score 61.5; DB 2; 27.2%; Pred. No. 1e+02; tive 11; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endo-1,3-beta-glucanase; Osg1 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1964;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from
probable DNA repair protein radC [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB0007
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AB0007

RESULT

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R;Boegre, L.; Jonak, C.; Mink, M.; Meskiene, I.; Traas, J.; Plant Cell 8, 417-428, 1996
A;Title: Developmental and cell cycle regulation of Alfalfa A;Reference number: Z16796; MUID:96361876; PMID:8721748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Gene: numr
C;Superfamily: nucleolin; ribonucleoprotein repeat homology
밁
                                                                                                                                                                                                               A;Cross-references: UNIPROT:059744; UNIPARC:UPI000006B51D; A;Experimental source: strain 972h-; cosmid c530
                                                                                                                                                                                                                                                                                                                                            R;Lyne, M.; Wood, V.; Rajandream, M.A.; submitted to the EMBL Data Library, May
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A; Residues: 1-635 < BOE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleolin homolog nuM1 - alfalfa N;Alternate names: nuM1 protein
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                                S
                                                                                                                                                                               A; Gene: SPDB: SPBC530.08
                                                                                                                                                                                                                                                                      A; Molecule type:
                                                                                                                                                                                                                                                                                     A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                        A Reference number: Z21934
A Accession: T40524
                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein SPBC530.08 - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                         T40524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPROT:Q40363; UNIPARC:UPI00000AA67F; EMBL:X88845; NID:g1279562; PII
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                                                                                                                                                                                                                                                     A;Residues: 1-815 <LYN>
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Best Local S
Matches 15
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;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                Accession: T40524
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Best Local Similarity
Matches 12; Conserv
                                                                       Matches
                                                                                      Query Match
Best Local
                                                                                                                                           Map position:
26-62/Domain:
                                                                                                                                                                                                  Genetics
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                                                                       20;
                                                                                        Similarity
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 EADSPAMOALKVPDR--QTAFTLACKCVDSAIVCVONLSHLSKGLKRTLD
                                   EIDGPAGQA -- EPDRAHYNIVTFCCKCDSTLRLCVQS-THVD---IRTLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPAKNGNVKKAQPETTS--EESDSDDISSDEEEVKKPAAKAVPSK 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TPTLHEYMLDLOPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDR
                                                                                                                                           GAL4 zinc binuclear cluster homology <GL4>
                                                                                                                                                                                                                                                                        DNA
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                                                                       Conservative
                                                                                    11.8%;
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                                                                     Score 61; DB 2;
Pred. No. 1.1e+0;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 61; DB 2;
Pred. No. 86;
8; Mismatches 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 61; DB
Pred. No. 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred.
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                                                              ,B 4,
..1e+02;
16;
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                                                                                                       Length 815;
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                                                                         Indels
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                                                                                                                                                                                                                                      EMBL: AL023634; PIDN: CAA19174.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ha, D.T.C.; Swoboda,
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hypothetical protein ZK632.4 - Caenorhabditis elegans
C; Species: Caenorhabditis elegans
C; Deccies: Caenorhabditis elegans
C; Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #te
C; Accession: S40936
R; Berks, M.
submitted to the EMBL Data Library, February 1993
A; Reference number: S40933
A; Accession: S40936
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-411 < BER>
A; Cross-references: UNIPROT: P34650; UNIPARC: UPI000012E
C; Genetics:
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A;Molecule type: DNA
A;Residues: 1-22 <KUR>
A;Cross-references: UNIP)
C;Genetics:
                                                                                                                         A;Title: Genome sequence of the nematode C. elegans: a platform for investigating A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: pee websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Project: A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 19; A;Accession: C89134
                                                                                                                                                                                                                                                     protein F25G6.6 [imported] - Caenorhabditis elegans C;Specites: Caenorhabditis elegans C;Specites: Caenorhabditis elegans C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004 C;Accession: C89134 R;anonymous, The C. elegans Sequencing Consortium. Science 282, 2012-2018, 1998 Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
C89134
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C;Superfamily: yeast mannose-6-phosphate isomerase
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C;Superfamily: DNA repair protein radc
                                                   A; Molecule type: DNA
A; Residues: 1-551 < STO>
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deno-Tarraga, A.M.; Cl
A; Note: Similar to asparagine
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  ;Cross-references: UNIPROT:016924; UNIPARC:UPI0000080118; GB:chr_V; PIDN:AAC25799.1; Note: Similar to asparagine synthetase; F25G6.6
                                                                                                      Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 CKC----DSTLRLCVQSTHVDIRTLEDLL 83
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37.8%;
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Pred. No. 6
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Pred. No. 31;
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N;Contains: SIL protein, short form
C;Species: Homo sapiens (man)
C;Date: 17-Uul-1992 #sequence_revision 17-Uul-1992 #text_change 09-Uul-2004
C;Accession: A41685
R;Aplan, P.D.; Lombardi, D.P.; Kirsch, I.R.
MO1. Cell. Biol. 11, 5462-5469, 1991
A;Title: Structural characterization of SIL, a gene frequently disrupted in A;Reference number: A41685; MUID:92017825; PMID:1922059
A;Accession: A41685
                                                                                              A;Wolecule type: mRNA
A;Residues: 1-1287 <APL>
A;Cross-references: UNIPROT:Q15468; UNIPARC:UPI0000072CA6;
A;Note: exon/intron borders were determined by genomic DNA
C;Genetics:
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A41685
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A; Cross references: UNIPROT: 043993;
A; Cross references: UNIPROT: 043993;
A; Cross references: UNIPROT: 043993;
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A;Gene: F25G6.6
A;Map position: 5
C;Superfamily: asparagine synthase (glutamine-hydrolyzing)
F;1-1287/Product: SIL protein #status predicted <MAT> F;1-165,213-1287/Product: SIL protein, short form #st
                                       C; Superfamily: human SIL protein C; Keywords: alternative splicing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change C;Accession: T14476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pslA protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
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24.4%; Pred. No. 2.10
tive 17; Mismatches
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Pred. No. 8
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Query Match

11.7%;

Score 60.5;

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Length 1287;

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A; MOLTECUAL VIEW A; Residues: 1-1826 <STO>
A; Cross-references: UNIPROT: Q92985;
A; Cross-references: Strain J138
                                                                                                                                                                                                                                                                                                                                                                                             R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138. A;Reference number: A86491; MJID:20330349; PMID:10871362
A;Accession: H86502
                                                                                                                                                                                                                   A;Gene: uvrA
C;Superfamily: Chlamydia trachomatis probable excinuclease ABC chain
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A;Title: gp180, a host cell glycoprotein that binds duck hepatitis A;Reference number: A57010; MUID:95318059; PMID:7797483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-1389 < KUR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: UNIPROT:Q90240; UNIPARC:UPI00000FC41C; EMBL:U25126; NID:g1008477;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: I50090
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                                                                                                                                                         Query Match
Best Local S
Matches 23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80
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                                   54 IVTFCCKCDSTLRICVQST--HVDIRTLEDLLMGTLG
                                                                                                                  10 EYMLDLQPETTDLYXY-----XQLNDSSEE-----EDEIDGPAGQAEPDRAHYN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6
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                                                                                                                                                           23;
                                                                                                                                                                            Similarity
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                                                                          DYVLELGPEGGDLGGYLLASCTPKDLIQLNTPTAKALAPYIEGSLDIPVVKSEPPSSPKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGGGGGEGGEP 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MHGDEPLARPLLIRLAQELVRGWAGGDERLGRLLNTTDLYLLPSLNPDGFERAREGDCGG 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MHGDTPTLHEYMLDLQPE----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YGLLQSSDNSEDEEEPPDNADSKSEYLLNQNLRSIPEQLGGQKEPSKNDHEIIN-CSNCE 1184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLRLCVQSTHVDIRTLEDL
                                                                                                                                                         Conservative
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-CDILIKDAYONNLKHIDLALPRNSLIAIAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -GTNADTPVLRNI 1198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.7%;
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                                                                                                                                                                            11.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 60.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 2.1e+02;
1; Mismatches 23;
                                                                                                                                                                            Score 60.5; DB 2;
Pred. No. 3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 2.30
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                   UNIPARC: UPI000016569B; GB: BA000008; NID: g8978469;
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.3e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                         32;
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966
                                                                                                                                                                                              Length 1826;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1389;
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                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F.; Ouchi, K.; Shiba,
                                                                                                                                                         25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B virus particles,
                                                                                                                                                         Gaps
                                                                                                                                                                                                                                      A; ATP-binding cas
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                                                                            936
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A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-172 <GRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invertase inhibitor homolog - common tobacco
C;Species: Nicotiana tabacum (common tobacco)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 31-Dec-2004
C;Accession: T03396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: uvrA; CP0678
C;Superfamily: Chlamydia trachomatis probable excinuclease ABC chain A;
F;609-885/Domain: ATP-binding cassette homology <ABC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Residues: 1-1826 <REA>
A;Cross-references: UNIPARC:UPI0000137E7B; GB:AE002226; GB:AE002161; NID:g7189592; PIDN:I
A;Experimental source: strain AR39, HL cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-1826 <ARN>
A;Cross-references: UNIPROT:Q9Z985; UNIPARC:UPI0000137E7B; GB:AE001595; GB:AE001363; N
A;Cross-references: UNIPROT:Q9Z985; N
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzber, Nucleic Acids Res. 28, 1397-1406, 2000
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          excinuclease ABC, chain A CP0678 [imported] - Chlamydophila pneumoniae (strains CWL029 C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: D72120; B81550
C;Accession: D72120; B81550
R;Kalman, S; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J. Nature Genet. 21, 385-389, 1999
                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: Z14924
A; Accession: T03396
                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Greiner, S.; Krausgrill, S.; Rausch, T. submitted to the EMBL Data Library, April 1997
                                                                                                                                                                                                                                                     A;Cross-references: UNIPROT:O49909; UNIPARC:UPI00000AC71C; EMBL:Y12806
A;Experimental source: strain petit havana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                          C; Superfamily: Ripening-related protein-like,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T03396
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Best Local Similarity
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                                                                                                                                          Local
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24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  54 IVTFCCKCDSTLRLCVQST--HVDIRTLEDLLMGTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 EYMLDLQPETTDLYXY------XQLNDSSEE-----EDEIDGPAGQAEPDRAHYN
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                                                                                                                                       Similarity
                                                  NIVTFCCKCDSTLRLCVQSTHVDIRTLE----DLLMGTLGIV 90
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  NIINTTCRATTNYPLCLTTLHSDPRTSEAEGADLT--TLGLV
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23.7%;
                                                                                                                                       38.1%;
                                                                                                                                                                     11.6%;
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; Pred. No. 3e+02;
17; Mismatches 32;
                                                                                                                                       Score 60;
Pred. No.
                                                                                                          Pred. No. 27;
6; Mismatches
                                                                                                                                             DB 2; Length 172
27;
                                                                                                                                                                                                                             contains similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88
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  63
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C;Accession: H86352
C;Accession: H86352
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn., L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M., D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86352
A;Status: preliminary
A;Residues: 1-465 <STO-
A;Residues: 1-465 <STO-
A;Residues: 1-465 <STO-
A;Residues: 1-465 <STO-
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A,Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A,Reference number: A70300; MUID:98196666; PMID:9537320

A,Accession: E770341

A,Status: preliminary; nucleic acid sequence not shown; translation not shown

A,Molecule type: DNA

A,Residues: 1-370 AAQF>

A,Cross-references: UNIPROT:066761; UNIPARC:UPI0000056374; GB:AE000690; GB:AE000657; A,Experimental source: strain VF5

C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conserved hypothetical protein aq_454 - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: E70341
$46281
P element - fruit fly
C;Species: Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: F2E2.2
A;Map position:
C;Superfamily: A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein F2E2.2 [imported] - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001
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C;Superfamily: conserved hypothetical protein yodO
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                                                                                     RESULT 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Superfamily: Arabidopsis thaliana hypothetical protein F17J16.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cross-references: UNIPROT:Q9LM64; UNIPARC:UPI000000A126E; GB:AE005172; NID:g9280695;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                              233 DTPSLVYLDYSGHVARRYTAEMGSLEEARLNLLPWEQLIDSDEEDDDFDGYGPRWEKRSK 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 DSSEEEDEIDGPAGQAEPDRAHYNIVTFCC-KCDSTLRLCVQSTHVDIRTLEDL 82
                                                                                                                                                                                                                                                                                                                                     4
                                                                                                                                                                                                                                                                                                                                                                                           27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             h 11.6%;
Similarity 33.3%;
                                                                                                                                                                                                                     HYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                                                                                                                                                                                                                     DTPTL-----HEY---MLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRA 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DALKEEGDIPG-LTHRYPDRVLLNVTTFCAVYCRHCMRKRIFSQGERARTKEEI 146
                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
        (Drosophila
bifasciata
                                                                                                                                                                        DATGLIAMIS---NVKTLH-LSSDSLEVIHSLCKVMP
                                                                                                                                                                                                                                                                                                                                                                                                               11.6%;
25.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                               Score 60;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 60; DB 1; Length 370 Pred. No. 62;
                                  ananassae)
                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Indels
                                                                                                                                                                                                                                                                                                                                                                                        36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #text_change 09-Jul-2004
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                                                                                                                                                                                                                                                                                                                                                                                        28;
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C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004 C;Accession: $46281  
R;Hagemann, S.; Miller, W.J.; Pinsker, W. Mol. Gen. Genet. 244, 168-175, 1994  
A;Title: Two distinct P element subfamilies in the genome of Drosophila bif; A;Reference number: $46281; MUID:94329069; PMID:8052236  
A;Accession: $46281
                                                                                        R;Brown, R.A.; Ho, L.K.F.; Weber-Hall, S.J.; Shipley, J.M.; Fry, Biochem. Biophys. Res. Commun. 233, 537-544, 1997 A;Title: Identification and cDNA cloning of a novel mammalian C2 A;Reference number: JC5500; MUID:97289668; PMID:9144573 A;Accession: JC5500
                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JC5500
                                                                                                                                                                                                                                                                 phosphoinositide 3-kinase (EC 2.7.1.-) - C;Species: Homo sariana (---)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: supposed to play a role in anchoring the terminal A;Note: specifically expressed in skeletal and cardiac muscle C;Keywords: skeletal muscle; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Luo, G.; Zhang, J.Q.; Nguyen, T.P.; Herrera, A.H.; Paterson, B.; Horowits, R. Cell Motil. Cytoskeleton 38, 75-90, 1997
A;Title: Complete cDNA sequence and tissue localization of N-RAP, a novel nebulin-related A;Reference number: Z21630; MUID:97439586; PMID:9295142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nebulin-related protein, skeletal muscle - mouse
C;Species: Mus musculus (house mouse)
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ś
A;Residues: 1-1634 <BRO>
A;Cross-references: UNIPROT:000750;
A;Experimental source: breast cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                          S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-1175 < LUO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A; Residues: 1-562 < HAG>
                                                                    A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                               맑
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary; translated from GB/EMBL/DDBJ
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 CVQSTHVDIR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                 AQQLSHVNYR 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKADYKHDVVD-YNYLPLHSILPNNDEAGSPEGCQLQAEHDRMKFSSVTNTPQIVQAKIN 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAG---QAEPDRAHYNIVTFCCKCDSTLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DAPHLIKLVRNHYLATGLHINGQTLTKSTVEQTITHCCKTDVTILFKVNESHLNVRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DVPTLYELIKKLHRRGYFVVSIVSDMGAGNQRLWRELGISEEKTWFGHPEDEDLKIFVFS 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DNA
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -AGQAEPDRAHYNI VTFCCKCDSTLRLCVQSTHVDIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 60; DB 2; L
Pred. No. 2.1e+02;
8; Mismatches 37;
                         UNIPARC: UPI0000131B5A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    97;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                         GB:Y11312;
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                                                                                                                                             domain-containing
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                         NID: g2808446;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            filaments in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78
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A; Map position: 1
A; Introns: 109/2
C; Superf
                                                                                                                                                                                                                              R;Li, Y.; Bachmann, S.; Maiss, E.; Commandeur, U.; Breyel, E.; Timpe, U.; Koenig, R. Arch. Virol. 129, 349-356, 1993
A;Title: Nucleotide sequence of the coat protein gene of pelargonium leaf curl virus A;Reference number: A48355; MUID:93228459; PMID:8470957
A;Accession: A48355; MUID:93228459; PMID:8470957
A;Accession: A48355
A;Accession: A48355
A;Accession: A48355
A;Cross-references: UNIPROT:Q86586; UNIPARC:UPIO0000F7BB9; GB:S58174; NID:g299096; PI A;Note: sequence extracted from NCBI backbone (NCBIN:129117, NCBIP:129118)
C;Superfamily: carnation mottle virus coat protein
C;Keywords: coat protein; glycoprotein
C;Keywords: coat protein; glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-333 <LYN>
A;Cross-references: UNIPROT:074739; UNIPARC:UPI00006C436; EMBL:AL031852; PIDN:CAA21253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Map position: 1q32-1q32
C;Superfamily: HeC2 phosphatidylinositol 3-kinase; protein kinase
C;Keywords: phosphotransferase
F;156-162,169-174/Domain: SH3 #status predicted <SH3>
F;1037-1320/Domain: catalytic #status predicted <CAT>
F;1498-1612/Domain: protein kinase C C2 region homology <KC2A>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Accession: T39642
R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conserved hypothetical protein SPBC1709.14 - fission yeast (Schizosaccharom C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Comment: This enzyme
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                   267 LHEINIEFRSRLTDSERKALEEEDKREKDELDGYMRPVSQATP 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               109/3; 168/3; 222/1; 235/1
ily: Saccharomyces cerevisiae hypothetical protein YPL096w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   341 HMLDILRSGSDIQDYFLTGYVWSAVTPSPEHLGDEVNLKV-TVLCDRLQ-EALTFTCNCS 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11 YMLDLQPETTDL-----YXYXQLNDSSEE-EDEIDGPAGQAEPDRAHYNIVTFCCKCD 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDG---PAGQAEP 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STVDLLIYQTLCYTHDDLRNVDVGDFVLKPCGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STLRLCVQS----THVDIRTLE--DLLMGTLGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.5%;
ilarity 32.6%;
Conservative
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Pred. No. 3.1e+02;
L7; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 59.5;
Pred. No. 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fission yeast (Schizosaccharomyces
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 333;
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ansen, N.F.; Hughës, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.;
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: C96640
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T25B24.14 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
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                                                                                                                                                                                                                  A;Cross-references:
                                                                                                                                                                                                                                                        A; Molecule type: DNA
                                                                                                                                                                                                                                                                          A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Accession: C96640
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Best Local
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26; Conserv
                                                                                               Similarity
TMALHNYIRDSQOEDSDFRHWEIVESYEQHGDENDGHVPYVPTG----DRVMENI 388
                                     TPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAHYNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEATLNIPCDRIKRYCDDSATVDHKLID---LGQLGI 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DQYTFNNVVLHYVPLCATTEVGRVAMYFDKDSEDVE---PADRVE--LANYGVLKETAPW 208
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                                                                            Conservative
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                                                                                                                                                                                                                  UNIPROT:Q9SY99; UNIPARC:UPI00000A6CC0; GB:AE005173; NID:g4585884; PII
                                                                                               11.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11.5%; Score 59.5; D
26.8%; Pred. No. 74;
tive 13; Mismatches
                                                                          Score 59.5; D
Pred. No. 77;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.J.; Federspiel, N.A.; Conway, A.B.; Conway, A.B.;
                                                                                                                   BB
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                                                                            23;
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Conway, A.R.; Creasy,
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                                                                                                               Length
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reasy, T.H.;
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: Dewar, K.;
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C69455

R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; D.; Fletschmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997 tungsten formylmethanofuran dehydrogenase, subunit F (fwdF) homolog - Archa
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004 C; Accession: C69455 Archaeoglobus Dodson, fulgi

A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.N. Smith, H.O.; Woese, C.R.; Venter, J.C. A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeor A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: C69455

shown

A;Residues: A; Molecule type: DNA A; Status: preliminary; nucleic acid sequence not shown; translation not

A;Cross-references: UNIPROT:028629; UNIPARC:UPI0000056C46; GB:AE000989; GB:AE000782; C;Superfamily: formylmethanofuran dehydrogenase, subunit F; ferredoxin 2[4Fe-4S] homo F;28-94/Domain: ferredoxin 2[4Fe-4S] homology /FFP-2 Query Match Best Local : Similarity 11.5**%**; 21.3**%**; Score Pred. No. 84; В <u>ی</u> Length 438

70

OSTHVDIRTLEDILMGTLGIVXPICSOK

97

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A;Gene: A1993/000
A;Map position: 4
C;Superfamily: Putative ternary complex factor MIP1
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-596 <STO>
A;Cross-references: UNIPROT:023178; UNIPARC:UPI000009E6AC; GB:NC_001268; NID:g7270657;
C;Genetics: CC:
                                                                                                                                                                                                                                                                                                                                                         Cispecies: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: A85438
R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Nature 402, 769-777, 1999
A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A;Reference number: A85001; MUID:20083488; PMID:10617198
A;Accession: A85438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:084760; UNIPARC:UPI00000D339E; GB:AE001348; GB:AE001273; A;Experimental source: serotype D, strain UW-3/Cx C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004 C;Accession: B71474 R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Pan, J.; Marathe, R.; Aravind,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein AT4g37080 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Peb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
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A;Reference number: A71570; MUID:99000809; PMID:9784136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable hsp60 chaperonin, mitochondrial - Chlamydia trachomatis (serotype D, C,Species: Chlamydia trachomatis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
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                                                                                        Matches
                                                                                                               Local
  262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  57 FCCKCDSTLRLCVQSTH-VDIRTLEDLLM 84
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EAAADKHSESTKLQLDDRLADQDKAQESVSGSSSE--
                                          EYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIVTFCCKCDSTLRLCVQSTHVDIRTLEDLL--MGTLGIVXPICSQK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DTTPLHELALKTLNSTQESGFVLGGGAALLYATQSLSSSPEHSQE-----
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24.3%; Pred. No. 16
                                                                                                             11.5%;
26.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell
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                                                                                     Score 59.5; DB 2;
Pred. No. 1.2e+02;
1; Mismatches 33
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A;Introns: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 37°C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructokin C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 152, 181-186, 1995
A;Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophosp
A;Reference number: Z16949; MUID:95137384; PMID:7835697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F14G6.15 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ঠ
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                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: F14G6.15
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A; Residues: 1-617 <STO>
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;Todd, J.F.; Blakeley, S.D.; Dennis, D.T.
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                                                                                                                                                          Matches
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                                                                  ----- bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting bulleting 
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                                                                                                                                                     11.5%; Score 59.5; DB 2; 24.0%; Pred. No. 1.2e+02; tive 15; Mismatches 29;
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Pred. No. 1.2e+02;
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                                                                          --- EIDGPAGQAEPDRAHYNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             S.; Khaykin, E.
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C;Species: Ar;
C;Date: 19-Fel
C;Accession:
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A;Residues: 1-1708 AMTH>
A;Residues: 1-1708 AMTH>
A;Cross-references: UNIPROT:026769; UNIPARC:UPI0000066625;
A;Experimental source: strain Delta H
C;Genetics:
                                                                                                                                                                                                                                                                                                                                RESULT 97
F69189
                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct A;Reference number: A69000; MUID:98037514; PMID:9371463
A;Accession: F69189
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: UNIPROT:064624; UNIPARC:UPI00000A9EDA; EMBL:AC003673; NID:g3004543; A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S., Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, submitted to the EMBL Data Library, April 1998
A;Description: Arabidopsis thaliana chromosome II BAC F19F24 genomic sequence. A;Reference number: Z14153
A;Accession: T01622
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A;Molecule type: DNA
A;Residues: 1-822 <STO>
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A; Residues: 1-822 < R
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    Best Loc
Matches
                                                                                                     Gene: MTH673
Superfamily: Methanobacterium thermoautotrophicum
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;Gene: At2g18940; F19F24.14
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  Similarity 23.9
28; Conservative
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11.5%; Score 59.5; DB 2; 23.9%; Pred. No. 3.7e+02; 2ive 12; Mismatches 46;
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Pred. No. 1.7e+02;
[0; Mismatches 17
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                                       Length 1708;
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31;
Gaps
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hypothetical 527K polyprotein -
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N.Contains: myosin ATPasse (EC 3.6.4.1)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A33977; S06116; A43422
R;Shohet, R.V.; Conti, M.A.; Kawamoto, S.; Preston, Y.A.; Brill, D.A.; Adelstein, R.S. Proc. Natl. Acad. Sci. U.S.A. 86, 7726-7730, 1989
A;Title: Cloning of the cDNA encoding the myosin heavy chain of a vertebrate cellular myoka, Reference number: A33977; MUID:90046668; PMID:2813355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPARC:UPI000008A46C
A;Experimental source: brush border
A;Note: sequence extracted from NCBI backbone (NCBIP:111947)
A;Note: sequence extracted from NCBI backbone (NCBIP:111947)
C;Superfamily: myosin heavy chain; myosin motor domain homology
C;Keywords: actin binding; ATP; coiled coil; hydrolase; methyla
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A;Note: this translation is not annotated in GenBank ent
R;Hodge, T.P.; Cross, R.; Kendrick-Jones, J.
J. Cell Biol. 118, 1085-1095, 1992
A;Title: Role of the COOH-terminal nonhelical tailpiece
A;Reference number: A43422; MUID:92381096; PMID:1512291
A;Accession: A43422
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A; Residues: 1-1959 <SHO>
A; Cross-references: UNIPROT: P14105; UNIPARC: UPI000012FB7F;
R; Katsuragawa, Y.; Yanagisawa, M.; Inoue, A.; Masaki, T.
Eur. J. Biochem. 184, 611-616, 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                       F;552-565/Region: actin binding #status predicted F;626-640/Region: actin binding #status predicted F;837-1936/Domain: coiled coil #status predicted <COI
                                                                                                                                                                                                                                                 F;1937-1959/Domain: carboxyl-terminal <CBT>
F;125/Modified site: N6,N6,N6-trimethyllysine ()
F;180/Binding site: ATP (Lys) #status predicted
F;694,704/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;84-764/Domain: myosin motor domain homology <MMOT>
F;174-181/Region: nucleotide-binding motif A (P-loop)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 716-1008 < KAT>
                                                                                                                                                                                                                                                                                                                                                                                                          F;837-1277/Region: S2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; not A;Molecule type: mRNA A;Residues: 1900-1959 <HOD>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Reference number: S06116; MUID:90032648; PMID:2806244
A;Accession: S06116
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                                                                                                                           Similarity
LEGDSSDLHDQIAELQAQIAEL -- KIQL --
                                                          MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNI 54
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Pred. No. 4.2e
14; Mismatches
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      SKKEEELQAALARVEEEAAQKNM
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A;Cross-references: UNIPROT:Q40712; UNIPARC:UPI00001101CF; EMBL:D32136; NID:g511666; PID A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
A;Note: only a part of the coding sequence is given
R;Fukuhara, T.; Moriyama, H.; Pak, J.Y.; Hyakutake, H.; Nitta, T.
Plant Mol. Biol. 21, 1121-1130, 1993
A;Title: Enigmatic double-stranded RNA in Japonica rice.
A;Reference number: S33529; MUID:93257627; PMID:8490131
A;Accession: S33529; MUID:93257627; PMID:8490131
A;Accession: S3529
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 3854-4370 < FUV>
A;Cross-references: UNIPARC:UPI0000179215; EMBL:D12639
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1992
C;Superfamily: rice hypothetical 527K polyprotein
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C;Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
C;Accession: S57908; S33529
R;Moriyama, H.; Nitta, T.; Fukuhara, T.
Mol. Gen. Genet. 248, 364-369, 1995
A;Title: Double-stranded RNA in rice: a novel RNA replicon in plants.
A;Reference number: S57908; MUID:96004703; PMID:7565598
                                                                                                                                                                                                                                                                                                                                              A;Accession: AP1164
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-214 <GLA>
A;Residues: 1-214 <GLA>
A;Cross-references: UNIPROT:Q8Y924; UNIPARC:UP100000556BC; GB:NC_003210; PIDN:CAC98796.
A;Experimental source: strain EGD-e
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science 294, 849-852, 2001
A; Authors: Kreft, J.; Kuln, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
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C; Keywords: polyprotein
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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STRAIN-ISOLATE African 1, and Isolate European German 131;
Terai M., Fu L., Ma Z., Burk R.D.;
"Cloning and sequencing of non-European human papillomavirus
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Song Y.S., Kee S.H., Kim J.W., Park N.H., Kang Submitted (NOV-1996) to the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBank/DDBJ of the EMBL/GenBa
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Beth-Giraldo E., Giraldo G.,
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RESULT 2
Q547B8 HPV16
ID 47847B8 HPV16
AC Q547B8;
DT 24-MAY-2005, s
DT 24-MAY-2005, s
DT 24-MAY-2006, e
DE 87 protein (Fx
GN Name=E7;
OS Human papillom
OC Viruses; dsDNA)
OC Alphapapilloma
OX NCBI TaxID=33
RN NUCLEOTIDE SEC
RA Zhang, J, Gao,
RT "Clonina.";
RL Submitted (MA)
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DR GO; GO:0005756
PT NON TER
RESULT 3
Q778G4 HPV16
ID Q778G4 HPV16
AC Q778G4;
DT 10-MAX-2005,
DT 10-MAX-2005,
DT 07-FEB-2006,
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Best Local (
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Best Local :
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24-MAY-2005, sequence of
07-FEB-2006, entry vers
E7 protein (Fragment).
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Zhang, J, Gao, Y, Yan
"Cloning and sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOTIF
                                                                                                                                                                                                                                                                                                           GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, DN
NON_TER
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                                                                                                                                                                                                                                                                                                                                                            EMBL; AF512012; AAM74160.1; -; Genomic_DNA.
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Viruses; dsDNA viruses no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
Transcription regulation.
Protein E7.
CHAIN 1 98 Protein E7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alphapapillomavirus.
NCBI_TaxID=333760;
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/FTIG=PRO_0000133414.

C-XX-C motif-1.

C-XX-C motif-2.

C-XX-C motif-2.
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Pred. No. 4.
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integrated into l sequence version entry version 3.

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PRELIMINARY;

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RESULT 4
Q77866 HPV16
AC Q77866;
AC Q77866;
DT 10-MAY-2005, E
DT 10-MAY-2005, E
DT 07-FEB-2006, E
DT 07-FEB-2016, E
DT 10-MAY-2005, E
DT 10-MAY-2005, E
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Best Local Similarity
Matches 95; Conserv
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Viruses; dsDNA viruses, no
Alphapapillomavirus.
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor acti
GO:0006355; P:regulation of transcripti
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GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
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Pred. No. 4
                                                                                                                                                              ion factor activity; IEA.
  of transcription, DNA-dependent;
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               9BD612534CD2C9EB
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Query Match

99.0%;

Score

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<u>ب</u>

Length

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RESULT 5
Q77868 H
AC Q77868;
DT 10-MAY-2
DT 10-MAY-2
DT 10-MAY-2
DT 10-MAY-2
DT 07-FEB-2
DE E7 prote
OS Human pa
OC Viruses;
OC Alphapap
OC VIRUSES;
OC NCBI_Tax
RN [1]
RAP NUCLEOTI
RAP NUCLEOTI
RAP Varhelje
RA Varhelje
RA Varhelje
RA Varhelje
RA T 53 codo
RL J. Gen.
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    RESULT 6
Q77869
ID Q7787
ID Q7788
AC Q7788
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DT 10-M
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DE E7 p
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COS Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E7 protein (Fragment).
Human papillomavirus type 16
Viruses, dsDNA viruses, no R
                                                               Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333760;
                                                                                                                                                                 10-MAY-2005, integrated into 1
10-MAY-2005, sequence version
07-FEB-2006, entry version 3.
E7 protein (Fragment).
                                                                                                                                                                                                                                                             Q778G9_HPV16
Q778G9;
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NCBI_TaxID=333760;
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NUCLEOTIDE SEQUENCE.
MEDLINE=20112892; PubMed=10644829;
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F:transcription i
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0; Mismatches
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 512; DB 2; Pred. No. 4.5e-52;
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                                                                                                                       stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      factor activity; IEA.
transcription, DNA-dependent;
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RESULT 7

Q778H1 HPV16
AC Q778H1;
DT 10-MAX-2005, a
DT 10-MAX-2005, a
DT 10-MAX-2005, a
DT 10-FEB-2006, a
DE E7 protein (FE
OS Human papillom
OC Viruses; dsDNN
OC Alphapapillom
OC Viruses; dsDNN
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OX NCBI_TAXID=333
RN (1)
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10-MAY-2005, integrated into L
10-MAY-2005, sequence version
07-FEB-2006, entry version 3.
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                           L; AJ388065; CAB45123.1; -; Genomic_DNA.
GO:0005622; C:intracellular; IBA.
GO:0003700; F:transcription factor activity;
                                                                                                                                                                                                                                                                                                                                                                     GO:0006355; P:regulation
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PF00527; E7; 1.
61
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                                                                                                                                                       Score 512; DB 2;
Pred. No. 4.5e-52;
0; Mismatches 3
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Q778H2 HPV16
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SEQUENCE
                                                                      MEDLINE-20112892; PubMed=10644829; van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Vooverheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers "Analysis of human papillomavirus type 16 E6 variants in p53 codon 72 polymorphism genotypes in cervical carcinoge J. Gen. Virol. 81:317-325(2000).
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Q778H7;
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MEDLINE=20112892; PubMed=10644829;

MEDLINE=20112892; PubMed=10644829;

van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.

Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;

"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
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Viruses; dsDNA viruses, no Rl
Alphapapillomavirus.
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Pfam; PF00527; E7; 1.
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GG:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity;
GO:0006355; P:regulation of transcription, Dr
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RESULT 11
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Q778H9;
10-MAY-2005, integrated into U
10-MAY-2005, sequence version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     L; AJ388060; CAB45113.1; -; Genomic_DNA.
GG:0005622; C:intracellular; IBA.
GO:0003700; F:transcription factor activit:
GO:0006355; P:regulation of transcription,
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Q778I1_HPV16
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
Pfam; PP00527; E7; 1.
NON_TER
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                                                                                                                                                       MEDLINE=20112892; PubMed=10644829; van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analysis of human papillomavirus type 16 E6 variants in relatic p53 codon 72 polymorphism genotypes in cervical carcinogenesis." J. Gen. Virol. 81:317-325(2000).
                                                                                                                                                                                                                                                                                       Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
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10-MAY-2005, integrated into UniProtKB/TrEMBL.
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MEDLINE=20112892; PubMed=10644829;
MEDLINE=20112892; PubMed=10644829;
van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.
verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;
"Analysis of human papillomavirus type 16 E6 variants in relation
p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";
J. Gen. Virol. 81:317-325 (2000).
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Pfam; PI
NON_TER
                           EMBL; AJ388058; CAB45109.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:000355; P:regulation of transcription, DJ
InterPro; IPR000148; Papvi_E7.
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RESULT 14
Q77815 HPV16
ID Q77815; HPV16
AC Q77815;
DT 10-MAY-2005, i
DT 10-MAY-2005, i
DT 07-FEB-2006, e
DE E7 protein (Fr
OS Human papilloma
OC Viruses; dsDNA
OX NCBI_TaxID=333
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Human papillomavirus type 16.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=333760;
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Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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. No. 4.5e-52
                               Papillomaviridae;
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RESULT 15
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ID Q77AI1 HPV16
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NCBI_TaxID=333760;
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van Duin M., Snijders P.J., Vossen
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GO:0005622; C:intracellular; IEA.
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                                                                                                                            NUCLEOTIDE SEQUENCE.

STRAIN-QEH-2076, QEH-186, PWH-Q42, QEH-525, QEH-453, QI
GEH-1220, QEH-400, PWH-Q27, QEH-318, and PWH-Q39;
QEH-1220, QEH-400, PWH-Q27, QEH-318, DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.]
Cheung J.L.K., Xu L.Y., Cheng A.F.,
"Human papillomavirus type 16 intratypic variant infector cervical neoplassa in southern China.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Terai M.,
Submitted
                                                                                                                                                                                                                                                                                                 MEDLINE=22242222; PubMed=12355268; DOI=10.1007/800239-002-2344-Y; DeFilippis V.R., Ayala F.J., Villarreal L.P.; "Evidence of diversifying selection in human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                 Terai M., Ma Z., Bur
Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=99434235; PubMed=10502513; DOI=10.1006/viro.1999.9868; Plores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.; "Establishment of the human papillomavirus type 16 (HPV-16) life cycle in an immortalized human foreskin keratinocyte cell line.";
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; AAO85409.1; -; (AAV91653.1; -; (AAV91661.1; -; (AAV91669.1; 
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Attribution-NoDerivs License
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07-FEB-2006,
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                               "Sequence variations and viral genomic statype 16 in penile carcinomas from Ugandan J. Gen. Virol. 78:2199-2208(1997).
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Beth-Giraldo E., Giraldo G.;
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                                                                                                                     by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                               sequence version
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AAM11884.1;
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AAV91685.
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Oli650;
Ol-JUL-1997, integrated into U
Ol-JUL-1997, sequence version
O7-FEB-2006, entry version 24
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Submitted (AUG-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048; Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., (Cheung J.L.K., Xu L.Y., Cheng A.F.; "Human papillomavirus type 16 intratypic variant infection for cervical neoplasia in southern China.";
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NUCLEOTIDE SEQUENCE.
MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
MEDLINE=97407827; PubMed=9264576; DOI=10.1006/gyno.1997.4756;
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AF4486326; AAL96632.1; -; G
L; AF4486327; AAL96632.1; -; G
L; AF4486320; AAL96632.1; -; G
L; AF4486330; AAL96635.1; -; G
L; AF4486331; AAL96636.1; -; G
L; AF4486333; AAL96639.1; -; G
L; AF4486334; AAL96639.1; -; G
L; AF4486336; AAL96641.1; -; G
L; AF4486336; AAL96651.1; -; G
L; AF4486336; AAL96651.1; -; G
L; AF4486336; AAL96651.1; -; G
L; AF4486350; AAL96655.1; -; G
L; AF4486351; AAL96655.1; -; G
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(JAN-2002)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Burk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Z., Burk R.D.;to the EMBL/GenBank/DDBJ databases.
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.3e-51;
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RESULT 20
Q778H5 HPV16
ID Q778H5 HPV16
AC Q778H5;
DT 05-JUL-2004, i
DT 05-JUL-2004, i
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Best Local
Matches
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Best Local
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H3 HPV16
Q778H3 HPV16
Q778H3;
05-JUL-2004, i
05-JUL-2004, g
07-FEB-2006, e
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0003700; F:transcription of transcription, DI
InterPro; IPRO0148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10995 MW; 81E53B534CC3281B CF
                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                              van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F. Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.; "Analysis of human papillomavirus type 16 E6 variants in relation p53 codon 72 polymorphism genotypes in cervical carcinogenesis."; J. Gen. Virol. 81:317-325 (2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type Viruses; dsDNA viruses, no Alphapapillomavirus.
                                                                                                                                                                                                                                                                              EMBL:
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                                                                                                                                                                                                       Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20112892; PubMed=10644829;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=333760;
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98
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1; Mismatches
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integrated into I sequence version

UniProtKB/TrEMBL

PRELIMINARY;

98

B

entry version 9.

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RESULT 21
QBGRD2_HPV16
ID QBGRD2_HPV16
AC QBQRD2;
DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 07-PEB-2006, s
DE 87 protein.
OS Human papillom
OC Viruses; dSDNA
OC Alphapapillom
OC NCBI_TAXID=333
RN [1]
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01-JUN-2002, integrated into U
01-JUN-2002, sequence version
07-FEB-2006, entry version 10
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                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., C
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:696-700(2002).
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                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, Alphapapillomavirus.
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E7 protein (
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                                                       L; AF486345; AAL96650.1; -; Genomic_DNA.
GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
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GO:0005622; C:intracciplular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-de
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PF00527; E7; 1.
                       Pro; IPR000148; Papvi_E7 PF00527; E7; 1.
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Pred. No. 1.7e-51;
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                                                        Human papillomavirus typ
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI TaxID=333760;
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07-FEB-2006,
07-FEB-2006,
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Q2MJT4_HPV16
Q2MJT4;
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QBQRD3;
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                                                                                                                                                                           E7 protein.
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NCBI_TaxID=333760;
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Viruses; dsDNA viruses, no
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GO:0006355; P:regulation of transcription, DNA-dependent;
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PF00527; E7; 1.
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1; Mismatches
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Pred. No. 1.7e-51;
1; Mismatches 3
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                                                                                                                stage;
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RESULT 24

O12338 HPV16
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EMBL; AF477385; AAM03025.1; -; Genomic_DNA.
GO; GO:0005522; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003755; P:regulation of transcription, DNA-dependent; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tornesello M.L., Buonaguro F.M., Meglio A., Buonaguro L., Beth-Giraldo E., Giraldo G.; Beth-Giraldo E., Giraldo G.; "Sequence variations and viral genomic state of human papillomavirus type 16 in penile carcinomas from Ugandan patients."; J. Gen. Virol. 78:2199-2208(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Jinhu X., Xinxing W., Yun T.; Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=97437474; PubMed=9292007;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alphapapillomavirus.
NCBI_TaxID=333760;
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01-JUL-1997, sequence version
07-FEB-2006, entry version 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses; dsDNA viruses,
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SEQUENCE 98 AA; 10992 MW; 9BD6125357D379EB CRC64;
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NCE 98 AA;
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94; Conservative
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                             CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
                                                                                                                                   MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
CDSTLRLCVQSTHVDICTLEDLLMGTLGIVCPICSQXP
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95.9%;
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95.9%;
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Pred. No. 3.9e-51;
0; Mismatches 4
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Pred. No. 1.7e-51;
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Attribution-NoDerivs License
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RESULT 26
QBQRD4 HPV16
QBQRD4;
DT QBQRD4;
DT 01-JUN-2002, s
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DT 01-JUN-2002, s
DT 01-JUN-2002, s
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DT 01-JUN-2002, s
DT 01-JUN-2002, s
DT 01-JUN-2011 on
OC Viruses; dSDW1
OC Viruses; dSDW1
OC Alphapapilloma
OX NCBI TAXID=333
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CR NUCLEOTIDE SEC
RP MUCLEOTIDE SEC
RP MEDLINE=221821
RN [1]
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MEDLINE=22182962; PubMed=12195358; DOI=10.1086/342048;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Cl
Cheung J.L.K., Xu L.Y., Cheng A.F.;
"Human papillomavirus type 16 intratypic variant infection
for cervical neoplasia in southern China.";
J. Infect. Dis. 186:896-700(2002).
                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus type Viruses, dsDNA viruses, no Alphapapillomavirus
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InterPro; IPR000148; PapviinterPro; PR00527; E7; 1.
Pfam; PF00527; E7; 1.
                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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Viruses; dsDNA viruses, no Rh
Alphapapillomavirus
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GO; GO:0005622; C:inftacellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-de
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                                Pfam; PF00527; E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jinhu X., Xinxing W., Yu
Submitted (DEC-2001) to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=333760;
                                                  InterPro; IPR000148;
L; AF486329; AAL96634...,
GO:0005622; C:intracellular; IEA.
GO:0005700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
GO:0006355; P:regulation of transcription, CNA-dependent;
CO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  integrated into
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.7%;
94.9%;
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to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                            16
                                                                                                                                                                                                                                                                                                                                                                                                       RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 500;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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RESULT 27
QBB5P6 HPV16
ID QBB5P6 H
AC QBB5P6;
DT 01-MAR-2
DT 01-MAR-2
DT 07-PEB-2
DT 07-PEB-2
DT 01-MAR-2
DT 01-DT S
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Best Local S
Matches 90
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Best Local Similarity
Matches 93; Conserv
                                                                                                                                                                                                                                OSODH6_HPV16 PRELIMINARY; PRI
OSODH6;
O1-MAY-2000, integrated into Unif
O1-MAY-2000, sequence version 1.
O7-FEB-2006, entry version 14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QBB5P6_HPV16 PRELIMINARY; PRT; 94 AA. QBB5P6; 01-MAR-2003, integrated into UniProtKB/TrEMBL. 01-MAR-2003, sequence version 1. 07-FEB-2006, entry version 10.
                                                                                                                                             Human papillomavirus type 16.
Viruses, dsDNA viruses, no RV
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ponglikitmongkol M., Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 16.
Viruses; dsDNA viruses, no RNA
Alphapapillomavirus.
                         NUCLEOTIDE SEQUENCE.
Lee H.P., Song Y.S.,
Submitted (SEP-1999)
                                                                                                                 NCBI_TaxID=333760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
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                                                                                                                                                                                                                      protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L; AF469197; AAO15692.1; -; Genomic_DNA.
GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; F:regulation of transcription, DNA-dependent;
erPro; IPR000148; Papvi_E7.
mr; PF00527; E7; 1.
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94 AA;
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ilarity 94.9%;
Conservative
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to the EMBL/GenBank/DDBJ databases.
                         Kim J.W., Roh J.W., Park N.H., Kang to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                        RNA
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Pred. No. 1.5e-50;
1; Mismatchės 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 486; DB 2;
Pred. No. 4.9e-49;
                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                      stage;
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                                               Kang S.B.;
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RESULT
Q9QDH4
ID Q9
AC Q9
DT 01
DT 01

JLT 30)H4 HPV16 Q5QDH4 HFV16 Q9QDH4; 01-MAY-2000, 01-MAY-2000,

PRELIMINARY;

PRT;

93

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sequence

integrated into UniProtKB/TrEMBL

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Q9QDH2
Q9QDH2
ACQQ9
ACQQ9
DT 011
DT 011
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Q9QDH2;
Q1-MAY-2000, integrated into UniProtKB/TrEMBL
Q1-MAY-2000, sequence version 1.
Q7-FEB-2006, entry version 14.
E7 protein (Fragment)
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
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Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                          Pfam;
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Alphapapillomavirus.
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GO:0006355; P:regulation of transcription, DNA-dependent;
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003770; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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QOODHB;
Q1-MAY-2000, integrated into U
01-MAY-2000, sequence version
07-FEB-2006, entry version 14.
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Alphapapillomavirus.
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-de
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NCE 93 AA; 10452 MW; |
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                                                                                                                                                                        Similarity
                                        MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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MHGDTPTLHEYMLDLQPETTDLYCYEQLSDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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(SEP-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        integrated into UniProtKB/TrEMBL
                                                                                                                                                                92.3%;
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to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA stage;
                                                                                                                            Score 477; DB 2; I
Pred. No. 5.6e-48;
1; Mismatches 3;
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Pred. No. 5.6e-48;
1; Mismatches 3
                                                                                                                                                                                                                                                                              83281BB2AE2C8A1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                     Length 93;
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RESULT
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Best Local
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07-FEB-2006, entry version 11.
E7 protein (Fragment).
Human papillomavirus.
Viruses, dsDNA viruses, no RNA sunclassified Papillomaviridae.
                                                                                                                                                                                                 Protein E7.
Name=E7;
                                                                                                                                                                                                                      01-AUG-1992,
01-AUG-1992,
07-FEB-2006,
                                                                                                                                                                                                                                                         VE7_HPV35
P27230;
                                                                                                                                               Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10587;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF469198; AAOJ5694 1; -; Genomic DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activit;
GO; GO:0006355; P:regulation of transcription,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2003,
                                NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=92124753; PubMed=1310198;
                                                                                           Delius H.,
                                                                                                      MEDLINE=94265501; PubMed=8205838;
                                                                                                                  STRAIN=Isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                        Marich
                                                                                                                            NUCLEOTIDE SEQUENCE
                                                                                                                                                                                     Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
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Submitted (JAN-2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10566;
          Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.; The phylogenetic relationship and complete nucleotide sequence of
                                                                    "Primer-directed sequencing Curr. Top. Microbiol. Immuno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [nterPro; IPR000148; Papvi_E7.
papillomavirus
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3R 77 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                    CDSTLRLCVQSTHVDIR
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                                                                                           Hofmann B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77 AA; 8782 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                       integrated into UniProtKB/Swiss-Prot. sequence version 1. entry version 32.
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                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77
                                                                                                                            [GENOMIC DNA]
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96.1%;
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type
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                                                                    encing of human papillomavirus Immunol. 186:13-31(1994).
                                                                                                                                                                          no RNA stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Score 406; DB 2
Pred. No. 1e-39;
1; Mismatches
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                                                                                                                                                                                                                                                                     PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            factor activity; IEA.

Concernation, DNA-dependent;
                                                                                                                                                                           Papillomaviridae;
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RESULT 34
Q76WP2 9PAPI
ID Q76WP2;
AC Q76WP2;
DT 05-JUL-2
DT 07-FEB-2
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Best Local S
Matches 72
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Best Local :
                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no RNA stage; unclassified Papillomaviridae. NCBI_TaxID=10566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004, integrated into UniProtKB/TrEMBL 05-JUL-2004, sequence version 1. 07-FEB-2006, entry version 10.
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EMMB: X74477; CAA52562.1; -; Genomic_DNA.
PIR; F40824; W7WLJS.
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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-- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000148; Papvi_E7. Pfam; PF00527; E7; 1. SEQUENCE 99 AA; 10954 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human papillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein

    II; D10597; BAA01448.1; -; Genomic_DNA.
    GO:0005622; C:intracellular; IEA.
    GO:0003700; F:transcription factor activity; IEA.
    GO:0003355; P:regulation of transcription, DNA-dependent;

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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61
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                                                                                                                                                                                                                                                                                               . Similarity 72; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                  KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                      MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSS-EEEDEIDGPAGQAEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCEATLRLCVQSTHIDIRKLEDLLMGTFGIVCPGCSQR 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHGETTTLQDYVLDLEPEATDLYCYEQLCDSSEEEEDTIDGPAGQAKPDTSNYNIVTSCC
KCEATLRLCVOSTHIDIRKLEDLLMGTFGIVCPGCSQR
                                                                                                                                               MHGEITTLQDYVLDLEPEATDLYCYEQLCDSSEEEEDTIDGPAGQAKPDTSNYNIVTSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein has both transforming and trans-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
95
10954 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                  1.
10954 MW; 8EAA8F248051E226 CRC64;
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73.5%;
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73.5%;
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/FTId=PRO_0000133433.

C-XX-C motif-1.

C-XX-C motif-2.
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                                                                                                                                                                                                                                                                                                                                     Pred.
                                                                                                                                                                                                                                                                                                                                                                    Score 381.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                         No. 1
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                                                                                                                                                                                                                                                                                                  1.1e-36;
nes 14;
                                                                                                                                                                                                                                                                                                                                                                    DB 2;
   98
                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                 Length
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                                                                                                                                                                                                                                                                                                                                                                            99;
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37 HPV31

VE7 HPV31

P17387;

P17387;

P17387;

P17387;

P1748-1990;

P1748-2006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOTIF
SEQUENCE
                                                                                                                                                                                                                                                          05-JUL-2004, integrated into 0 05-JUL-2004, sequence version 07-FEB-2006, entry version 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDILINE-89299478; PubMed=2545036;
Goldsborough M.D., Disilvestre D., Temple G.F.
"Nucleotide sequence of human papillomavirus
neoplasia-associated virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10585;
                                                             NUCLEOTIDE SEQUENCE.
Fiedler M., Fitzky B., D
Submitted (OCT-2003) to
                                                                                                                                                                                                E7 transforming protein variant. Human papillomavirus type 31. Viruses; dsDNA viruses, no RNA s
                                                                                                                                                                                                                                                                                                                                            Q6T377_HPV31
Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                  Alphapapillomavirus.
NCBI_TaxID=10585;
                                                                                                                                                                                                                                                                                                                                 Q6T377;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation.

CHAIN

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98
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PIR; B32444; W7WL31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
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-!- FUNCTION: E7 protein ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus type 31. Viruses; dsDNA viruses, no RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [nterPro;
                                                                                                                                                                                                                                                                                                                                                                             _HPV31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CKSTLRLCVQSTQVDIRILQELLMGSFGIVCPNCSTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
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91
AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                               integrated into UniProtKB/TrEMBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entry version 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
94
10918 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.0%;
                                                                Durst M., Zwerschke W., Jansen-Du
o the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                   no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                has both transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protein E7.
/FTId=PRO_0000133429.
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 372; DB 1;
Pred. No. 1.4e-35;
                                                                                                                                                                                                                                                                                                                                                          PRT;
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    see http://www.uniprot.org/terms
Attribution-NoDerivs License
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                                                                                         Jansen-Durr P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
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RESULT 38
O90724 HPV67
ID O90724 HPV67
AC O90724;
DT 01-NOV-1998, 4
DT 01-PEB-2006, 6
DE ORF E7.
OS Human papillon
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IDBS633
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163 9PAPI

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QBB563;
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:00003700; P:regulation of transcription, DNA-dependent;
InterPro; IPRO0148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10917 MW; 9D31DFF1CF9064B1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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07-FEB-2006,
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unclassified Papillomaviridae.
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity
GO:0006355; P:regulation of transcription,
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PF00527; E7; 1.
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  papillomavirus
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                                           integrated into UniProtKB/TrEMBL. sequence version 1. entry version 17.
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95.4%;
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Pred. No. 5.4e-35;
L5; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 343; DB 2;
Pred. No. 2.2e-32;
1; Mismatches 2
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transcription, DNA-dependent;
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01-JAN-1988,
07-FEB-2006,
Protein E7.
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P06429;
EMBL;
                                                                                                                                                                                                                                                                                                                        Snijders P.J.F., van den Brule A.J.C., Schrijnemakers H.F. Snijders D.J.F., van den Brule A.J.C., Schrijnemakers H.F. Raaphorst P.M.C., Meijer C.J.L.M., Walboomers J.M.M.; "Human papillomavirus type 33 in a tonsillar carcinoma gen putative E7 mRNA via two E6* transcript species which are at different early region poly(A) sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-86200464; PhDMed=3009902; Cole S.T., Streeck R.E.;
                                                                                                                                                                                                                                                             at different early region poly(A) sites.";
J. Virol. 66:3172-3178(1992).
-!- FUNCTION: E7 protein has both transforming
                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniproDistributed under the Creative Commons Attribution-NoDerivs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Genome organization and nucleotide sequence type 33, which is associated with cervical cay. Virol. 58:991-995(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92219410; PubMed=1313922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10586;
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Alphapapillomavirus.
NCBI_TaxID=37120;
                                                                                                                                                                                                  -!- SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [MRNA]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=E7;
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Distributed under the Creative Commons Attribution-NoDerivs License
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Virus Genes 17:117-121(1998).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99073695; PubMed=9857984; DOI=10.1023/A:1008002905588;
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Pfam; PF00527; E7; 1
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GO:0003700; F:transcription factor activity;
GO:0006355; P:regulation of transcription, D
M12732; AAA46959.1;
X64084; CAA45430.1;
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¬ RNA ►
                                                                                                                                                                                                  the papillomaviruses E7 protein
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   mRNA
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Pred. No. 5.5e-29;
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                                                                                                                                see http://www.uniprot.org/terms
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Matches 56
Query Match
Best Local Similarity
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1_HPV52
VE7_HPV52
P36831;
                                                                  MOTIF
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Takami Y., Kondoh G., Saito J., Noda K., Sudiro T.M., Sjahrurachman A., Warsa U.C., Yutsudo M., Hakura A.; "Cloning and characterization of human papillomavirus type 52 cervical carcinoma in Indonesia."; Int. J. Cancer 48:516-522(1991).

-!- FUNCTION: E7 protein has both transforming and trans-activeness.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X64085; CAA45434.1; -; mRNA.
PIR; A03689; W7WL33.
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
Transcription regulation.
Protein E7.
CHAIN
Protein E7.
                                                                                                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein E7.
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07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-1994,
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                                                                                                                                                                Transcription regulation. CHAIN 1 99
                                                                                                                                                                                                                                                                                                      EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                          "Primer-directed sequencing of human papillomavirus types."; Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=E7;
                                                                                                                                                                                                                                                      InterPro; IPR000148; Papvi_E7
                                                                                                                                                                                                                                                                                PIR; S36574; S3657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91258022; PubMed=1646174;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Delius H., Hofmann B.;
                                                                                                                                                                                                                DNA-binding; Early
                                                                                                                                                                                                                                   PF00527; E7;
                                                                                                                                                                                                                                                                                                 X74481; CAA52586.1; -; Genomic_DNA.
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AA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence version entry version 32
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91
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                                                                       96
11032 MW;
                                                                                                                                                                                                        protein; Oncogene;
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    56.9%;
57.1%;
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                                                                  Protein E7.

/FTId=PRO 0000133448.

C-XX-C motif-1.

C-XX-C motif-2.

C-XX-C motif-2.
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Pred. No. 1.
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C-XX-C motif-2.
    Score 294; DB 1; Pred. No. 2.2e-26;
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.6e-26;
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RESULT 41
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01-AUG-1992, sequence versi
07-FEB-2006, entry version
Protein E7.
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Ben-Saadon R., Fajerman I.,
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PubMed=15254040; DOI=10.10
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Kirii Y., Iwamoto S., Matsukura T.;
"Human papillomavirus type 58 DNA sequence.";
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NCBI_TaxID=10598;
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Viruses, dsDNA viruses, no
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DNA-binding; Barly protein;
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-!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
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KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK
                                                                   MRGNNPTLREYILDLHPEPTDLFCYEQLCDSSDEDEIGLDGPDGQAQPATANYYIVTCCY
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I., Ziv T., Hellman U.,
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                                                                                                                                                            16;
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                                                                                                                                                        Score 289.5;
Pred. No. 7.2e
6; Mismatches
                                                                                                                                                                                                                                                 Peptide (Met-Gly) (interchain with in ubiquitin) (by host).
D719984F3CF48D12 CRC64;
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C-XX-C motif-2.
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Q547M4;
24-MAY-2005,
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07-FEB-2006,
E7 protein.
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OSOCZ1;
O1-MAY-2000, integrated into Unil
O1-MAY-2000, sequence version 1.
O7-FEB-2006, entry version 17.
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GO; GO:00
SEQUENCE
NUCLEOTIDE SEQUENCE.
STRAIN=E6/E7-HK-1, E
E6/E7-HK-16;
                                                                                                                                                                                                                                     Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
NCBI_TaxID=10598;
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MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,
Cheung J.L.K., Cheng A.F.;
"Association of human papillomavirus type 58 variant with the risk of cervical cancer.";
J. Natl. Cancer Inst. 94:1249-1253(2002).
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Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10598;
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Chan P.K.S., Lam C.W.,
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                                                                                                                      Cheng A.F.;
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Li; AF478134; AAL85385.1; -; Genomic_DNA.
Li; AF478134; AAL85388.1; -; Genomic_DNA.
Li; AF478136; AAL85381.1; -; Genomic_DNA.
Li; AF478136; AAL85381.1; -; Genomic_DNA.
GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:000375; P:regulation of transcription, DNA-dependent;
GO:0006355; P:regulation of transcription, DNA-dependent;
GO:0006376; P:regulation of transcription, DNA-dependent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                               (OCT-1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             integrated into UniProtKB/TrEMBI
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                      E6/E7-HK-11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.0%;
57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      type 5
                                                                                               ដ
                                                                                                                                          Chan
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                                                                                               the
                                                                                                                                                                                                                                                                                                                     58.
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O RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                          RNA stage;
                                                                                               EMBL/GenBank/DDBJ
                                                                                                                                             м. у. м.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 289.5; DB z;
Pred. No. 7.2e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                         E6/E7-HK-14,
                                                                                                                                             Li W.W.H.,
                                                                                                                                                                                                                                                                                            Papillomaviridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                3
                         E6/E7-HK-15,
                                                                                                                                          Cheung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98
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                                                                                                                                             J.L.K.,
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F0 HPV58
QBQSF0;
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STRAIN=66/E7-HK-8;

MEDIXINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;

Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan Cheung J.L.K., Chang A.F.;

"Association of human papillomavirus type 58 variant with the recervical cancer.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus ty
Viruses; dsDNA viruses,
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EMBL; AF478132; AAL85377.1; -; Genomic DNA.
EMBL; AF478142; AAL85387.1; -; Genomic DNA.
EMBL; AF478146; AAL85391.1; -; Genomic DNA.
EMBL; AF478147; AAL85392.1; -; Genomic DNA.
EMBL; AF478147; AAL85390.1; -; Genomic DNA.
EMBL; AF478147; AAL85390.1; -; Genomic DNA.
EMBL; AF478145; AAL85390.1; -; Genomic DNA.
GO; GO:0005352; P:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, DN
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J. Natl. Cancer Inst. 94:1249-1253(2002).
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                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10598;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphapapillomavirus.
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                                                                                                                                                                                                                                          (BL; AF478139; AAL85384.1, 197, 200, 60:0005622; C:intracellular; 0; G0:0003700; F:transcription 0; G0:0006355; P:regulation of 00:0006355; P:regulation of 00:0006555; P:regulation of 00:0006555; P:
                                                                                                                                                                                 rPro; IPR000148;
; PF00527; E7; 1.
ENCE 98 AA; 10
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                                                    Similarity
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Conservative
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                                                                                                                                                                                                                                                                                                                                                             AAL85384.1; -; Genomic_DNA.
C:intracellular; IEA.
F:transcription factor activity;
                                                                                                                                                              10833 MW;
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56.1%;
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Score 286.5; DB:
Pred. No. 1.6e-25
7; Mismatches 29
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Pred. No. 9.4
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                                                                                                                                                                                          8248DD5321354CC9 CRC64;
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RESULT 45
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  RESULT 46
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ID QQQHQZ_H
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Matches 56
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O7-FEB-2006,
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QEQHN7;
01-JUN-2002;
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EMBL; AF478135; AAL85380.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=E6/E7-HK-3, and E6/E7-HK-4;
MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan i
Cheung J.L.K., Cheng A.F.;
"Association of human papillomavirus type 58 variant with the recervical cancer.";
NUCLEOTIDE SEQUENCE.
STRAIN=E6/E7-HK-17, and E6/E7-HK-18;
STRAIN=E6/E7-HK-17, and E6/E7-HK-18;
MEDLINE=221/6796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan
                                                                                                                                                                              Human papillomavirus type
Viruses; dsDNA viruses, no
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                                                                                                                         NCBI_TaxID=10598
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                                                                                                                                                         Alphapapillomavirus.
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GO:0006355; P:regulation of transcription, DNA-dependent;
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PF00527; E7; 1.
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ilarity 57.1%;
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       м. у.м.,
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Best Local (
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 Best Local Similarity
              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9QCZ2 HPV58
Q9QCZ2;
01-MAY-2000,
01-MAY-2000,
07-FEB-2006,
                                                                                                                                                                                                                               STRAIN=E6/E7-HK-2, and E6/E7-HK-6;
MEDLINE=22176796; PubMed=12189229; DOI=10.109
Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H.
Cheung J.L.K., Cheng A.F.;
"Association of human papillomavirus type 58
                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type s
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cervical cancer.";
J. Natl. Cancer Inst. 94:1249-1253(2002).
                                     SEQUENCE
                                                                                                                  EMBL;
                                                                                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                    cervical
                                                                                                                                                                                                                                                                                                                           Submitted (OCT-1999) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                Chan P.K.S., Lam C.W., Chan M.Y.M., Li W.W.H.,
                                                                                                                                                                                                                                                                                                                                                                STRAIN=E7-HK-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        E7 protein
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EMBL; AF478149; AAL85394.1; -; Genomic_DNA.
GO; GO:0005622; C:intraccellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; F:regulation of transcription, DN
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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"Association of human papillomavirus type
                                                                                                                              EMBL;
                                                                                                                                                                                                        J. Natl. Cancer Inst. 94:1249-1253 (2002).
                                                                                                                                                                                                                                                                                                                                        Cheng A.F.;
                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10598;
                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                 InterPro; IPR000148; Papvi
Pfam; PF00527; E7; 1.
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_HPV58
                                                                          L; AF192269; AAF13690.1; -; Genomic_DNA.
L; AF478133; AAL85378.1; -; Genomic_DNA.
L; AF478137; AAL85382.1; -; Genomic_DNA.
G0:0005522; C:intracellular; IEA.
G0:0003700; F:transcription factor activity; IEA.
G0:000355; P:regulation of transcription, DNA-dependent;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence version entry version 16
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10803 MW;
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55.0%;
                                        ME.
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Pred. No. 2.1e-25;
 Score 284.5; DB 2; Pred. No. 2.8e-25;
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                                        ED3C57B911355721
                                                                                                                                                                                                                                                                                                                                                                                                                               stage; Papillomaviridae;
                                                                                                                                                                                                                                                          DOI=10.1093/jnci/94.16.1249;
, Li W.W.H., Lo K.W.K., Chan
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                                        CRC64;
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RESULT 49
Q80SE8 HPV58
ID Q80SE8;
AC Q80SE8;
DT 01-UUN-2002, EDT 07-FEB-2006, EDT 07-FEB-2006, EDT 07-FEB-2011lon
OC Viruses; dsDNJ
OC Alphapapillon
OX NCBI_TAXID=10;
RN [1]
RN NUCLEOTIDE SEC
RC STRAIN=E6/E7-F
RX MEDLINE=22176;
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AC QQQSE9 H
AC QQQSE9 H
AC QQQSE9 T
DT 01-JUN-2
DT 07-FEB-2
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NUCLEOTIDE SEQUENCE.
STRAIN=E6/E7-HK-13;
MEDLINE=22176796; PubMed=12189229; DOI=10.1093/jnci/94.16.1249;
                                                                                                                                                                                                                                                 01-JUN-2002, integrated into U01-JUN-2002, sequence version 07-FEB-2006, entry version 16
                                                                                                                                              Human papillomavirus type 58. Viruses; dsDNA viruses, no Ri Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type 58.
Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
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QBQSE9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                 NCBI_TaxID=10598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7
Pfam; PF00527; E7; 1.
SEQUENCE 98 AA; 10833 MW; ED24DEA180BC4FA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J. Natl. Cancer Inst. 94:1249-1253(2002).
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Pred. No. 3.7e-25;
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Ol-MAY-2000, integrace version 01-MAY-2000, sequence version 01-MAY-2006, entry version 16.
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MEDLINE=99429608; PubMed=10501500;
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, DN
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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NCBI_TaxID=31552;
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Cheung J.L.K., Cheng A.F.;
"Association of human papillomavirus type
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Pfam, PF00527; E7; 1.
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                                                                                                                                                                                                                                                                                                                                                    JLT 52
HPV6B
                                                                                                                                                                          VE7_HPV6B
P06464;
01-JAN-1988,
01-JAN-1988,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VE7 HPV11 STANDARY,
P04020;
23-OCT-1986, integrated into UniProtKB/Swiss-Prot.
23-OCT-1986, sequence version 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUCLEOTIDE SEQUENCE [GENOMIC DNA].

Pife K.H., Fan L., Fritech M.H., Bryan J., Brown D.R.;

Pife K.H., Fan L., Fritech M.H., Bryan J., Brown D.R.;

Pife K.H., Fan L., Fritech M.H., Bryan J., Brown D.R.;

Pife K.H., Fan L., Fritech M.H., Bryan J., Brown D.R.;

Pifer M.H., Brown D.R.;

Submitted (OCT-1994) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: E7 protein has both transforming and trans-activating
Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; M14119; AAA46928.1; -; Genomic_DNA.
EMBL; L36108; AAA21704.1; -; Genomic_DNA.
PIR; A03690; W7WL11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activities.
-!- SIMILARITY: Belongs to the papillomaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                   Name=E7
                                                                                                                                             Protein E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00527; E7;
DNA-binding; Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=86181601; PubMed=3008427;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transcription
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCDSNVRLVVECTDGDIRQLQDLLLGTLNIVCPICAPKP, 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
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91
                                                                                                                                                                             sequence version entry version 37
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                                                                                                                                                                                                                                                      integrated into UniProtKB/Swiss-Prot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        regulation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10889 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.4%;
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                                                                           <u>6</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
                                    RNA stage; Papillomaviridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RNA stage;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 245; DB 1;
Pred. No. 1.3e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein E7.
/FTId=PRO_0000133410.
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AACA9A60C933E1F6 CRC64;
                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 98;
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                                                                                                                                                                                                                                                                                                                                                                                     RESULT 53
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Best Local S
Matches 52
                                                                                                                                                                                                                                                                                                                                                                      7_HPV6A
                                                                                                                   NUCLEOTIDE SEQUENCE (GENOMIC DNA).

MEDILINE=95.97152; PubMed=7778283;

Hofmann K.J., Cook J.C., Joyce J.G., Brown D.R., Schul-
George H.A., Rosolowsky M., Fife K.H., Jansen K.U.;

"Sequence determination of human papillomavirus type 6,

"Sequence determination of Saccharomyces cerevisiae.";

"Irology 209:506-518(1995).

"Irology 209:506-518(1995).
                                                                                                                                                                                                                                                                                                                                                 VE7_HPV6A
Q84292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type 6b.
EMBO J.
                                                                                                                                                                                                                                                                                                            15-JUL-1998, integrated into UniProtKB/Swiss-Prot. 01-NOV-1996, sequence version 1. 07-FEB-2006, entry version 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=84131949; Pubmed=6321162;
MEDLINE=84131949; Pubmed=6321162;
Schwarz E., Durst M., Demankowski C., Lattermann O., Zech R.,
Wolfsperger E., Suhai S., Zur Hausen H.;
"DNA sequence and genome organization of genital human papillomavirus
Pfam; PF00527
DNA-binding;
                                    EMBL; L41216; AAA74212.1; -; Genomic
                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                              Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
                                                                                                                                                                                                                                                                                      Name=E7;
                                                                                                                                                                                                                                                                                               Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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1 98 Protein E7.
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                                                                                      -!- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA-binding; Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Belongs to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10600;
                         InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                              CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                                                                                                                                                                                                                           CGCDSNVRLVVQCTETDIREVQQLLLGTLNIVCPICAPK 97
                         IPR000148;
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10887
  protein; Oncogene; Transcription;
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52.5%;
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o RNA
                         E7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 243;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           997CB5095A39C4CD
                                                                                                                                                                                                                                                           stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                      DNA.
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3.2e-20;
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                                                                                                                          and trans-activating
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RESULT 55
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Best Local S
Matches 48
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Best Local (
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7 HPV34
VE7 HPV34
P36828;
01-JUN-1994,
                                                                                                                                                                              MOTIF
MOTIF
SEQUENCE
                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
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                                                                                                                                                                                                                                                                                            EMBL ;
                                                                                                                                                                                                                                                                                                                                                    -
                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE [GENOMIC DNA]
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein E7.
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                                                                                                                                                                                                                                             DNA-binding; Early protein; Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                   "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-!- FUNCTION: E7 protein has both transforming and trans-activating
                                                                                                                                                                                                                                                                                                                                                                                                       Delius H., Hofmann B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=333764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOTIF
                                                                                                                                                                                                                         Transcription regulation.
                                                                                                                                                                                                                                                                                                                                             activities.
SIMILARITY: Belongs to the papillomaviruses E7
                                                                                                                                                                                                                                                                               ; X74476; CAA52556.1; -; Genomic_DNA.
S36516; S36516.
                                                                                                                                                                                                                                                           PF00527; E7; 1.
                                               59
                                                                   60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59
                                                                                                                                     48;
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                        MHGDTPTLHEYMLDLQPET-TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHGDTPTLHEYMLDLQ-PETTDLYXYXQLNDSSEEE-DEIDGPAGQAEPDRAHYNIVTFC 58
                                               RCQSTVCLTIESTHADLLVLEDLLMGALKIVCPNCSRR 96
                                                                   KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGCDSNVRLVVQCTETDIREVQQLLLGTLDIVCPICAPK 97
                                                                                          MHGKKPSVQDIVLDLKPTTETDLTCYESL-DNSEDEDETDSHL-ERQAEQAWYRIVTDCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC
                                                                                                                                                                                                                                                                   IPR000148; Papvi_E7.
                                                                                                                                                                                 97
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                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                57
90
7 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry version 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         integrated into UniProtKB/Swiss-Prot.
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91
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                                                                                                                                                                                 10985 MW;
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93
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94
                                                                                                                                               43.0%;
49.0%;
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52.5%;
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o RNA stage;
                                                                                                                                      18;
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                                                                                                                                     Score 222.5;
Pred. No. 5.5e
18; Mismatches
                                                                                                                                                                                         /FTId=PRO_0000133432.
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 242; DB 1;
Pred. No. 2.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protein E7.
/FTId=PRO_0000133404.
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                          Protein E7.
                                                                                                                                                                                19E3C9D1F12BF4F6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      997CBDAB5A39C4CD CRC64;
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                                                                                                                                     i.5e-18;
ies 29;
                                                                                                                                                        DB 1;
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RESULT 56
091194 HPV16
091194 HPV16
ID 091194;
AC 091194;
DT 01-DEC-2001, integrated into UniProtKB/TrEMBL
DT 01-DEC-2001, sequence version 1.
DT 01-DEC-2006, entry version 12.
DE Truncated E7 protein.
                                                                              SON BERGCOCCEPAN X OOC DETENDED ACC
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Best Local Similarity
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Best Local :
                          Query Match
                                                                                                 Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AY057438; AAL14205.1; -; Genomic_DNA.
GO; GO:0005522; C:intracellular; IEA.
GO; GO:000370; F:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, DY
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
Zhao M., Wu X.X., Ding X.H.;
Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                            SEQUENCE
                                                                                                                                                GO; GO:0005622; C:intracellular; IEA.

GO; GO:0003700; F:transcription factor activity;
GO; GO:0006355; P:regulation of transcription, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human papillomavirus type
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Terai M., Burk R.D.;
"Identification and characterization of 3 novel genital human papillomaviruses by overlapping polymerase chain reaction: candHPV89,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Putative transforming protein E7.
Human papillomavirus - cand90.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q8JNAO_9PAPI
Q8JNAO;
                                                                                                                                                                                                                            EMBL; AF393782; AAK84003.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                              Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                         Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          candHPV90,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
MEDLINE=22079881; PubMed=12085327; DOI=10.1086/340824;
                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=333760;
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                                                                                                   PF00527; E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MHGDTPTLHEYMLDL-QPETTDLYXYXQLNDSSEEEDEIDG--PAGQAEPDRAHYNIVTF
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45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHGQRPTLKDIFLELDQPDAVDLHCNEQLASSEEEDNREDGEQPTQPTEPAQQAYRVVTS
                                                                                                                           IPR000148;
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Dis. 185:1794-1797(2002).
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                                                                    1.
4903 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10944 MW;
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42.7%;
95.3%;
                                                                                                                           Papvi_E7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no RNA stage; Papillomaviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RNA stage; Papillomaviridae;
Score
Pred.
                                                                            19A57D4E52FB14D6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 221.5; DB 2
Pred. No. 7.4e-18;
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221;
No. :
3.1e-18;
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                                                                                                                                                        DNA-dependent;
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                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98
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                            43;
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RESULT 57

VET RHPV1

VET RHPV1

AC P2216

PT 01-AI

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

DT 07-F1

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DT 07-F1

CC ---

CC C---

CC
RESULT 58

Q9WHG1 9PAPI
ID Q9WHG1,
AC Q9WHG1;
DT 01-NOV-1999, integrated into UniProtKB/TrEMBL.
DT 01-NOV-1999, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE Putative transforming protein E7.
OS Human papillomavirus - cand85.
OC Viruses; daDNA viruses, no RNA stage; Papillomav OC Alphapapillomavirus.
OX NCBI TaxID-151757;
RN [1]
RP NUCLEOTIDE SEQUENCE.
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Matches
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01-AUG-1991,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VE7_RHPV1
P22161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; M60184; AAA79312.1; -; Genomic_DNA.
PIR; B38503; W7WLR1.
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ostrow R.S., Labresh K.V., Faras A.J.;
"Characterization of the complete RhPV 1 genomic sequence integration locus from a metastatic tumor.";
Virology 181.424-429(1991).
-!- FUNCTION: E7 protein has both transforming and trans-
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Viruses; dsDNA viruses, no
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MEDLINE=91135018; PubMed=1847267;
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NA-binding; Early protein; Oncogene; Transcription;
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113 AA;
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13; Mismatches
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/FTId=PRO 0000133470.

C-XX-C motif-1.

C-XX-C motif-2.
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                                                                                                      Papillomaviridae;
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RESULT 59
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P21736;
01-MAY-1991,
01-JUN-1994,
07-FEB-2006,
Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Delius H., Hofmann B.; "Primer-directed sequencing of human papillomavirus types."; Curr. Top. Microbiol. Immunol. 186:13-31(1994).
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                                                                                                                           EMBL; X74479; CAA52574.1; -; Genomic_DNA.
EMBL; M38198; AAA46974.1; -; Genomic_DNA.
PIR; S36562. $35562.
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE [GENOMIC DNA].
Kaplan J.B., Burk R.D.;
Submitted (AUG-1990) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus type
Viruses; dsDNA viruses, no
Alphapapillomavirus.
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                                                                                                                                                                                                                                                           Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
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DNA-binding; Early protein;
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                             Transcription regulation.
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GO:0006355; P:regulation of transcription, DNA-dependent;
erPro; IPR000148; Papvi_E7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.

Sastre-Garau X., Favre M., Couturier J., Orth G.;

"Distinct patterns of alteration of myc genes associated with integration of human papillomavirus type 16 oe type 45 in two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1999, integrated into u
01-NOV-1999, sequence version
07-FEB-2006, entry version 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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Q9Y4Y3;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE SEQUENCE
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Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
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G0:0005622; Cintracellular; IEA.
G0:0003700; Fitranscription factor activity
G0:0006355; P:regulation of transcription,
                                                                                                                                                                                                                                                                                                                                                                                                 Pro; IPR000148;
PF00527; E7; 1
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      PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                       Papvi_E7
                                                                                                                                                                                                                                                                                    41.0%; Score 212; DB 2;
43.8%; Pred. No. 1.1e-16;
tive 15; Mismatches 32
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Pred. No. 8.1e-17;
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C-XX-C motif-2.

G -> E (in Ref. 2).

R -> Q (in Ref. 2).

4C53808A7285AD41 CRC64;
      PRT;
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factor activity, I&A.
DNA-dependent;
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Q8B5W9;
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01-JUL-1997,
01-JUL-1997,
07-FEB-2006,
            Pfam;
  SEQUENCE
                                    EMBL; AF436130; AAO15456.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                     Terai M., Burk R.D.; Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                  Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                   01-MAR-2003, sequence versi
07-FEB-2006, entry version
                                                                                                  Copyrighted by the UniProt Consortium, see http://www.uniprot.org/to
                                                                                                                                                                                     NCBI_TaxID=44028;
                                                                                                                                                                                                                           Human papillomavirus type
                                                                                                                                                                                                                                     Putative transforming protein E7.
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GO; GO:0006355; P:regulation of transcription,
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NCBI_TaxID=10593;
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            Pro; IPR000148; Papvi
PF00527; E7; 1.
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sequence version 1.
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43.8%;
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Query Match

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Matches 47
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Matches 4
                                                            77_HPV53

VB7_HPV53

P36832;

01-JUN-1994, 1

01-JUN-1994, 8

07-FEB-2006, e
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VB7 HPV30
VB67826;
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MOTIF
SEQUENCE
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CHAIN 1 105 Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA]. MEDLINE=94265501; PubMed=8205838;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activities.
-!- SIMILARITY: Belongs to the papillomaviruses E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Primer-directed sequencing of human papillomavirus types.";
Curr Top. Microbiol. Immunol. 186:13-31(1994).
-1- FUNCTION: E7 protein has both transforming and trans-act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Delius H., Hofmann B.;
                         Name=E7;
                                           Protein E7.
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S36504; S36504.
papillomavirus
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47; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PF00527; E7;
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                                                                                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPET-TDLYXYXQLNDSSEE-EDEIDG---PAGQAEPDRAH--YN
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                                                         sequence version entry version 32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /FTId=PRO 0000133428.
C-XX-C motif-1.
C-XX-C motif-2.
; 6166758B14B44D67 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 209.5; DB 1; Length Pred. No. 2.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein E7
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                               EMBL; Y15175; CAA75464.1; -; Genomic DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity
GO; GO:0006355; P:regulation of transcription,
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
NUCLEOTIDE SEQUENCE.
MEDLINE=98118461; PubMed=9454709; DOI=10.1006/viro.1997.8943;
Delius H., Saegling B., Bergmann K., Shamanin V., de Villiers
The genomes of three of four novel HPV types, defined by dif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47_9PAPI
056947_9
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                                                                                                                                                                               Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                 Alphapapillomavirus.
NCBI_TaxID=69986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E7 protein
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Transcription regulation.
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NCBI_TaxID=333765;
  SEQUENCE
                                                                                                                                                                                                                                                      Virology
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Curr. Top. Microbiol. Immunol. 186:13-31(1994).
                          Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000148; Papvi_E7.
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  PF00527; E7;
NCE 90 AA;
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12162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNA stage; Papillomaviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 208.5; 1
Pred. No. 2.7e
23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein E7.
/FTId=PRO 0000133449
C-XX-C motif-1.
C-XX-C motif-2.
  ABAB4EADABACF33B CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEA7E2E8D0C1F7EC
                                                                                        factor activity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.7e-16;
hes 29;
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ed by differences
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Query Match

Score 207.5;

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Best Local 9
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                                                                                                                                                                                                                                    908 9PAPI
Q6EGQ8 9PAPI
Q6EGQ8;
16-AUG-2004,
16-AUG-2004,
07-FEB-2006,
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006_HPV73
082006_HPV73
082006;
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=120686;
[1]
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MEDLINE=96213783; PubMed=8635859;

DOI=10.1002/(SICI)1097-0215(19960516)66:4<453::AID-IJC7>3.0.CO;2-V;

Voelter C., He Y., Delius H., Roy-Burman A., Greenspan J.S.,

Greenspan D., de Villiers E.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X94165; CAA63883.1; -; Genomic_DNA.
GO; GO:0005622; C::Intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus type 73.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Novel HPV types present in oral papillomatous with HIV infection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-FEB-2006, entry version 20. E7 protein.
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                                                                                                                                Human papillomavirus type 71.
                                                                                                                                                                           Name=E7;
                                                                                                                                                                                                       Putative transforming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KCQCTVCLAIESNKADLRVIEELLMGTLGIVCPNCSR
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                                                                                                                                                                                                                                           entry version
13
                                                                                                                                                                                                                                                                                                                   integrated into UniProtKB/TrEMBL
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                                                                                                   RNA stage;
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Pred. No. 3.
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                                                                                                   Papillomaviridae;
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QZVJC6;
                                                                                                      EMBL; DQ080082; AAZ39514.1; SEQUENCE 95 AA; 10541 MW
                                                                                                                                                                                                                                                                                                               PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510. Narechania A., Chen Z., Desalle R., Burk R.D.; "Phylogenetic Incongruence among Oncogenic Genital Papillomaviruses."; J. Virol. 79:15503-15510(2005).
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EMMBL; AY330623; AAQ95199.1; -; Genomic_DNA.
EMBL; AY330620; AAQ95178.1; -; Genomic_DNA.
EMBL; AY330620; AAQ95178.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity
GO; GO:00003755; P:regulation of transcription,
                                                                                                                                                                                                                Distributed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Qv28897
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                                                                                                                                                                                                            under the Creative Commons
                                                                                                                                                                                                                                                 by the UniProt Consortium,
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7_HPV29
VE7 HPV29
P50784;
01-OCT-1996, 4
01-FEB-2006, 6
                                                                                                                                                 ULT 70
1_HPV18
VE7_HPV18
P06788;
Human papillomavirus type
Viruses; dSDNA viruses, n
Alphapapillomavirus.
NCBI_TaxID=333761;
                                                                       01-JAN-1988,
01-APR-1990,
07-PEB-2006,
Protein E7.
Name=E7;
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SEQUENCE
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Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human papillomavirus type 29.
Human papillomavirus type 29.
Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
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Pred. No. 6.7e
l2; Mismatches
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/FTId=PRO 00001
C-XX-C motif-1.
C-XX-C motif-2.
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RESULT 71
Q6FGF1 HUMAN
ID Q6FGF1,
AC Q6FGF1;
DT 05-JUL-2004,
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EMBL; X05015; CAA28665.1; -; Genomic_DNA.
EMBL; M20324; AAA99513.1; -; mXNA.
EMBL; M20325; AAA99515.1; -; mRNA.
EMBL; M26798; AAA46947.1; -; Genomic_DNA.
EMBL; X04773; CAA28467.1; -; Genomic_DNA.
EMBL; X04773; CAA28467.1; -; Unassigned_DNA.
EMBL; A06324; CAA00540.1; -; Unassigned_RNA.
EMBL; A06328; CAA00543.1; -; Unassigned_RNA.
PIR; B26165; W7WL18.
FIRETPO; IPR000148; Papvi_E7.
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MEDLINE=87283882; PubMed=3039146;
Cole:S.T., Danos O.;
"Nucleotide sequence and comparative analysis of the human "Nucleotide sequence and comparative despillomavirus papillomavirus type 18 genome. Phylogeny of papillomaviruses repeated structure of the E6 and E7 gene products.";
J. Mol. Biol. 193:599-608(1987).
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MEDLINE=87218459; PubMed=3034571;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE [GENOMIC DNA] MEDLINE=87053870; PubMed=3023067;
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MEDLINE=88188247; PubMed=2833614;
Inagaki Y., Tsunokawa Y., Takebe I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription patterns of human papillomavirus
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                                                                                                                                                                                                                                                                                                               Similarity 42; Conserv
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HTMLCMCCKCEARIKLVVESSADDLRAFQQLFLNTLSFVCPWCASQ
                                               MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
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98
73
105 AA;
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C-XX-C motif-1.
C-XX-C motif-2.
C-XX-B (in Ref. 1 and K -> B (in Ref. 1)
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2CDB119534D0186A CRC64;
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RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soarce M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Raha S.S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Richards J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Willalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Wilting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Wilting M., Madan A., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
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Best Local S
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                                                                                      SULT 72
7 HPV13
VE7 HPV13
V02271;
01-APR-1993, 1
01-APR-1993, 8
07-FEB-2006, 6
                            Protein E7. Name=E7;
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Pfam; PF00527; E7; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
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07-FEB-2006,
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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papillomavirus
                                                                                                                                                                                                                                                                                                                                                                         59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
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                                                                                      sequence version
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type
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Pred. No. 1.4e
21; Mismatches
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ches 32;
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Attribution-NoDerivs License
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RESULT 73
Q76296 HPV18
ID Q76296;
AC Q76296;
DT 10-MAY-2005, 6
DT 10-FEB-2006, 6
DT 07-FEB-2006, 6
DT 10-MAY-2005, 6
DT 10-MAY-2005, 6
DT 10-MAY-2005, 6
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Best Local
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SEQUENCE
                                            "Small tumor virus genomes are integrated attachment regions in transformed cells.", J. Virol. 75:12339-12346(2001).
                                                                                                                MEDLINE=21568387; PubMed=11711624; DOI=10.1128/JVI.75.24.12339-12346.2001; Shera K.A., Shera C.A., McDougall J.K.;
                                                                                                                                                                                                                                                Narechania A., Chen Z., Des "Phylogenetic Incongruence Papillomaviruses.";
                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE.
PubMed=16306621; DOI=10.1128/JVI.79.24.15503-15510.2005;
Narechania A., Chen Z., Desalle R., Burk R.D.;
Narechania A., Chen Z., Desalle R., Burk R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                        Human papillomavirus
Viruses; dsDNA viruse
Alphapapillomavirus
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PIR; B42955; W7WL13.
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                                                                                                                                                                                    NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=333761;
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MEDLINE=92391075; PubMed=1325697;
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NCBI_TaxID=10573;
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44.7%;
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    Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 200.5; DB 1
Pred. No. 2.3e-15;
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C-XX-C motif-1.
C-XX-C motif-2.
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RESULT 74
QGEGQ1 9PA
ID EGGQ1
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AC QGEGQ
DT 16-AI
DT 07-F
DE PUTA
OC HUMBA
OC VITU
OC Alpi
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RESULT 75
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ID Q9QNI
AC Q9QNI
DT 01-M2
DT 01-M2
DT 07-F1
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Best Local S
Matches 42
1P7_HPV18

Q9QNP7_HPV18

Q9QNP7;

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01-MAY-2000,

07-FEB-2006,

E7_protein.
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EMBL; AF339139; AAL34458.1; -; Genomic_DNA.
GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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88,68
88,74
88,88
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16-AUG-2004, sequence versi
07-FEB-2006, entry version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 94 AA; 10499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Putative transforming protein E7. Human papillomavirus type 71.
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Fu L., Burk R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=120686;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L, AY330622; AAQ95192.1; -; Genomic_DNA.
GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-de
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                                                                                                                               PRELIMINARY;
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                             version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.6%; Score 199.5; DB 2;
43.6%; Pred. No. 2.7e-15;
43.6%; Mismatches 37;
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39.6%; Pred. No. 2.4e-15;
tive 20; Mismatches 33
                                                      version
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0003755; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
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NUCLEOTIDE SEQUENCE.
MEDLINE=89259065; PubMed=2542593;
MEDLINE=89259065; PubMed=2542593;
                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/toDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                          Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases.
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Matsukura T., Delius
Submitted (JAN-2004)
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J. Virol. 63:2829-2834(1989)
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Alphapapillomavirus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10591;
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NCE 105 AA; 12010 MW; 24799BB534D4496A CRC64;
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the EMBL/Ge
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                                                                           see http://www.uniprot.org/terms
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Schmidt B.
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RESULT 78
Q81965 HPV59
ID Q81965 HPV59
AC Q81965;
DT 01-NOV-1996;
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OJONP6;
O1-MAY-2000, integrated into 1
O1-MAY-2000, sequence version
O7-FEB-2006, entry version 14
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GO; GO:0003700; F:transcription facto
GO; GO:0006355; P:regulation of trans
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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Laassri M., Gul'ko L.,
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Viruses; dsDNA viruses, no RN
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Veiko V.P.
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GG:0005622; C:intracellular; IEA.
GO:0003709; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
erPro; IPR000148; Papvi_E7.
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                                                                                                                                                                                                                                                                                                                                                                                 42;
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                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                              HTMLCMCCKCEARIELVVESSADDLRAFQQLFLKTLSFVCPWCASQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAH-YNIVTFCC 59
                                                                                                                                                                                                                             YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                          WHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHGKKPTIRDYVLTMQPEPRSLTCNEQL-DSSDSEDEREQPTQQDQQVNLQVYRVVTECT
                                                                                                                                                                                                                                                                                 MHGPKATLQNIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
  integrated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               integrated into UniProtKB/TrEMBL
                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.3%;
                                                                                                                                                                                                                                                                                                                                                                                                        38.0%; Score 196.5; 39.6%; Pred. No. 7e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vinokurova
       into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     no RNA stage;
                                                                                                                                                                                                                                                                                                                                                                              19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 198; DB 2
Pred. No. 4.4e-1
L4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 7e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of transcription,
     UniProtKB/TrEMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CAE98EACB2C34EE3
                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C4979555DAD4A960 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human
                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor activity;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Papilloma Virus Type 18 and its Mutants.";
                                                      107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kisseljova N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Papillomaviridae,
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                                                                                                                                                                                                                                                                                                                                                                              34;
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VE7_PCP
ID VE
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Best Local
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                                                    [nterPro;
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VE7_PCPV1
Q02272;
Q1-APR-1993,
Q1-APR-1993,
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NUCLEOTIDE SEQUENCE.

MEDLINE=94303229; PubMed=8030272;

POY-Burman A., Kim H., de Villiers E.-M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-FEB-2006, entry version ORF putative E7 protein. Name=ORF putative E7; Human papillomavirus type EViruses; dsDNA viruses, no
                                                                                                                                                                                           "Human papillomavirus type 13 and pygmy chimpanzee 1: comparison of the genome organizations."; Virology 190:587-596(1992).
-!- FUNCTION: E7 protein has both transforming and
                                                                                                                                                                                                                                                                        van Ranst M., Fuse A., Fiten P., Beuken Opdenakker G.;
                                                                                                                                                                                                                                                                                                                                                                                       Pygmy chimpanzee papillomavirus type: Viruses; dsDNA viruses, no RNA stage; Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-FEB-2006,
Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Nucleotide sequence and phy
papillomavirus type 59.";
Virology 203:158-161(1994).
                                                            EMBL; X62844; CAA44656.1; -;
                                                                                              Copyrighted by the UniProt Consortium, see http://www.unipro
                                                                                                                                                                                                                                                                                                          MEDLINE=92391075; PubMed=1325697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=37115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996, sequence version 07-FEB-2006, entry version 21.
Pfam; PF00527;
DNA-binding; E:
                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alphapapillomavirus.
                                                                                                                                                       -I- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR000148; Papvi_E7.
                                                                                                                                                                             activities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF00527; E7; 1.
NCR 107 AA; 12042 MW; A8F2B6973D727163 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --HNIVCVCCKCNNQLQLVVETSQDGLRALQQLFMDTLSFVCPLCA 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WHGDTPTLHEYMLDLQP---ETTDLYXXXQL--NDSSEEEDEIDGP----AGQAEPDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHGPKATLCDIVLDLEPQNYEEVDLVCYEQLPDSDSENEKDEPDGVNHPLLLARRAEPQR
                                        IPR000148; Papvi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
      Early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entry version 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD
  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17;
                                          E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RNA stage; Papillomaviridae;
  Oncogene; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 9.4e
7; Mismatches
                                                            Genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 195.5;
Pred. No. 9.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                            DNA.
                                                                                                                                                                                                                                                                                                                                                                                           1.
; Papillomaviridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                  see http://www.uniprot.org/terms
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                                                                                                                                                                                                                                                                                            Pfister H.,
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                                                                                                                                                                                               and trans-activating
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                                                                                                                                                                                                                                                      papillomavirus type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
                                                                                                                                                                                                                                                                                            Burk R.D.,
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                                                                                                  License
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RESULT 81
Q885X6_HPV54
ID Q885X6;
AC Q885X6;
DT 01-MAR-2003, 6
DT 07-FEB-2006, 6
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Shera K.A., Shera C.A., McDougall J.K.;
"Small Tumor Virus Genomes Are Integrated near Nuclear Matrix
Attachment Regions in Transformed Cells.";
J. Virol. 75:12339-12346(2001).
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Viruses; dsDNA viruses, no
Alphapapillomavirus.
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E7 protein.
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activit;
GO:0006355; Piregulation of transcription,
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00527; E7; 1.
105 AA; 12
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tive 21; Mismatches
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C-XX-C moTif-1.

C-XX-C moTif-2.
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EMBL; Y18455; --
GO; GO:0005622;
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                                                                                                                                                                                                                                         "Cloning of E6 and E7 Genes of Transformation Potential of E7 Virus Genes 182:139-149(1999).
                                                                                                                                                                                                                                                                                                          Laassri M.,
Kisseljev F.
                                                                                                                                                                                                                                                                                                                                                                                                                         Human papillomavirus type 1 Viruses; dsDNA viruses, no Alphapapillomavirus
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01-MAY-2000,
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Narechania A., Chen Z., DeBalle R., Burk R.D.;
"Phylogenetic Incongruence among Oncogenic Genital Alpha
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Veiko V.P.,
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity;
GO:0006355; P:regulation of transcription, DN
                                 Y18493; CAB53099.1; -; Genomic_DNA.
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                                                                          by the UniProt Consortium, see http://www.uniprot.org/terms under the Creative Commons Attribution-NoDerivs License
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in Evolution; Genomic sequence of AE9,
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            C:intracellular;
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                                                                                                                                                                                                                                                                                                                                  Vinokurova S., Kisseljova N., Veiko
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                                                                                                                                                EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   stage; Papillomaviridae;
                                                                                                                                                                                                                                                                 Gene
                                                                                                                                                                                                                                                                                       Human Papilloma Virus Type 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oncogenic Genital Alpha Human
                                                                                                                                                                                                                                                                 and its Mutants.";
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RESULT 84
Q21283 HPV13
ID Q21283 HPV13
AC Q21283;
DT 07-MAR-2006, i
DT 07-MAR-2006, e
DT 07-MAR-2006, e
DE E7.
GN Name=E7;
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OBJUTG/J

ID JGG/G

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Best Local
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'G7_9PAPI
Q8JTG7_9PAPI
Q8JTG7;
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GO; GO:0005622; C:intracellular; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human papillomavirus - (
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI TaxID=202252;
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GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
SEQUENCE 105 AA; 11952 MW; 247BF448A6BBB4FA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Identification and characterization of 3 novel genital human papillomaviruses by overlapping polymerase chain reaction: car
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
MEDLINE=22079881; Pu
Terai M., Burk R.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002,
01-OCT-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  candHPV90, and candHPV91.";
J. Infect. Dis. 185:1794-1797(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQ-AEPDRAHYNIVTFCC 59
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                                                                                                                                                                                                                                                                                                                                      SCYCSIRLVVKCSSSDIKTLEELLLGTLQIVCPLCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          MYGKEPTLRDYVLTLQPEPRSLTCDEQL-DSSDSEDEREQSTQQDQQVDLQVYKVVTECT
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                                                                    entry
                                                                                       sequence version
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                                                                    version
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Pred. No. 2.7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 191; DB 2;
Pred. No. 2.9e-14;
                                                                                                                                                                                     PRT;
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RESULT 85
Q98005_9PAPI
ID Q98005_9PAPI
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Best Local &
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GO; GO:0003700; F:transcription factor activity; IBA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent;
InterPro; IPR00148; Papvi_E7.
Pfam; PP00527; E7; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                   Longuet M., Cassonnet P., Orth G.;
"A novel genital human papillomavirus (HPV),
immunosuppressed patients.";
J. Clin. Microbiol. 34:1859-1862(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
MEDLINE=96379050; PubMed=8784613;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus ty
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E7 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1997, integrated into 0
01-FEB-1997, sequence version
07-FEB-2006, entry version 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human papillomavirus type 13.
Viruses; dsDNA viruses, no RN
Alphapapillomavirus.
NCBI_TaxID=10573;
                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                Copyrighted by the UniProt Consortium, see http://www.uniprot.org/termsDistributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alphapapillomavirus.
NCBI_TaxID=44028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q98005;
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Distributed
                                                                                                                                                                                                                                                                                                                             EMBL; U40822; AAC55128.1; -; Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (DEC-2005) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amazon."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
Borborema-Santos C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Sequencing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DQ344807; ABC79058.1; -; Genomic DNA. NCE 98 AA; 10738 MW; 97D6627CB7CF8
                                  60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          58
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                                                                                                                                            45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRA----HYNIVTF
                                                                                                                                                             Similarity
                                                                                                    MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH-YNIVTFCC
                                  KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK
VCNRSLRLVVQCTGPDINNLHTLLLGTLNLVCPLCAPK
                                                                    WHGKYSTLKEIVLELQPDPVGLHCNEQLDSSEEEVDEL---ATQATQQLTQAYQIVTCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CSKCCSNVRLVVECTGPDIHDLHDLLLGTLNIVCPLCAPK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHGQYTTLKDIVLDLTPDPVGLHCNEQLDSS---EDEVDEQATQATQHSTLLQCYQILTS
                                                                                                                                                                                                                 96 AA;
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                                                                                                                                                                                                                   10522 MW;
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45.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74
                                                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 190; DB 2;
; Pred. No. 3.8e-14;
12; Mismatches 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA stage; Papillomaviridae,
                                                                                                                                          Score 189; DB
Pred. No. 4.8e
12; Mismatches
                                                                                                                                                                                                                   8DF8480CEE5CCEA3 CRC64;
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                                                                                                                                                               .8e-14
                                                                                                                                                                                DB 2;
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3 isolated in the
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98
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                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                           74,
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                                                                                                                                            Gaps
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                                                                        57
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RESULT 87
VE7 HPV42
ID - VE7 H
AC P2723
DT 01-AU
DT 07-FE
DE Prote
GN Name=
OS Human
OC Virus
OC Alpha
OX NCBI
RN [1]
RN [1]
RN MUCLI
RN MEDLI
RA Phili
RT "Hum
RT organ
RT organ
RT viro;
CC -1-|
CCC -1-|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VE7_HPV28
ID VE7 H
AC P5078
AC P5078
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Best Local S
Matches 43
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VE7 HPV28

P50783;

01-OCT-1996,

01-OCT-1996,

07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                           VE7_HPV42
P27231;
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SEQUENCE
                                                                                                                                                                                                                                     Human papillomavirus ty,
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10590;
                                                                                                                                                                                                                                                                                                                                                                           01-AUG-1992,
07-FEB-2006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=37111;
                                                                  Virology 186:331-334(1992).
                                                                                                                            NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=92087479; PubMed=1309278;
Philipp W., Honore N., Sapp M., Col
"Human papillomavirus type 42: new
                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1992, integrated into UniProtKB/Swiss-Prot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   activities.
-!- SIMILARITY: Belongs to the papillomaviruses E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases --- FUNCTION: E7 protein has both transforming and trans
                                                                                                            organization.";
                                                                                                                                                                                                                                                                                                                                 Name=E7
                                                                                                                                                                                                                                                                                                                                                        Protein E7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOTIF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U31783; AAA79423.1; -;
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Viruses; dsDNA viruses, no RNA stage;
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DNA-binding; Early
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                         SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                        sequence version entry version 31
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83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
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                      Belongs to the papillomaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53
86
9625 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein;
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44.8%;
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                                                                                                                                                                                                                                                                      2 42.
                                                                  has both transforming
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/FTId=PRO_0000133426.

C-XX-C motif-1.

C-XX-C motif-2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 186; DB 1;
Pred. No. 9.7e-14;
1; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genomic_DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4A3692CED16BCD60 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                      вtage;
                                                                                                                                                       Cole
                                                                                                                                le S.T., Streeck R.E. sequences, conserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription;
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                                                                                                                                                                                                                                                                                      Papillomaviridae;
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                                                                  and
                      E7
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                    protein family.
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RESULT 88
VE7_HPV66
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Query Match
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Q80956;
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SEQUENCE
                                    MOTIF
                                                                          EMBL; M75123; -; NOT ANNOTATED CDS; Genomic_DNA.

EMBL; U31794; AAA79500.1; -; Genomic_DNA.

IRE B44890; B44890.

InterPro; IPR000148; Papvi_E7.

Pfam; PF00527; E7; 1.

DNA-binding; Early protein; Oncogene; Transcription;

Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                                               Human papillomavirus tyn
Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=37119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1998, integrated into UniProtKB/Swiss-Prot. 01-NOV-1996, sequence version 1. 07-FBB-2006, entry version 30.
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Pfam; PF00527; E7; 1.
DNA-binding; Early protein; Oncogene; Transcription;
Transcription regulation.
CHAIN
Protein E7.
                       SEQUENCE
                                                                    CHAIN
                                                                                                                                                                            Copyrighted by the UniProt Consortium, see http://www.uniprot.org/t.
Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                              Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
-- FUNCTION: E7 protein has both transforming and trans-activating activities.
-- SIMILARITY: Belongs to the papillomaviruses E7 protein family.
                                                                                                                                                                                                                                                                                                 carcinoma of the uterine cervix. J. Clin. Microbiol. 29:2656-2660
                                                                                                                                                                                                                                                                                                                      Tawheed A.R., Beaudenon S., Favre M., Orth "Characterization of human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein E7.
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PIR; F39451; W7WL42.
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                                                                                                                                                                                                                                                              Delius H.;
                                                                                                                                                                                                                                                                          NUCLEOTIDE SEQUENCE [GENOMIC DNA].
                                                                                                                                                                                                                                                                                                                                                            NUCLEOTIDE SEQUENCE [GENOMIC DNA].
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                       105
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86
AA;
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89
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 35.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                           RNA stage;
                                 /FTId=PRO_0000133459.
C-XX-C motif-1.
C-XX-C motif-2.
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C-XX-C motif-1.
C-XX-C motif-2.
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Pred. No. 2.1e-13
 Score 183.5;
                                                                    Protein E7.
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                       C09339F42F62AFFA CRC64;
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                                                                                                                                                                                                                                                                                                                                    Orth G.;
                                                                                                                                                                                                                                                                                                                                                                                                           Papillomaviridae;
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Length 105;
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RESULT ID 7386

ID 7386

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                                                                                                                                                                                                                                                                SULT 90
7 HPV54
0081019;
15-JUL-1998, 3
01-NOV-1996, 6
07-FEB-2006, 6
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037386_CCPV1
037386;
01-JAN-1998,
01-JAN-1998,
07-FEB-2006,
                  Submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases -i- FUNCTION: E7 protein has both transforming and trans
                                                                                                                                                      Viruses; dsDNA viruses, Alphapapillomavirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Common chimpanzee
NCBI_TaxID=66261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Common chimpanzee papillomavirus type 1. Viruses; dsDNA viruses, no RNA stage; Papillomaviridae; unclassified Papillomaviridae; primate papillomaviruses;
                                                                                                                            NCBI_TaxID=333766;
                                                                                                                                                                                                                         Protein E7
Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scinicariello F., Soza I., Brasky K.M., Hilliard J.K.; Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                   Delius H
                                                                                                                                                                                                  Human papillomavirus type 54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUCLEOTIDE SEQUENCE.
Scinicariello F., So
                                                                                       NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    L; AF020905; AAB71705.1; -; Genomic DNA.
GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity
GO:0006355; Piregulation of transcription,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pro; IPR000148; Papvi_E7.
PF00527; E7; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MHGDTPTLHEYMLDLQPET-TDLYXYXQLNDS-SEEEDEID-----GPAGQAEPDRAHY
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                                                                                                                                                                                                                                                                integrated into UniProtKB/Swiss-Prot.
sequence version 1.
entry version 30.
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                                                                                       [GENOMIC DNA]
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                       has both transforming and trans-activating
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17; Mismatches 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 180.5; DB 
Pred. No. 5e-13;
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J. Clin. Microbiol. 34:738-744(1996).
-!- FUNCTION: E7 protein has both transforming and trans-activating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=97060129; PubMed=8904450;
Longuet M., Beaudenon S., Orth G.;
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MEDLINE=96249586; PubMed=8815087;
Forslund O., Hansson B.G.;
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EMBL; U22461; AAC54881.1; -; Genomic_
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"Human papillomavirus type 70 genome cloned from overlapping PCR "Human papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping PCR "Thuman papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned from overlapping papillomavirus type 70 genome cloned fr
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DNA-binding; Early protein; Oncogene; Transcription;
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/FTId=PRO_0000133462.

C-XX-C motif-1.

C-XX-C motif-2.
                                                                                                                                                                                                                                                         Oncogene; Transcription;
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  01-JUN-1994,
01-JUN-1994,
07-PEB-2006,
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MEDLINE=91188699; PubMed=1964523; DOI=10.1016/0168-1702(90)90091-0;

Hirsch-Behnam A., Delius H., de Villiers E.M.;

"A comparative sequence analysis of two human papillomavirus (HPV)

types 2a and 57.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human papillomavirus ty
Viruses; dsDNA viruses,
Alphapapillomavirus.
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P22160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Virus Res. 18:81-98(1990).
-!- FUNCTION: E7 protein has both transforming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation.
CHAIN 1 92
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Pfam; PF00527; E7; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; X55965; CAA39431.1; -; Genomic_DNA.
S15622; S15622.
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integrated into UniProtKB/Swiss-Prot.
sequence version 1.
entry version 31.
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                                                                                          STANDARD,
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83
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Pred. No. 8.5e-13;
4; Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein E7.
/FTId=PRO_0000133453
C-XX-C motif-1.
C-XX-C motif-2.
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ches 31;
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VET_HPVO7

ID VET_H
AC P3681
DT 01-UU
DT 07-FE
DE PTOCE
GN Name=
OS Human
OC Virus
OC Alpha
OX NCB1.
RN NUCL1
RR NUCL1
RR NEDL1
RP NUCL
RX MEDL1
RP CUrri
CC -1- E
CC -1- E
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CC Copy
DR PIR;
DR Inte:
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P36816;
01-JUN-1994,
01-JUN-1994,
07-FEB-2006,
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MOTIF
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-!- FUNCTION: E7 protein has both transforming and trans-act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=10596;
             EMBL; X74463; CAA52477.1; -; Genomic_DNA.
PIR; S36585; S36585.
                                                  Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                          Human papillomavirus type 7.
Viruses; dsDNA viruses, no RNA
Alphapapillomavirus.
                                                                                                                                                                                                                                                                  Protein E7.
Name=E7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE [GENOMIC DNA].
MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein E7.
                                                                                     "Primer-directed sequencing of human papillomavirus Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-!- FUNCTION: E7 protein has both transforming and t
                                                                                                                                                                       NUCLEOTIDE SEQUENCE [GENOMIC DNA]. MEDLINE=94265501; PubMed=8205838;
                                                                                                                                                                                                            NCBI_TaxID=10620;
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DNA-binding; Early pro
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                                                                                                                                                          Delius H., Hofmann B.;
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    IPR000148;
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/FTId=PRO 00001
C-XX-C motif-1.
C-XX-C motif-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 178.5; DB 1
Pred. No. 9.3e-13;
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Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                       stage; Papillomaviridae;
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Best Local
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Best Local Similarity
Matches 45; Conserv
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7 HPV51
VE7 HPV51
P26558;
01-AUG-1992;
01-AUG-1992;
07-FEB-2006;
                                                                                                                              MOTIF
SEQUENCE
                                                                                                                                                                                                                                                                                                                                MEDLINE-91303675; PubMed=1649326;
Lungu O., Crum C.P., Silverstein S.J.;
"Biologic properties and nucleotide sequence
papillomavirus type 51.";
J. Virol. 65:4216-4225(1991).
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MOTIF
SEQUENCE
                                                                                                                                                                                                                                                                 Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms Distributed under the Creative Commons Attribution-NoDerivs License
                                                                                                                                                                                                                                                                                                                                                                                                                       Human papillomavirus ty,
Viruses; dsDNA viruses,
Alphapapillomavirus.
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PF00527; E7; 1.
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APCCRCSSVVQLAVESSGDTLRVVQQMLMGELSLVCPCCA
                   TECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                         MRGNVPQLKDVVLHLTPQTEIDLQCYEQF-DSSEEEDEVDNMRDQLPERRAGQATCYRIE
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111 AA;
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107
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98 C
11339 MW;
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es, no RNA stage;
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                                                                                                                             Protein E7.

/FTId=PRO 0000133447.

C-XX-C motif-1.

C-XX-C motif-2.

C-XX-C motif-2.

M; 65E85C554099801A CRC64;
                                                                                  Score 178; DB 1;
Pred. No. 1e-12;
16; Mismatches ?
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/FTId=PRO 00001:
C-XX-C motif-1.
C-XX-C motif-2.
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Pred. No. 9.
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RESULT 96
VE7_HPV55
ID VE7_H
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VE7_HPV
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Best Local (
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InterPro; IPRO00148; Papva_
Pfam; PP00527; E7; 1.

DNA-binding; Early protein; Or
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01-MAY-1992, s
07-FEB-2006, e
Protein E7.
Name=E7;
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P25485;
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01-NOV-1996,
07-FEB-2006,
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Q80935;
                                                                                        NUCLECTIDE SEQUENCE [GENOMIC DNA].

MEDLINE=91188699; PubMed=1964523; DOI=10.1016/0168-1702(90)90091-0;

Hirsch-Behnam A., Delius H., de Villiers E.M.;

"A comparative sequence analysis of two human papillomavirus (HPV)

types 2a and 57.";
                                                                                                                                                                                                                        Human papillomavirus tyr
Viruses; dsDNA viruses,
Alphapapillomavirus.
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Submitted
                                                                      Virus Res.
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                                                   runction: E7 protein
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o RNA stage; Papillomaviridae;
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Pred. No. 1.5e-12;
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C-XX-C motif-2
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01-OCT-2000,
07-FEB-2006,
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SEQUENCE
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Kino N., Sata T., Sato Y., Sugase M., Matsukura T.;
"Molecular cloning and nucleotide sequence analysis of a novel human
papillomavirus (type 82) associated with vaginal intraepithelial
                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=129724;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human papillomavirus type
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091R58;
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PIR; S15615; S15615
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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                                                                                                                                                                                                                                                                                                Clin. Diagn. Lab. Immunol. 7:91-95(2000).
                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                               neoplasia.";
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GO:0005622; C:intracellular; IEA.
GO:0003700; F:transcription factor activity
GO:0006355; P:regulation_of transcription,
                                                                                                                                                                  Pro; IPR000148; Papvi_E7.
PF00527; E7; 1.
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                        TFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                                  WRGNVPQLKDIVLELTPQPEIDLQCYEQF-DSSDEEDEVDNWRDQPARQAGQDTC-YRIK
                                                                           WHGDTPTLHEYMLDLQPE-TTDLYXYXQLNDSSEEEDEIDG----PAGQAEPDRAHYNIV
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40.0%; Pred. No. 2e-1
tive 18; Mismatches
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Pred. No. 1.8e-12;
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C-XX-C motif-1.
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ID VE7.HPV10
AC P36818;
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DE Protein E7;
GN Name=E7;
GN Name=E7;
OS Human papil
OC Viruses; de
OC Alphapapill
OX NCBI_TAXIDD
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01-JUN-1994,
01-JUN-1994,
07-FEB-2006,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Viruses; dsDNA viruses,
Alphapapillomavirus.
NCBI_TaxID=333759;
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Viruses; dsDNA viruses, no RNA stage;
Alphapapillomavirus.
  DNA-binding; Early protein; Oncogene; Transcription; Transcription regulation.

CHAIN 1 86 Protein E7.
                                                                            PIR; S36533; S36533.
InterPro; IPR000148; Papvi_E7.
Pfam; PF00527; E7; 1.
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Narechania A., Chen Z., Desalle R., Burk R.D.;
"Phylogenetic Incongruence among Oncogenic Genital Alpha Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE STRAIN=Qv34077;
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10-JAN-2006,
                                                                                                                                                                                                                       Copyrighted by the UniProt Consortium, Distributed under the Creative Commons
                                                                                                                                                                                                                                                                                                                                                    "Primer-directed sequencing of human papillomavirus types.";
Curr. Top. Microbiol. Immunol. 186:13-31(1994).
-!- FUNCTION: E7 protein has both transforming and trans-act
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human papillomavirus type i
Viruses; dsDNA viruses, no
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NCE 96 AA; 10594 MW; E
                                                                                                                                                              X74465; CAA52490.1; -; Genomic_
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QUERY MATCH
Dash Local Similarity 42.5%; Fred. No. 2.8e-12; Indels 9; Gape 2;

MATCHES 40; Conservative 10; Mismatches 33; Indels 9; Gape 2;

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1 MIGREPHTVOTELSIALEDIEV-----CVAQUEEEYTDA----VEPAQOAYEVTECTK 51

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; SEQ ID NO 8
; LENGTH: 220
; TYPE: PRT
; ORCANISM: Homo sapien
US-09-485-885-8
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                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Munger, Karl
APPLICANT: Jones, D. Leanne
TITLE OF INVENTION: METHOD AND KIT FOR EVALUATING
TITLE OF INVENTION: TRANSFORMED CELLS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: GB 9
PRIOR TILING DATE: 197-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
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                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                       CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Ann-Louise Kerner,
STREET: 200 State Street
                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                      CITY: Boston
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Local Similarity 96.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     114 MHGDTPTLHEYMLDLQPETTDLYGYQQLNDSSEEEDEIDGPÄGQÄEPDRÄHYNIVTFCCK 173
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  McDaniels, Patricia A.
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Gerard, Catherine Marie Ghislaine
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Cabezon Silva, Teresa
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                                                INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGIH: 98 amino acids
TYPE: amino acid
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Best Local Similarity 96.9%;
Matches 95; Conservative
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Veri
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/075,541D
ETILING DATE: 10-JUN-1993
                                                                                                                                       ATTORNET, ALAN S
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 25-567-2020
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                                                                                                                                                                                                                                           APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: AU pk 3876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FERNANDO, GERMAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
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LENGTH: 98 amino acids
TYPE: amino acid
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ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
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MOLECULE TYPE:
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                                    STRANDEDNESS:
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Pred. No. 8e-60;
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RESULT 5
US-08-944-368A-4
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                         Patent No. 6228368
GENERAL INFORMATION:
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APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/382,616A
CURRENT FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
PRIOR FILING DATE: 1999-08-25
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TYPE: PRT
ORGANISM: Papillomavirus sylvilagi
                                                                                                                                                                                                                                                                                        APPLICANT: Gissman, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                     COUNTRY: United States of America ZIP: 60606-6402
COMPUTER READABLE FORM:
SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/944,368A
                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 21
                                                                                                                                                                           STREET: 233 Sc
CITY: Chicago
                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                233 South Wacker Drive, 6300 Sears Tower
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96.9%;
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Pred. No. 8e-60;
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Pred. No. 8e-60;
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GENERAL INFORMATION:
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Best Local Similarity
Matches 95; Conserv
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                                                                                           TELEFAX: (202) 672-5
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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NAME: Williams Jr., Joseph.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET NUMBER: 27
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve;
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/99/820,764
FILING DATE: 30-Mar-2001
CLASSIFICATION: CURROWN>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 98 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
TOPOLOGY: linear MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                            APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W
                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
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                                                         TYPE: amino acid
                                                                                                                                                                                        REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/09820764
                                                                         ENGTH: 98 amino acids
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Pred. No. 8e-60;
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GENERAL INFORMATION:
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Best Local S
                                                                                                                                       Matches
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SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                       Local
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FILING DATE: 07-No. 6562351-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: US 09/026,896
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTIN Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
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HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                      1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/09986118A
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                    MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                                                                             TYPE: amino acid
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STATE: D.C.
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Pred. No. 8e-60;
0; Mismatches
                                                                                                                                                    Score 512; DB 2; Length 98; Pred. No. 8e-60;
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US-09-824-017-4
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Patent No. 6641994
GENERAL INFORMATION:
APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application US/09824017
Patent No. 6649167
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
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Best Local (
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SOFTWARE: PatentIn Ve
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CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Papillomavirus sylvilagi
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Ver

CURRENT APPLICATION DATA:

APPLICATION UNMBER: US/99/824,017

FILING DATE: 03-Apr-2001

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 09/026,896

FILING DATE: 1998-02-20

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                             NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington
LENGTH: 98 amino acids
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Pred. No. 8e-60;
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; TOPOLOGY: linear; ; MOLECULE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-824-017-4
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US-09-637-746-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 11613.29USW1
CURRENT APPLICATION NUMBER: US/09/637,746
CURRENT FILING DATE: 2000.08-11
PRIOR APPLICATION NUMBER: PCT/US99/04142
PRIOR PILING DATE: 1999-02-25
PRIOR PPLICATION NUMBER: US 60/079,567
PRIOR FILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR PILING DATE: 1998-02-25
PRIOR PILING DATE: 1998-03-27
PRIOR PILING DATE: 1998-03-31
SOPTWARE: PATENTIN VETSION 3.1
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LENGTH: 98
TYPE: PRT
ORGANISM: Human papillomavirus
S-09-637-746-3
                                                         GENERAL INFORMATION:
APPLICANT: TZYY-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
CURRENT APPLICANTION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
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APPLICANT: Thorgeirsen, Snorri S.
APPLICANT: Woitach, Joseph T.
APPLICANT: Zhang, Minghuang
TITLE OF INVENTION: CDNA ENCODING A GENE BOG
TITLE OF INVENTION: PRODUCT
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Best Local :
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NUMBER OF SEQ ID NOS: 25
SOPTWARE: PastSEQ for Wil
SEQ ID NO 7
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Similarity 96.9%;
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                   Windows Version 4.0
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Pred. No. 8e-60;
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; LENGTH: 98
; TYPE: PRT
; ORGANISM: human papillomavirus
US-09-501-097A-7
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US-09-613-303-12
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
                                                                                                     Sequence 12, Application Patent No. 6495347 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 12, Application US/09980523A Patent No. 6783763
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Best Local (
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Pred. No. 8e-60;
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Pred. No. 8e-60;
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GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCT:
FILE REFERENCE: 12071/00200
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US-09-613-303-35
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; OTHER INFORMATION:
US-10-267-311-12
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US-10-267-311-12
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PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 12
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SOFTWARE: FastSEQ for
SEQ ID NO 12
LENGTH: 121
                                                                                                                     Sequence 35, Application Patent No. 6495347
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Patent No. 6657055
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Best Local Similarity
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Best Local
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US/10/267,313
CURRENT APPLICATION NUMBER: US/09/613,303
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ORGANISM: Artificial
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TYPE: PRT
ORGANISM: Artificial Sequence
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                                                               Siegel, Marvin
Chu, N. Randall
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                  N: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO 12071/002001
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Pred. No. 1.1e-59;
0; Mismatches 3
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Pred. No. 1.1e-59;
0; Mismatches 3
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CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 198
TYPE: PRT
ORGANISM: Artificial Sequence
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US-09-485-885-1
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APPLICANT: Siegel, Marvin
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
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      GENERAL INFORMATION:
APPLICANT: Bruck, C
APPLICANT: Cabezon
APPLICANT: Delisse,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 35
LENGTH: 198
                                                                                  Sequence 1, Application US/09485885 Patent No. 6342224
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Best Local Similarity
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PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
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                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161
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                                                                                                                                                                                                    161
                                                                                                                                                                                                                                                                               101 MHGDTPTLHEYMLDLOPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                                      61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                            95;
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                                                                                                                                                                                                                                                                                                     1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 198
                                                                                                                                                                                                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
Bruck, Claudine
Cabezon Silva, Teresa
Delisse, Anne-Marie E
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ilarity 96.9%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                            99.0%;
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Pred. No. 2.1e-59;
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 512; DB 2;
Pred. No. 2.1e-59;
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                                                                                                                                                                                                                                                                                                                                                                                                  Length 198;
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Eva Fernande

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; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-1
RESULT 19
US-08-459-818-20
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                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 12
LENGTH: 239
TYPE: PRT
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                                                                                                                                                                                                                                                                 Query Match
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapien
-09-485-885-12
                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: GB
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR PILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITLE OF INVENTION:
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                                                                                                                                                                                                                                               Local
                                                                                                                                                    133 MHGDTPTLHEYMLDLÓPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
NT: Bruck, Claudine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              174 CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          114 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   95;
                                                                                                                                                                        1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                            h 99.0%;
Similarity 96.9%;
95; Conservative
                                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                           CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 230
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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                                                                                                                                                                                                                          Score 512; DB 2; Length 239; Pred. No. 2.7e-59; O; Mismatches 3; Indels
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Pred. No. 2.4e-59;
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Sequence 20,

Application US/08459818

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                                                                                                                                                                                                                                                                            sequence 20, Appl
Patent No. 588557
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: FASTSEQ 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,818
FILING DATE: 02-UN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                    APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
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NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34,
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CORRESPONDENCE ADDRESS:
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APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
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COMPUTER READABLE FORM:
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CITY: Los Angeles
STATE: California
                                                  CITY: Los Angeles
STATE: California
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REFERENCE/DOCKET NUMBER: 30436.35US02
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                               COUNTRY:
                                                                                    STREET:
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                                                                                                       ADDRESSEE:
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                                                                                        11150 Santa Monica Blvd.,
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                                                                                                                                                                                           Ledbetter, Jeffrey
Damle, Nitin K.
Brady, William
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                                 USA
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                                                                                                     Merchant & Gould
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Pred. No. 2.9e-59;
                                                                                      Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 253;
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Patent No. 5855...
Patent No. 5855...
Pinsle
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Matches
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APPLICATION NUMBER: US 08/375:

FILING DATE: 18-JAN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
REGISTRATION NUMBER: 34/470
REFERENCE, JOCKET NUMBER: 30436
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,666
FILING DATE: 08-JUL-1997
CLASSIFICATION: 435
PRIOR APPLICATION: 435
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TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,078 FILING DATE: 05-JUN-1995
                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Plopby disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/375390
                                                                                                                                                                                                                                                                                  STREET: 11150 Santa
CITY: Los Angeles
STATE: California
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 215
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11150 Santa Monica Blvd.,
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                                                                                              05-JUN-1995
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RESULT 22
US-08-725-776-20
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 310-445-1140
TELEPAX: 310-445-9031
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 253 amino acids
TYPE: amino acid
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Matches
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                                                                                                            TELEFAX: 310-445-9031
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Adriano, Sarah B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          ZIP: 90025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/725,776
                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Linsley, Peter S.
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Damle, Nitin K.
APPLICANT: Brady, William
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MOLECULE TYPE:
                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kiener, Peter A.
TITLE OF INVENTION: CTLA4 Receptor and Uses Thereof
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: C
                                                                                                                                                                                      REGISTRATION NUMBER: 34,470
REFERENCE/DOCKET NUMBER: 30436-35US01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 11150 Santa Monica Blvd., Suite 400 CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 95; Conserv
              TOPOLOGY:
                                  STRANDEDNESS
                                                                                                                                                TELEPHONE:
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                                                                      LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                  amino acids
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nilarity 96.9%;
Conservative (
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                linear
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TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-488-062-20
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                                                                                                                                                   Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/488,062 FILING DATE: 07-7UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 08/375390
FILING DATE: 18-JAN-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 310-445-1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: CTLA4 Receptor NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Merchant & Gould STREET: 1150 Santa Monica Blvd., CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Adriano, Saral REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: California
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                                                                156 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 215
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                     61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                    1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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Similarity 96.9%;
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CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 253
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                                                                                                                                                                                                                                                                                         253 amino acids
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Damle, Nitin K.
Brady, William
                                                                                                                                      Conservative
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                                                                                                                                                   Score 512; DB 1;
Pred. No. 2.9e-59;
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                                                                                                                                    Mismatches
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                                                                                                                                                                   DB 1; Length 253;
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                                                                                                                                              Matches
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                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,083
FILING DATE: 10-SEP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REGISTRATION NUMBER: 24,190
                                                                                                                                                                 Best
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 263 amino acids
                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: Protein
LOCATION: 1..263
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: A-TELECOMMUNICATION INFORMATION: TELEPHONE: 415-781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H. Dreger
STREET: 4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human TITLE OF INVENTION: Papilloma Virus Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                       162
                  61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                            1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                              95;
                                                                                                                                                               Similarity
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 259
                                                                       MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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Inglis, Stephen C.
Munro, Alan J.
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                                                                                                                                                                                                                                                                                                                                            ESS: single
linear
                                                                                                                                              Conservative
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                                                                                                                                                           99.0%;
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                                                                                                                                           Score 512; DB 1;
Pred. No. 3.1e-59;
0; Mismatches 3
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                                                                                                                                                                                DB 1;
                                                                                                                                                                            Length 263;
                                                                                                                                              Indels
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; Sequence 10, Application US/08860165
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian

RESULT 25 US-08-860-165-10

Application US/08860165A

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CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157
EARLIER FILING DATE: 1994-12-20
UNMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
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US-09-359-382-10
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LENGTH: 266
TYPE: PRT
ORGANISM: Human papillomavirus type
5-09-359-382-10
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                                                                                                                                                                Matches
                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS FILE REFERENCE: 017227/0148

CURRENT APPLICATION NUMBER: US/09/359,382

CURRENT FILING DATE: 1999-07-23

EARLIER APPLICATION NUMBER: US 08/860,165

EARLIER FILING DATE: 1997-09-22

EARLIER FILING DATE: 1997-09-22

EARLIER APPLICATION NUMBER: PCT/AU95/00868

EARLIER FILING DATE: 1995-12-20

EARLIER FILING DATE: 1995-12-20

EARLIER APPLICATION NUMBER: AU PN0157/94

EARLIER APPLICATION NUMBER: AU PN0157/94

EARLIER FILING DATE: 1994-12-20

NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS FILE REFERENCE: 17227/130
                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 266
                                                                                                                                                                                  Local Similarity
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221 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 258
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                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                              MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                               99.0%;
                                                                                                                                                              Score 512; DB 2;
Pred. No. 3.2e-59;
0; Mismatches 3
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Pred. No. 3.2e-59;
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RESULT 27 US-09-367-309A-1

US-09-613-303-33

Patent No. 6495347 GENERAL INFORMATION:

APPLICANT:

Siegel, Chu, N.

Marvin Randall Sequence 33, Application US/09613303 Patent No. 6495347

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FILE REFERENCE: 017227/0149

CURRENT APPLICATION NUMBER: US/09/367,309A

CURRENT FILING DATE: 1999-08-11

PRIOR APPLICATION NUMBER: PCT/AU98/00080

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: AU PO 5178

PRIOR APPLICATION NUMBER: AU PO 5178

PRIOR FILING DATE: 1997-02-19

NUMBER OF SEQ ID NOS: 6

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No. 6734173
GENERAL INFORMATION:
APPLICANT: TZYY-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HS
FILE REFERENCE: 2240-163349
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US-09-501-097A-25
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RESULT 29
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                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 287
TYPE: PRT
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APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Human papillomavirus type
                                                                                                                                                                                                                                                                                 ORGANISM: Human papillomavirus/Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 266
                                                                                                                                                                                                            y Match 99.0%;
Local Similarity 96.9%;
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les 95; Conserv
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                                                                                                                      MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEBDBIDGPAGQAEPDRAHYNIVTFCCK
                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 287
                                                                                   CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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Pred. No. 3.5e-59;
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Pred. No. 3.2e-59;
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CURRENT APPLICATION UNMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PastSEQ for Windows Version 4 ^
SEQ ID NO 33
LENGTH: ^^-
                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
LENGTH: 295
RESULT 31
US-09-613-303-25
; Sequence 25, Application US/09613303
; Patent No. 6495347
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Best Local (
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mizzen, Lee A. TITLE OF INVENTION: INDUC
                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                  61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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Pred. No. 3.6e-59;
0; Mismatches 3
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GENERAL INFORMATION:

APPLICANT: Siegel, Marvin

APPLICANT: Ciu, N. Randall

APPLICANT: Mizzen, Lee A.

TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN

FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT APPLICATION NUMBER: US/09/613,303

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR APPLICATION NUMBER: US 60/143,757
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US-10-267-311-25
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                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 55
SOFTWARE: FRANSEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 324
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Patent No. 66570:
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SEQ ID NO 25
                                                                                                                                                     Matches
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                                                                                                                                                                                       Query Match
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PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE.
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CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
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APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                    ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                            TYPE: PRT
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                                    61 CDSTLRLCVQSTHVDIRTLEDILMGTLGIVXPICSQKP 98
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                                                                                                  1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/10267311
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                                                                                                                                                     Conservative
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96.9%;
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Pred. No. 4.1e-59;
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Pred. No. 4.1e-59;
LMCTLGIVCPICSOKP 324
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                                                                                                                                                                                       Length 324;
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; SOFTWARE: FastSEQ for F
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6
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US-09-485-885-14
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US-09-485-885-14
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                    SOFTWARE:
SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 14,
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APPLICANT:
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CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR PILING DATE: 1998-08-17
PRIOR PILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fer
APPLICANT: Gerard, Catherine Marie Ghi
APPLICANT: Lombardo-Benchekk, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE:
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                                                                                                                                                                                                                                                LENGTH: 390
TYPE: PRT
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Local Similarity 96.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                        284 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 343
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5. 6342224
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                                                                                1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                            FastSEQ for Windows Version 3.0
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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                                                                                                                         Conservative
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                                                                                                                                          96.98;
                                                                                                                     Score 512; DB 2; Length 390; Pred. No. 5.4e-59; O; Mismatches 3; Indels
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US-10-267-311-19
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                                                                                ; OTHER INFORMATION: fusion sequence US-10-267-311-19
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Query Match
Best Local Similarity
Matches 95; Conserv
                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 6657055
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 19, Applicat Patent No. 6495347 GENERAL INFORMATION:
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Best Local
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
PRIOR FILING DATE: 1999-07-08
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CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Chu, N. Randall APPLICANT: Mizzen, Lee A. TITLE OF INVENTION: INDUCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randal
APPLICANT: Mizzen, Lee A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                 ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                        TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: fusion sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                           LENGTH:
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6495347
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         Conservative
                          99.0%;
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96.9%;
         <u>,</u>
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       Score 512; DB 2; 1
Pred. No. 7.4e-59;
0; Mismatches 3;
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                                              Length 493
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1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60

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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE REFILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASTSEQ for Windows V
SEQ ID NO 17
LENGTH: 639
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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US-09-613-303-17
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                                                                                        ; OTHER INFORMATION: fusion sequence US-10-267-311-17
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GENERAL INFORMATION:
  Query Match 99.0%;
Best Local Similarity 96.9%;
Matches 95; Conservative
                                                                                                                                                                                                                   SOFTWARE: PastSEQ for Windows Version 4.0 SEQ ID NO 17
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Patent No. 6495347
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CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 55
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PRIOR FILING DATE: 1999-07-08
                                                                                                                                 TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                LENGTH: 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    602
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Score 512; DB 2;
Pred. No. 1.1e-58;
0; Mismatches 3
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                                        Length 639;
  Indels
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  Gaps
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GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/9/613,303
PRIOR TILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
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CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 641
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US-10-267-311-51
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US-09-613-303-51
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                                                                           SOPTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 51
LENGTH: 641
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Patent No. 6657055
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Patent No. 6495347
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APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
                                                                                                                                                NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT ORGANISM: Artificial Sequence
OTHER INFORMATION: fusion sequence
                 ORGANISM: Artificial Sequence FEATURE:
                                                              TYPE: PRT
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les 95; Conserv
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Pred. No. 1.1e-58;
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Query Match

DB 2; Length 641;

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CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FABESEQ for Windows Version 4.0
SEQ ID NO 53
LENGTH: 647
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US-10-267-311-53
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCT
FILE REFERENCE: 12071/0020
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US-09-613-303-53
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
FILE REFERENCE: 12071/002001
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No. 6495347
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 53
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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TYPE: PRT
ORGANISM: Artificial Sequence
ORGANISM: Artificial Sequence FEATURE:
                                     TYPE: PRT
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Chu, N. Randall
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Pred. No. 1.1e-58;
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Pred. No. 1.1e-58;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/566,420
CURRENT FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,752
PRIOR FILING DATE: 1999-05-06
PRIOR PELING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 19
SEQ ID NO 19
SEQ ID NO 19
LENGTH: 98
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; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-09-566-420-19
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US-10-201-764-19
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                              CURRENT APPLICATION NUMBER: US/10/201,764
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/566,420
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,752
PRIOR APPLICATION NUMBER: 60/132,750
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: 60/132,750
PRIOR FILING DATE: 1999-05-06
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PATENTIN Ver. 2.0
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                                                                                                                                                                                                                      Sequence 19, Application US/10201764
PATCHI NO. 6716623
GENERAL INFORMATION:
APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
TITLE OF INVENTION: METHODS AND COMPOSITIONS
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: TBA
CHERENT APPLICATION
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Matches 95; Conserv
SEQ ID NO 19
LENGTH: 98
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Patent No. 6500641
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Best Local
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nes 94; Conservative
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Pred. No. 3.7e-59;
1; Mismatches 3;
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Pred. No. 1.1e-58;
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ORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: fusion sequence
US-09-613-303-8
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; ORGANISM: Human papillomavirus type
US-10-201-764-19
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US-09-613-303-8
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SEQ ID NO 8
LENGTH: 98
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Patent No. 6657055
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
PILE REFERENCE: 12071/002001
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Best Local 9
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Patent No. 6495347
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Best Local Similarity
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                                                     CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
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CURRENT FILING DATE: 2000-07-10
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APPLICANT: Chu, N. Randal
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUC
FILE REFERENCE: 12071/002
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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Similarity 95.9%;
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Chu, N. Randall
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95.9%;
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Pred. No. 3.7e-59;
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; SEQ ID NO 29
; LENGTH: 648
                                                                                                      GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
                                                                                                                                                                                                                     Sequence 29, Application US/10267311 Patent No. 6657055
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTI
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Pred. No. 1.7e-57;
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Pred. No. 1.2e-58;
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Sequence 41, Application US/09613303
Patent No. 6495347
GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILLING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-267-311-41
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US-09-613-303-41
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                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                              Sequence 41, Application US/10267311 Patent No. 6657055
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Best Local
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 711
TYPE: PRT
ORGANISM: Artificial Sequence
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95.9%;
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95.9%;
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Pred. No. 1.9e-57;
0; Mismatches 4
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Pred. No. 1.7e-57;
                                                                        RESPONSE IN VITRO
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US-10-267-311-45
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US-09-613-303-45
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                                                                                Sequence 45, Application US/10267311
Patent No. 6657055
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/613,303
CURRENT FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASTSEQ for Windows Version 4.1
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 45, Application US/09613303 Patent No. 6495347 GENERAL INFORMATION:
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SEQ ID NO 41
LENGTH: 711
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                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
TITLE OF INVENTION: 12071/002001
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Best Local
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION
FILE REFERENCE: 12071/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 724
TYPE: PRT
ORGANISM: Artificial Sequence
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95.9%;
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Pred. No. 1.9e-57;
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Pred. No. 1.9e-57;
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                    TH1-LIKE
                      RESPONSE
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; Sequence 20, Application US/09501097A
PALENT NO. 6734173
; GENERAL INFORMATION:
APPLICANT: TZYY-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: INFOVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
; CURRENT APPLICATION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
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US-09-501-097A-20
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US-09-501-097A-22
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US-09-501-097A-22
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FEATURE:
OTHER INFORMATION: fusion sequence
US-10-267-311-45
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PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 724
TYPE: PRT
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Best Local 9
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CURRENT FILING DATE: 2000-02-09
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tzyy-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
FILE REFERENCE: 2240-169349
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CURRENT FILING DATE: 2002-10-09
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NUMBER OF SEQ ID NOS:
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Local Similarity 96.9%;
                                                                                                                                                                                                                                                                                     377
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2000-02-09
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95.9%;
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; TYPE: PRT
; ORGANISM: human papillomavirus/Mycobacterium tuberculosis
US-09-501-097A-20
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Sequence 12, Application US/08860165A
PATENT NO. 6004557
GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
APPLICANT: FRAZER, Ian
FITCE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
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SOFTWARE: PatentIn Ve
SEQ ID NO 2
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SEQ ID NO 20
LENGTH: 723
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Best Local (
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CURRENT APPLICATION NUMBER: US/09/462,993
CURRENT FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: FR 97/09152
PRIOR FILING DATE: 1997-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KIENY, Marie-Paule
APPLICANT: BALLOUL, Jean-Marc
APPLICANT: BIZOUARNE, Nadine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Derivated from human papillomavirus, st. OTHER INFORMATION: HPV-16, E7 fusion signals of the rabies OTHER INFORMATION: glycoprotein, clone E7*TWR.
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                              1 MHGDTPTLHEYMLDLQPETTDLYXXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                                                                                                                                            MHGDTPTLHEYMLDLQPETT-----
                                                                                                                                                                                                                                       CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 117
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                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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96.9%;
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                                                                                                                                                                                                                                                                                                                                                                              Score 478; DB 2
Pred. No. 6e-55;
0; Mismatches
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Pred. No. 4.8e-57;
0; Mismatches 3
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RESULT 58
US-08-860-165-14
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CURRENT FILING DATE: 1999-07-23
EARLIER APPLICATION NUMBER: US 08/860,165
EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER APPLICATION NUMBER: AU PN0157/94
EARLIER FILING DATE: 1994-12-20
NUMBER: OF SEQ ID NOS: 27
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US-09-359-382-12
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                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 12
LENGTH: 172
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
                                                                                                                                                                                                                                                                              Best
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EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 172
Sequence 14, Application Patent No. 6004557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Appl: Patent No. 630639'
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human papillomavirus type 16-09-359-382-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver.
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ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                Similarity
                                                                                                            CDSTLR 164
                                                                                                                                                 CDSTLR 66
                                                                                                                                                                                   MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
                                                                                                                                                                                                           MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                 US/08860165A
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; Pred. No. 1.8e-38;
. Migmatches 2;
                                                                                                                                                                                                                                                         Score 353; DB 2; Length 172; Pred. No. 1.8e-38; 0; Mismatches 2; Indels
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GENERAL INFORMATION:
APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZER, Ian
ITITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 17227/130
CURRENT APPLICATION NUMBER: US/08/860,165A
CURRENT FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION
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EARLIER FILING DATE: 1997-09-22
EARLIER APPLICATION NUMBER: PCT/AU95/00868
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1995-12-20
EARLIER FILING DATE: 1994-12-20
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PALENTIN VET. 2.0
SEQ ID NO 14
LENGTH: 172
TYPE: PRT
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APPLICANT: EDWARDS, Stirling John
APPLICANT: COX, John Cooper
APPLICANT: WEBB, Elizabeth Ann
APPLICANT: FRAZEK, Ian
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
FILE REFERENCE: 017227/0148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Appli
Patent No. 6306397
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Best Local Similarity
                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/359,382
CURRENT FILING DATE: 1999-07-23
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TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Human papillomavirus type
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94 CSQKP 98
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                                                                         EEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPI
                                                                                                            EEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPI
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llarity 98.5%;
Conservative
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Pred. No. 2e-37;
0; Mismatches
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Pred. No. 2e-37;
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                                                                                                                                                                                                                                                                          Length 172;
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                                                                             RESULT 61
US-08-606-288-10
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                    Sequence 10, Application US/08606288 Patent No. 5955087 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 398-324
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US 60/
FILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 951
FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,288
FILING DATE: 23-FEB-1996
PRIOR APPLICATION NUMBER: B9 9503786.7
PILING DATE: 24-FEB-1995
PRIOR APPLICATION NUMBER: GB 9503786.7
PILING DATE: 24-FEB-1995
PRIOR APPLICATION NUMBER: 16 60/000024
                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
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    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A.63284/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
                                                                                                                                                           551 CGCDSNVRLVVQCTETDIREVQQLLLGTLNIVCPICAPK 589
                                                                                                                                                                                                                                    493 MHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDBVDGQ--DSQPLKQHYQIVTCC
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5. 5955087
                                                                                                                                                                                                                                                                                                                  53;
                                                                                                                                                                                             59 CKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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Whittle, N.R.
                                                                                                                                                                                                                                                                                                                  Conservative
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53.5%;
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Best Local Similarity
Matches 53; Conserv
                                                                                                                                                          Sequence 7, Application US/09347483 Patent No. 6123948
                                                                                                                                                                                                 -09-347-483-7
                                                                                                                        APPLICANT: Whittl
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APPLICANT:
APPLICANT:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/606,288
              APPLICANT: Thompson, H. APPLICANT: Wilson, M.J. TITLE OF INVENTION: Pol-
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ANTI-SENSE: 1
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LENGTH: 601 amino acid
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REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 0
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ATTORNEY/AGENT INFORMATION:
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                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 601 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Suite 3400, Four Embarcadero Center
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                                                                                                        Whittle, N.R. Carmichael, J.P.
                                                                                       Connor, S.E.
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Polypeptides Useful as Immunotherapeutic Agents, and Methods of Polypeptide Preparation 10
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                                                                      H.S.G.
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-347-483-7
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Best Local Similarity
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APPLICATION NUMBER: US 60/000
FILING DATE: 08-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 951547
FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dreger
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEPHONE: (415) 781-1989
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INFORMATION FOR SEQ ID NO:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                             TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Agents, and
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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LENGTH: 601 amino acids
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MEDIUM TYPE: Floppy (
COMPUTER: IBM PC com)
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
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                                                            STATE: C
                                                                                            ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Suite 3400, Four Embarcadero Center
CITY: San Francisco
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
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                                                                                                                                                                                                                                                                                                                                         0, Application US/09347483
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Suite 3400, Four Embarcadero Center
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53.5%;
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                                                                                                                                                                                          Immunotherapeutic Polypeptide Preparation
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Patent No. 6365160
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 601 amino acid
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FILING DATE: 28-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Walter H. Dreger
REGISTRATION NUMBER: 24,190
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 60 FILING DATE: 08-JUN-1995 PRIOR APPLICATION DATA:
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SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
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              COUNTRY: U.S.A.
ZIT: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
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amino acid
GY: linear
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                                                                                                                                           STATE: D.C.
                                                                                                                                                      CITY: Washington
                                                                                                                                                                              STREET:
                                                                                                                                                                          ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09000094
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                                                                                                                                                                                                                                                                                                                                                                                                           WEBB, Elizabeth Ann
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                                                                                                                                                                                                                                                                                                                     MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
                                                                                                                                                                                                                                                                                                                                                                        MARGETTS, Mary Brigid
COX, John Cooper
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Release #1.0, Version #1.25 (EPO)
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Pred. No. 1e-23;
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                    Version #1.30
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RESULT 65
US-10-011-749-46
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Patent No. 6726912
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                   ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION UMBER: US/10/011,749
FILING DATE: 11-Dec-2001

CLASSIFICATION: CUNKNOWN>
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REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
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PILING DATE: 21-Apr-1998
CLASSIFICATION: Unknown>
PRIOR APPLICATION DATA:
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 46:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 50 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1587 amino acids
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TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  839 MHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC 896
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                                                                                                                                                                                                                                                                                                                                                      CITY: Washington STATE: D.C.
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                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3000 K Street, N.W.
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
                                                                                                                                                                                                                                                                                                                                   COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: FOLEY & LARDNER
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WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
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Best Local Similarity
Watches 52; Conserve
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                                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION: Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,7
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              897 CGCDSNVRLVVQCTETDIREVQQLLLGTLNIVCPICAPK 935
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                                                                                                                                                                                                                                                                                                                                                                                 STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
                                                                              APPLICATION NUMBER: WO PCT/AU96/00473 FILING DATE: 26-JUL-1996 APPLICATION NUMBER: AU PN 4439/95 FILING DATE: 27-JUL-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1587 amino acids
TYPE: amino acid
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TELEFAX: (202) 672-5399
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                    NAME: BENT, Stephen A.
REGISTRATION NUMBER: 2
REFERENCE/DOCKET NUMBER: 017227/0137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Application US/09000094
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WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
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John Cooper
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52.5%; Pred. No. 1.3e-22;
tive 15; Mismatches 28
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                                                                                                                                                                                                                                                                            Version #1.30
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RESULT 67
US-10-011-749-22
Sequence 22, Application US/10011749
Patent No. 6726912
GENERAL INFORMATION:
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                                     INFORMATION
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/10/011,749
FILING DATE: 11-Dec-2001
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
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Local Similarity 51.5%;
see 51; Conservative 1
                                                                                                                                                 NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
TELECOMMUNICATION INFORMATION:
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ADDRESSEE: FOLEY & LARDNER
SEQUENCE CHARACTERISTICS
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TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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TYPE: amino acid
                                                                                                                TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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MARGETTS, Mary Brigid
COX, John Cooper
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                                                                      (202) 672-5300
202) 672-5399
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(02) 672-5399
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US-09-000-094-24
US-09-000-094-24
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Patent No. 6365160
GENERAL INFORMATION:
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                                                                                                                      INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/000,094
FILING DATE: 21-Apr-1998
CLASSIFICATION - UNKnown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
FILING DATE: 26-JUL-1996
FILING DATE: 26-JUL-1996
FILING DATE: 26-JUL-1996
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FILING DATE: 27-7UL-1995
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 017227/0137
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
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                                                                            LENGTH: 465 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20007-5109
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                                                                                                                                                                                   TELEPHONE: (202)
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WILLIAMS, Mark Philip
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John Cooper
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Pred. No. 4.5e-23;
6; Mismatches 28
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; LENGTH: 465 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-10-011-749-24
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US-10-011-749-24
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Patent No. 6726912
GENERAL INFORMATION:
                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local
                                          Matches
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TELEPAX: (202) 672-5:
INFORMATION FOR SEQ ID NO: 24:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/10/011,749
PILING DATE: 11-Dec-2001
CLASSIFICATION: Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EDWARDS, Stirling John
TITLE OF INVENTION: PAPILLOMAVIRUS POLYPROTEIN CONSTRUCTS
NUMBER OF SEQUENCES: 50
                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: 017227/0137 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                          51;
1 MHGDTPTLHEYMLDLQ-PETTDLYXYXQLNDSSEEE-DEIDGPAGQAEPDRAHYNIVTFC 58
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51; Conservative
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FILING DATE: 21-Apr-1998
APPLICATION NUMBER: WO PCT/AU96/00473
FILING DATE: 26-JUL-1996
APPLICATION NUMBER: AU PN 4439/95
FILING DATE: 27-JUL-1995
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                                                                                                                                                                                                                                                                                                                                                                                 NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
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                                       46.4%; Score 240; DB 2; Length 465; ilarity 51.5%; Pred. No. 6.1e-23; Conservative 16; Mismatches 28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCMILLAN, Nigel Alan John
WILLIAMS, Mark Philip
MOLONEY, Margaret Bridget
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                                                                                                                                                                                                                                                                                                 672-5399
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US-09-501-097A-6
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                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1998-08-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
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Patent No. 6342224
GENERAL INFORMATION:
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APPLICANT: TZYY-Choou Wu
APPLICANT: Chien-Fu Hung
TITLE OF INVENTION: IMPROVED HSP DNA VACCINES
FILE REFERENCE: 2240-169349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/09501097A Patent No. 6734173
                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                SOFTWARE: 1
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 6
LENGTH: 38
                                                                                                                                                                                               Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cabezón Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/501,097A
CURRENT FILING DATE: 2000-02-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                                                                                                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 100.0%; Pred. No. 2.4 ses 38; Conservative 0; Mismatches
                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    152 LHGRHVTLKDIVLDLQPPDPVGLHCYEQLVDSSEDEVDEVDGQ--DSQPLKQHFQIVTCC 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        210 CGCDSNVRLVVQCTETDIREVQQLLLGTLNIVCPICAPK 248
  172 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 217
                                                                            114 MHGPKATLQDIVLHLEPQNEIPVDLLGHQQLSDSEEENDEIDGVNHQHLPARRAEPQR--
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                                  52 YNIVTECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                          42;
                                                                                                                 1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                     FastSEQ for Windows Version 3.0
                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claudine
                                                                                                                                                                          39.0%; Score 201.5; DB 2
39.6%; Pred. No. 2.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             40.4%; Score 209; DB 2;
100.0%; Pred. No. 2.4e-20;
                                                                                                                                                          20;
                                                                                                                                                          Mismatches
                                                                                                                                                                                                 DB 2;
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                                                                                                                                                                                               Length 227;
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US-08-117-083-13
                                                                                                                                                                                                                                                                                                                                                                        Matches
Sequence 23, Application US/09485885
Patent No. 6342224
GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Gerard, Catherine Marie Ghislaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 13, Application US/08117083
Patent No. 5719054
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
COMPUTER: IBM PC compo
OPERATING SYSTEM: PC-
SOTTWARE: Patentin Re
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APPLICANT: Inglis, Stephen C.
APPLICANT: Munro, Alan J.
TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
TITLE OF INVENTION: Papilloma Virus Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Walter H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/117,083 FILING DATE: 10-SEP-1993 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: Protein LOCATION: 1..272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 4 Embarcade:
CITY: San Francisco
STATE: CA
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                                                                                                                                                                                                                 222 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 267
                                                                                                                                                                                                                                                                                            164 MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
                                                                                                                                                                                                                                                        52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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4 Embarcadero Center, Suite 3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272 amino acids
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SYSTEM: PC-DOS/MS-DOS
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RESULT 75
US-08-934-915-52
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PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 97
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows V
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 16
LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, 7
APPLICANT: Delisse, Anne-M
APPLICANT: Gerard, Catherin
Sequence 52, Application US/08934915 Patent No. 5932412
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LENGTH: 383
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Best Local
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CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Lombardo-Bencheikh, Angela TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/09/485,885
CURRENT FILING DATE: 2000-02-18
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                                                                                                                                                                                                                                                                                                                                                 LENGTH: 227
TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                              52 YNIVTECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                  MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                     MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDEVNHQHLPARRAEPQR--
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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BER: PCT/EP98/05285
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38.7%;
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                                                                                                                                                                                                                                                            20;
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Pred. No. 7.7e-18
                                                                                                                                                                                                                                                                              Score 192.5; DB :
Pred. No. 4.3e-17
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                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                               Length 227;
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                                                                                                                                                                                                                                                            11;
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GENERAL INFORMATION: APPLICANT: DILLNE

APPLICANT:

CHENG,

DILLNER, JOAKIM DILLNER, LENA HWEE-MING

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; MOLECULE TYPE: peptide
US-08-934-915-52
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                                                                                                                                                                                                                                                                                                                                                                                    RESULT 76
                                                        NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hopfi, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin
FILE REFERENCE: 032929-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/09486394 Patent No. 6478749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                 CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
PILING DATE: 22-SEP-1997
CLASSIPICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO:
                         TYPE: PRT
DRGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946.6
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U.S.A.

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
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TITLE OF INVENTION:
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TITLE OF INVENTION: DI
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MASON & ASSOCIATES, P.A.
STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    44 QAEPDRAHYNIVTFCCKCDSTLRLCVQSTH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30;
                                         30
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 QAEPDRAHYNIVTFCCKCDSTLRLCVQSTH 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33.1%; So ilarity 100.0%; E Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8, 11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 171; DB 1; 
; Pred. No. 1.8e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                               Tests,
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                                                                                                                                                                                                                                                               and Method
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                                                        Matches
                                                                    Query Match
Best Local Similarity
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APPLICANT: DILLNE
                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 19.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                    FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: F
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 22-SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                            TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: CLEARWATER
                                                                                                                                                                                                                                   TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 PAGQAEPDRAHYNIVTFCCKCDSTLRLCVQ 70
                           58 CCKCDSTLRLCVQSTHVDIRTLEDLLMGTL 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DILLNER, JOAKIM
DILLNER, LENA
CHENG, HWEE-MING
                                                                                                                                                                       30 amino acids
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                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                              22-SEP-1997
                                                31.3%; 50.
100.0%; Prr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11, 16, 18, 31, 33 AND 56, USEFUL IN IMMUNOASSAY FOR DIAGNOSTIC PURPOSES 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SYNTHETIC PEPTIDES OF HUMAN PAPILLOMAVIRUS 1, 5, 6, 8,
                                                                                                                                                                                                                                                                                                                                                       07/949,836
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                                                                      Score 162;
Pred. No.
                                                      Mismatches
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30
                                                                      2.8e-1
                                                                                      DB 1;
                                                                                   Length 30
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
SEQ ID NO 1
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US-08-934-915-51
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TYPE: PRT
ORGANISM: Human papillomavirus type 16
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
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Patent No. 6478749
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Patent No. 593241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                         COUNTRY: U.S.A.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
NAME: LOUISE A. FOULCh
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 194
TELECOMMUNICATION INFORMATION:
TELECHOONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR
TITLE OF INVENTION: DIAGNOSTIC PURPOSES
                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MASON & A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                               STREET: 17757 U.S
CITY: CLEARWATER
                                                                                                                                                                                                        APPLICATION NUMBER: US/01
FILING DATE: 22-SEP-1997
                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal
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Similarity 93.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08934915
                                                                                                                                                                                                                                                                                                                                                                                                                          E: MASON & ASSOCIATES, P.A.
17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DILLNER, LENA
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                                                                                                                                                                                                                           US/08/934,915
                                                               37, 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 154; DB 2;
Pred. No. 3.2e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; NAME/KEY: PEPTIDE
; LOCATION: (1)..(30)
; OTHER INFORMATION: E7 peptide.
US-09-486-394-4
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                                                                                                                                                                                                                                                                                                                              US-08-075-541D-7
                                                                                                                                                                                                                                                                                                                                                   RESULT 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 4
                                                                                                                                                                                                                                                                      Sequence 7, Application US/08075541D Patent No. 6183745
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09486394 Patent No. 6478749
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 30
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Human papillomavirus type 16 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL,
STREET: 1601 MARKET STREET, 36TH FLOOR
CITY: PHILADELPHIA
                                                                                                                                                                                APPLICANT: TINDLE, ROBERT
APPLICANT: FERNANDO, GERWAIN
APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                         ZIP: 19103-2398
                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                        61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIV 90
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)GY: linear
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                                                                         PENNSYLVANIA
                                                          USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.6%; Score 153; DB 2;
100.0%; Pred. No. 4.4e-13;
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Pred. No. 4.4e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 30;
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                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/828,645
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/194,796
PRIOR PILING DATE: 2000-04-05
NUMBER OF SEQ ID NOS: 8
SOFTMARE: Patentin version 3.1
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/09828645
Patent No. 6743593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 29.1%;
Best Local Similarity 56.6%;
Matches 30; Conservative
                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: pct/au91/005:
APPLICATION NUMBER: pct/au91/005:
APPLICATION NUMBER: pct/au91/005:
APPLICATION NUMBER: pct/au91/005:
APPLICATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2220
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Hu, Yao Xiong
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
FILE REFERENCE: 146-1-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                   OTHER INFORMATION: Derived from the E7 early region of HPV-16 NAME/KEY: misc feature LOCATION: (19)...(19)
OTHER INFORMATION: Xaa = L-carboxymethylcysteine
                                                                                                                                                                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                         ENGTH: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/075,541D FILING DATE: 10-JUN-1993 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino a STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patentl
                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 EYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCD 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EYMLDA----
                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acids
                                   PTLHEYMLDLOPETTDLYXXXQLNDSSEEE 35
 PTLHEYMLDLQPETTDLYXYEQLNDSSEEE 30
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER: pct/au91/00575
12-DEC-1991
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                                                                                         28.6%;
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                                                                       Score 148; DB 2; Length 30; Pred. No. 2e-12; 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8795-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
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RESULT 83

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US-08-363-586-1
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Best Local Similarity
Matches 28; Conserv
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                                                            NUMBER OF SEQ ID NOS: SOFTWARE: PatentIn ver SEQ ID NO 3
                                                                                                                                                                                                                                                                 Sequence 3, Application US/09828645
Patent No. 6743593
GENERAL INFORMATION:
                                                                                                                       CURRENT APPLICATION NUMBER: US/09/828,645
CURRENT FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 60/194,796
PRIOR FILING DATE: 2000-04-05
                                                                                                                                                                                            APPLICANT: Hu, Yao Xiong
TITLE OF INVENTION: Immunological Methodology for Discerning Human Papillomavirus
FILE REFERENCE: 146-1-002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/909,296
FILING DATE: 09-UUL-1992
APPLICATION NUMBER: EP 91111720.8
FILING DATE: 13-UUL-1991
ATTORNEY/AGENT INFORMATION:
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ORGANISM: Artificial Sequence
                       LENGTH: 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Wadler, Linda A.
REGISTRATION NUMBER: 33,218
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6 and E7-Gene Derived
TITLE OF INVENTION: Peptides for the Diagnostic Purpose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 1300 1 50
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
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ZIP: 20005-3315
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STREET: 1300 I Street, N.W.
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                                                                                PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 30 amino acids
amino acid
GY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          PTLHEYMLDLOPETTDLYXXXQLNDSSEEE 35
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llarity 93.3%;
Conservative
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RESULT 86
US-09-486-394-2
; Sequence 2, Application US/09486394
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; MOLECULE TYPE:
US-08-934-915-54
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; OTHER INFORMATION: Derived from the E7 early region of HPV-16
US-09-828-645-3
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                                                                                                                                                            Matches
                                                                                                                                                                          Query Match
Best Local Similarity
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/934,915
FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
PRIOR APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 30 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                              NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: DILLNER, JOAKIM APPLICANT: DILLNER, LENA APPLICANT: CHENG, HWEE-MING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: F
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CTTY: CLEARWATER
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                                                                                                          69 VQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                   813-538-3820
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                          peptide
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                                                                                                                                                                          28.2%;
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Pred. No. 2.7e-12;
0; Mismatches 2
                                                                                                                                                          Score 146; DB 1; Length 30; Pred. No. 3.7e-12; O; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn version 3.1 SEQ ID NO 2
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GENERAL INFORMATION:
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Best Local Similarity
                                             APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-JUN-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
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TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 30
TYPE: PRT
TELEFAX: 21
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NAME/KEY: PEPTIDE
LOCATION: (1)..(30)
OTHER INFORMATION: E7 peptide.
                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TINDLE, ROBE APPLICANT: FERNANDO, GE APPLICANT: FRAZER, IAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 19103-2398
                                    TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: PHILADELPHIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 DLYXYXQLNDSSEEEDEIDGPAGQAEPDRA 50
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                  215-567-2991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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                                    215-567-2020
SEQ ID
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Pred. No. 5e-12;
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; LOCATION: (1)..(28)
; LOTHER INFORMATION: E7 peptide.
US-09-486-394-5
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TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-47
                                                                                                                                                                                                                                                                                                                                                                                        US-08-363-586-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/486,394
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/04773
PRIOR FILING DATE: 1998-07-30
PRIOR APPLICATION NUMBER: DE 197 37 409.3
PRIOR FILING DATE: 1997-08-27
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-486-394-5
                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08363586 Patent No. 5629161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 5
LENGTH: 28
TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09486394 Patent No. 6478749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 27.7%; Score 143; DB 2; Best Local Similarity 100.0%; Pred. No. 7.2e-1 Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hopfl, Reinhard
TITLE OF INVENTION: Diagnostic Kit for Skin Tests, and Method
FILE REFERENCE: 032929-001
                                                                                                                                     NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
CORRESPONDENCE Finnegan, Hender
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                          APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Use of HPV-16 E6
TITLE OF INVENTION: Peptides for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                   STREET: 1300 I SU
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71 STHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 AHYNIVTFCCKCDSTLRLCVQSTHV 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 26.5%; l Similarity 96.4%; 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 STHVDIRTLEDLLMGTLGIVCPICSQKP 28
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                                                                                                                                                                                 Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 137; DB 2; Length 28; Pred. No. 5.2e-11;
                                                                                                                                                                                                                                            and E7-Gene Derived
Diagnostic Purpose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
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                                                                                                                                                                                              COUNTRY: USA
ZIP: 19103-2398
ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/08/075,541D
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Best Local Similarity
Matches 25; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 amino acids
                                                                                             CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
BEFFFFF DOCKFT NUMBER: 8795.4
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 13-JUL-1991
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Wadler, Linda A. REGISTRATION NUMBER: 33, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 09-JUL-1992
APPLICATION NUMBER: EP 91111720.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 23-DEC-1994
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                                                                                                                                                                                                                                                                                                                                                                                                          CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29 NDSSEEEDEIDGPAGQAEPDRAHYN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0, Application US/08075541D 6183745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              202-408-4000
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, 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56
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TELEFAX: 215-567-2991 INFORMATION FOR SEQ ID NO:

40:

TELEPHONE:

215-567-2020

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                                                                                           ; MOLECULE TYPE: peptide US-08-934-915-71
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US-08-934-915-71
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                                             Query Match
Best Local Similarity
                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 71, Appli
Patent No. 5932412
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                                                                                                                                                                                              TELEX:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: CHENG, HWI
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 26 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: MASON & I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: MASON & ASSOCIATES, P.A. STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500 CITY: CLEARWATER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y Match 24.4%;
Local Similarity 96.2%;
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0
FILING DATE: 22-SEP-1997
                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
58 CCKCDSTLRLCVQSTHVDIRTLEDLLMGT 86
                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 THVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25;
                                                                                                                                            : 30 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLORIDA
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                                Conservative
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CHENG, HWEE-MING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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                                               23.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SYNTHETIC PEPTIDES OF HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                                                                                                                                                             07/949,836
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                                                                                                                                                                                                                                                                                           37, 133
                                4; Mismatches
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                                                                                                                                                                                                                                                                               1946.6
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Pred. No. 1.3e-09;
                                               Score 122; DB 1; Length 30; Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 26;
                                Indels
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                            Gaps
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TYPE: PRT
; ORGANISM: Human Papillomavirus
US-09-980-523A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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US-08-075-541D-10
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GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Best Local Similarity 95.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRISS, ESTELLE
TITLE OF INVENTION: POLYEPTOPIC PROTEIN FRAGMENTS OF THE E6 AND E7
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE
FILE REFERENCE: WOBL AO INS
CURRENT APPLICATION NUMBER: US/09/980,523A
CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: PCT/FR00/01513
PRIOR APPLICATION NUMBER: FR 99/07012
PRIOR APPLICATION NUMBER: FR 99/07012
PRIOR APPLICATION NUMBER: FR 99/07012
PRIOR APPLICATION NUMBER: FR 99/07012
                                                                                                                                                                                ZIP: 19103-2398
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: TINDLE, RAPPLICANT: FERNANDO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: CHOPPIN,
APPLICANT: BOURGAU
APPLICANT: GUILLET
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FRAZER, IAN
TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE AND
TITLE OF INVENTION: PEPTIDES FOR USE THEREIN
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS: ADDRESSE: PANTICH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION NUMBER: pct/au91/0
APPLICATION NUMBER: pct/au91/0
                                                                                   APPLICATION NUMBER: US/08/075,541D FILING DATE: 10-JUN-1993 CLASSIFICATION: 424 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                            CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 GDTPTLHEYMLDLQPETTDLYXY 25
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                                                                                                                                                                                                                                                                                                                                                                      PENNSYLVANIA
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                                                                                                                                                                                                                                                                                                                                                   USA
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pct/au91/00575
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Pred. No. 5.2e-09;
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                                                                                                                                                                                                           Version #1.25
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US-08-934-915-48
; MOLECULE TYPE: US-08-934-915-48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5932412
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 48, Application US/08934915
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NAME: NADEL, ALAN S

REGISTRATION NUMBER: 27,363

REFERENCE/DOCKET NUMBER: 8795-
TELECOMMUNICATION INFORMATION:

TOT.EPHONE: 215-567-2020
                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
                                                                                                                                                            FILING DATE:
ATTORNEY AGENT INPORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 194C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/949,836
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 17757 U.S
CITY: CLEARWATER
STATE: FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: 811
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/934,915 FILING DATE: 22-SEP-1997
                                TOPOLOGY:
                                                                                                                                              TELEFAX: 813-538-3820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 GOAEPDRAHYNIVTFCCKCD 62
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17757 U.S. HWY. 19 NORTH, SUITE 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DILLNER, LENA
CHENG, HWEE-MING
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               peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNTHETIC PEPTIDES OF HUMAN PAPILLOWAVIRUS 1, 5, 6, 8, 11, 16, 11, 33 AND 56, USEFUL IN IMMUNOASSAY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23.2%; Score 120; DB 2;
100.0%; Pred. No. 5.8e-09;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DIAGNOSTIC PURPOSES
                                                                                                                                                                                                                  37, 133
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Sequence 74, Application US/09980177A

Patent No. 6838084

Patent No. 6838084

Patent No. 6838084

Patent No. 6838084

Patent No. 6838084

Patent No. 6838084

Patent No. 6838084

Patent No. 6838084

Patent No. 6838084

Patent No. 6838084

Patent Jochmus, Ingrid

Applicant: Jochmus, Ingrid

Applicant: Nieland, John

Patent Of Invention: Papilloma Virus L1-protein and Use Thereof in Diagnosis and

Patent Patent Patention: 50125/036001

Patent Patention Number: US/09/980,177A

CURRENT PILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: PCT/EP00/05006

PRIOR PATENT APPLICATION NUMBER: PCT/EP00/05006

PRIOR PILING DATE: 2000-05-31

PRIOR APPLICATION NUMBER: DE 19925199.1

PRIOR PILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 77

SOPTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      片
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                                                                                 ; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-980-177A-73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-980-177A-74
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SEQ ID NO 73
LENGTH: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                  Query Match
Best Local Similarity
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Patent No. 683808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jochnus, Ingrid
APPLICANT: Viceland, John
ITLE OF INVENTION: Cyptotoxic T-Cell Epitopes of the
TITLE OF INVENTION: Cyptiloma Virus L1-Protein and Use Thereof in Diagnosis and
TITLE OF INVENTION: Therapy
FILE REFERENCE: 50125/036001
CURRENT APPLICATION NUMBER: US/09/980,177A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: PCT/EP00/05006
PRIOR APPLICATION NUMBER: DE 19925199.1
PRIOR PILING DATE: 1999-06-01
NUMBER: OF SEQ ID NOS: 77
NUMBER OF SEQ ID NOS: 77
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                  22.4%; Score 116; DB 2; 1 100.0%; Pred. No. 1.9e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22.8%; Score 118; DB 2; 100.0%; Pred. No. 1.1e-08;
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                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 20;
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Indels
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Matches

Conservative

<u>,,</u>

Mismatches

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Gaps

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RESULT 98
US-08-934-915-46
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US-08-075-541D-3
                                                                                                                Sequence 46, Application US/08934915
Patent No. 5932412
                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/075,541D
FILING DATE: 10-UW-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: pct/au91/00575
PILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REGISTRATION NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: TINDLE, ROBE
APPLICANT: FERNANDO, GE
APPLICANT: FRAZER, IAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 215-567-2991
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                      APPLICANT:
APPLICANT:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETI
TITLE OF INVENTION: PAPILLOM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE TITLE OF INVENTION: PEPTIDES FOR USE THEREIN NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                             44 QAEPDRAHYNIVTFCCKCD 62
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PAPILLOMAVIRUS 1, 5, 6, 8,
                      SYNTHETIC PEPTIDES OF HUMAN
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                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6183745
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: LOUISE A. Foutch
REGISTRATION NUMBER: 37,133
REFERENCE/DOCKET NUMBER: 1946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 813-538-3800
                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: 1601 MARKET STREET, 36TH FLOOR
                                                                                                                                                                                                                                                                 TITLE OF INVENTION: SUBUNIT PAPILLOMA VIRUS VACCINE TITLE OF INVENTION: PEPTIDES FOR USE THEREIN NUMBER OF SEQUENCES: 56
                                                                                                                                                                                                                                                                                                                     APPLICANT: TINDLE, ROBE APPLICANT: FERNANDO, GE APPLICANT: FRAZER, IAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 3.0
SOFTWARE: Microsoft word 6.0
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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FILING DATE: 22-SEP-1997
CLASSIFICATION: 435
                                                                                                                                                                                              CITY: PHILADELPHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                          COUNTRY:
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CITY: CLEARWATER
STATE: FLORIDA
FILING DATE:
                  APPLICATION NUMBER:
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/ 1ve. 0; Mismatches
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              US/08/075,541D
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Pred. No. 4.9e-08;
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Sequence 69, Application US/09980177A

Patent No. 6838084

Patent No. 6838084

GENERAL INFORMATION:

APPLICANT: Jochnus, Ingrid

APPLICANT: Nieland, John

TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the

TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and

TITLE OF INVENTION: Therapy

FILE REFERENCE: 50125/036001

CURRENT PELICATION NUMBER: US/09/980,177A

CURRENT PILING DATE: 2001-11-29

PRIOR APPLICATION NUMBER: PCT/EP00/05006

PRIOR PILING DATE: 2000-05-31

PRIOR PILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 77

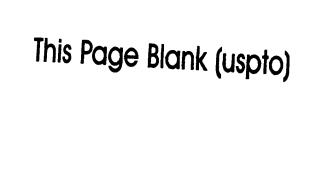
SOFTMARE: PastSEQ for Windows Version 4.0

SEQ ID NO 69

LENGTH: 20

ORGANISM: Human papillomavirus type 16

US-09-980-177A-69
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TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-075-541D-43
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US-09-980-177A-69
Search completed: May 27, 2006, 05:18:34 Job time : 30.7309 secs
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TELEPAX: 215-567-2991
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                     Query Match 21.7%; Score 112; DB 2; Length 20; Best Local Similarity 100.0%; Pred. No. 6.6e-08; Matches 20; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: AU pk 3876
FILING DATE: 12-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: pct/au91/00575
FILING DATE: 12-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: NADEL, ALAN S
REFERENCE/DOCKET NUMBER: 27,363
REFERENCE/DOCKET NUMBER: 8795-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-567-2020
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Maximum Match 100%
Listing first 100
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| S-09-986-118A-4
| S-10-654-129-4
| S-10-772-998-3
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| S-10-657-399-1
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Result No.

Minimum Maximum

DB DB

Title: Perfect

protein 9:

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                                                                                 ; LENGTH: 220
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-8
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US-10-000-903-8
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Matches
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/10000903
Publication No. US20020182221A1
GENERAL INFORMATION:
      Matches
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LENGTH: 248
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                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Human papillomavirus type 16
-10-530-253-11
                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Bruck, Claudine
APPLICANT: Cabeson Silva,
APPLICANT: Delisse, Anne-N
APPLICANT: Gerard, Catheri
APPLICANT: Lombardo-Benche
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Vaccine FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: PatentIn version 3.1
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Local Similarity 96.
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95; Conser
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Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
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                     99.2%;
  Score 513; DB 4; Length 220; Pred. No. 3.8e-53; O; Mismatches 3; Indels
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              APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Susan P. McElhiney
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2007-10-03
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
SEQ ID NO 9
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APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 8
LENGTH: 220
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Publication No. US20050031638A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and mutated E7 from Human papilloma OTHER INFORMATION: virus type 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
LENGTH: 248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           174
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Pred. No. 3.8e-53;
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US-10-367-095-9
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                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein US-10-367-095-9
RESULT 6
US-10-368-046-9
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Best Local S
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SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR PILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/356,154
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,135
PRIOR FILING DATE: 2002-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/356,113
PRIOR FILING DATE: 2002-02-14
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CURRENT FILING DATE: 2003-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: No. US20030228696A1el Insect Cell Line FILE REFERENCE: 44149-1US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/356,123 PRIOR FILING DATE: 2002-02-14
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                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 805
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                   471 MHGDTPTLHEYMLDLQPETTDLYGYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 530
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                                                                                                                                                                                             1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                          Similarity
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                                                                                 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 568
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Pred. No. 4.4e-53;
                                                                                                                                                                                                                                                                        Score 513; DB 4; Length 805; Pred. No. 1.9e-52;
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Sequence 9, Application US/10367367

Publication No. US20040121465A1

GENERAL INFORMATION:
APPLICANT: Robin A. Robinson
ITILE OF INVENTION: Optimization of Gene Sequences of
ITILE OF INVENTION: Virus-Like Particles for Expression
FILE REFERENCE: 44149-2US1
CURRENT APPLICATION NUMBER: US/10/367,367

CURRENT FILING DATE: 2003-02-15
PRIOR APPLICATION NUMBER: US 60/356,119
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,118
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR APPLICATION NUMBER: US 60/356,133
PRIOR FILING DATE: 2002-02-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-367-367-9
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LENGTH: 8
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SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2003-02-15
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PRIOR APPLICATION NUMBER: US 60/356,156
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PRIOR APPLICATION NUMBER: US 60/356,157
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95; Conserv
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Pred. No. 1.9e-52;
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PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR FILING DATE: 2002-02-14
NUMBER OF SEQ ID NOS: 13
SOPTWARE: FASUSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 805
TYPE: PRT
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PRIOR APPLICATION NUMBER: DCT/US03/04473
PRIOR FILING DATE: 2002-02-14
PRIOR PELLYG DATE: 2003-02-14
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PRIOR APPLICATION NUMBER: US 60/356,161
PRIOR PELLYG DATE: 2002-02-14
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PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR APPLICATION NUMBER: US 60/356,157
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR PELLYG DATE: 2002-02-14
PRIOR APPLICATION NUMBER: US 60/356,156
PRIOR APPLICATION NUMBER: US 60/356,123
PRIOR APPLICATION NUMBER: US 60/356,123
PRIOR PELLYG DATE: 2002-02-14
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                                                                                                                                                                             SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 805
TYPE: PRT
ORGANISM: Artificial Sequence
  Matches
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Publication No. US20050118191A1
GENERAL INFORMATION:
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Best Local
                                                     Query Match
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TITLE OF INVENTION: Optimization of Gene Sequences
TITLE OF INVENTION: Chimeric Virus-Like Particles
FILE REFERENCE: 19065/2132
                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2002-02-14
                                                                                                          FEATURE:
OTHER INFORMATION: HPV-16 L2/E7/E2 fusion protein
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                           Local Similarity
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     95;
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     Conservative
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96.9%;
Score 513; DB 5; Length 805; Pred. No. 1.9e-52; O; Mismatches 3; Indels
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Pred. No. 1.9e-52
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  Gaps
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RESULT 10
US-09-820-765-4
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US-09-728-466-1
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publication No. US20020039584A1
GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILICHOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOPTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 98
TYPE: PRT
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APPLICANT: Fisher,
APPLICANT: He, Wan
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/09/728,466
CURRENT FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
PRIOR FILING DATE: 1999-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral Agents
FILE REFERENCE: 28341/6216
                                                 COMPUTER: IBM PC compatible
operating system: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/820,765
FILING DATE: 30-Mar-2001
CLASSIFICATION: CUNknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/026,896
FILING DATE: 20-FEB-1998
                                                                                                                                                                                            ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                          CITY: Washington STATE: D.C. COUNTRY: U.S.A.
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Pred. No. 1.8e-53;
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RESULT 11
US-09-824-017-4
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US-09-824-017-4
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Best Local Similarity 96.9%;
Matches 95; Conservative
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TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 4:
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                                                                                        INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIN Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/824,017

FILING DATE: 03-Apr-2001

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                         NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
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TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
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LENGTH: 98 amino acids
                   TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPILLOMA VIRUS CAPSOMERE VACCINE
FORMULATIONS AND METHODS OF USE
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                                                                                                                                                                                   TELEPHONE: (202)
TELEFAX: (202) 6
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TOPOLOGY: linear;

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: S
US-09-986-118A-4
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US-09-986-118A-4
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
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MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/986,118A

FILING DATE: 07-NO. US20030021806A1-2001

CLASSIFICATION: CUnknown>

PRIOR APPLICATION DATA:

OF THE PRIOR DATA:

CLASSIFICATION DATA:

CONTROL OF THE PRIOR DATA:
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FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: BURGER, Alexander
HALLEK, Michael
TITLE OF INVENTION: PAPLILOMA VIRUS CAPSOMERE VACCINE FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
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                   61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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l Similarity 96.9%;
95; Conservative
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                                                                                                       1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: FOLEY & LARDNER STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
                                                                                                                                                            Conservative
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                                                                                                                                                          Score 512; DB 3; I Pred. No. 1.8e-53; 0; Mismatches 3;
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Pred. No. 1.8e-53;
0; Mismatches 3
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RESULT 13 US-10-177-390-8

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TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear TITLE OF INVENTION: Improved Transfection of Eucaryotic Cells with Linear FILE REFERENCE: 021505wo/JH/ml
CURRENT APPLICATION NUMBER: US/10/177,390
CURRENT FILING DATE: 2002-06-20
NUMBER OF SEQ ID NOS: 34
SEQ ID NO 8
LENGTW. C.
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
INFORMATION
                                               APPLICATION NUMBER: US/09/824,017
FILING DATE: 03-Apr-2001
APPLICATION NUMBER: 09/026,896
FILING DATE: 1998-02-20
ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
FILING DATE: 04-Sep-2003
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: BURGER, Alexander
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C.
               TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
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Pred. No. 1.8e-53
0; Mismatches
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US-10-772-988-3
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GENERAL INFORMATION:
APPLICANT: Kirin Beer Kabushiki Kaisha
TITLE OF INVENTION: Novel E7 antigen epitope from human
TITLE OF INVENTION: CD4+ T cells activated thereby
FILE REFERENCE: 137240PX
CURRENT APPLICATION NUMBER: US/10/479,541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 98
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APPLICANT: Thorgeirsson, Snorri S.
APPLICANT: Woitach, Joseph T.
APPLICANT: Zhang, Minghuang
                                                                                                                     Sequence 5, Application US/10479541 Publication No. US20040151723A1
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TITLE OF INVENTION: CONA ENCODING A GENE BOG (BST OVER-EXPRESSED GENE) AND ITS PROTEIN
TITLE OF INVENTION: PRODUCT
FILE REFERENCE: 11613.29USW1
CURRENT APPLICATION NUMBER: US/10/772,988
CURRENT FILING DATE: 2004-02-05
PRIOR APPLICATION NUMBER: US/09/637,746
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: PCT/US99/04142
PRIOR APPLICATION NUMBER: PCT/US99/04142
PRIOR APPLICATION NUMBER: US 60/079,567
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR APPLICATION NUMBER: US 60/075,922
PRIOR FILING DATE: 1998-02-25
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95; Conserv
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Pred. No. 1.8e-53;
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Pred. No. 1.8e-53;
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CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: 173803/2001
PRIOR FILING DATE: 2001-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 5
LENGTH: 98
LENGTH: 98
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US-10-657-399-1
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US-10-479-541-5
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CURRENT FILING DATE: 2002-04-29
PRIOR APPLICATION NUMBER: US/9/632,286
PRIOR APPLICATION NUMBER: US 09/632,286
PRIOR APPLICATION NUMBER: US 08/944,368
PRIOR APPLICATION NUMBER: US 08/944,368
PRIOR PRILING DATE: 1997-10-06
NUMBER OF SEQ ID NOS: 28
SOFTWARE: PATENTIN VETBION 3.3
SEQ ID NO 4
LENGTH: 98
TYPE: PRT
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APPLICANT: Fisher, Christopher
APPLICANT: He, Wanxia
TITLE OF INVENTION: Methods to Identify Anti-Viral.
FILE REFERENCE: 28341/6216
CURRENT APPLICATION NUMBER: US/10/657,399
CURRENT FILING DATE: 2003-09-08
PRIOR APPLICATION NUMBER: US/09/728,466
PRIOR PILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 09/382,616
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llarity 96.9%;
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RESULT 20
US-10-343-448-5
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Sequence 5, Application US/10343448
publication No. US20050054820A1
GENERAL INFORMATION:
APPLICANT: WU, TZYY-Choou
APPLICANT: HUNG, Chien-Fu
TITLE OF INVENTION: MOLECULAR VACCINE LINKING AN ENDOPLASMIC RETICULUM CHAPERONE
TITLE OF INVENTION: MOLECULAR VACCINE LINKING AN ENDOPLASMIC RETICULUM CHAPERONE
TITLE OF INVENTION: MOLECULAR VACCINE LINKING AN ENDOPLASMIC RETICULUM CHAPERONE
TITLE REFERENCE: 2240-186463
CURRENT APPLICATION UNMEER: US/10/343,448
CURRENT FILING DATE: 2003-01-31
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APPLICANT: CHOPPIN, JEANNINE
APPLICANT: BOURGAULT VILLADI
APPLICANT: GUILLET, JEAN-GEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 43
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
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SOFTWARE: PatentIn Ver.
SEQ ID NO 12
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APPLICANT: GUILLET, JEAN-GERARD
APPLICANT: CONNAN, FRANCINE
APPLICANT: FERRIES, ESTELLE
TITLE OF INVENTION: POLYEPITOPIC PROTEIN FRAGMENTS OF THE E6 PROTEIN
TITLE OF INVENTION: OR TO OF HPV, THEIR PRODUCTION AND THEIR USE
TITLE OF INVENTION: PARTICULARLY IN VACCINATION
FILE REFERENCE: 0508-1037-1
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CURRENT FILLING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: FR 9907012
PRIOR FILING DATE: 1999-06-03
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Pred. No. 1.8e-53;
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Pred. No. 1.8e-53;
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APPLICANT: Cuthill, Scott;
APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A;
APPLICANT: Ooi, Chean Eng
TITLE OF INVENTION: Complexes and Methods of
FILE REFERENCE: 21402-559
CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
VUMBER OF SEQ ID NOS: 198
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 17
LENGTH: 98
TYPE: PRT
ORGANISM: Homo sapiens
US-10-367-057-17
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US-10-530-253-14
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US-10-367-057-17
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LENGTH: 98
TYPE: PRT
                                                           GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 17, Application US/10367057 Publication No. US20050100554A1 GENERAL INFORMATION:
                                                                                                                                                       Sequence 14, Application US/10530253 Publication No. US20060014926A1
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Best Local Similarity
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APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US01/24134
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/222,902
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
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APPLICANT: FRAZER; Ian Hector
TITLE OF INVENTION: Gene Expression System Based on
FILE REFERENCE: 10338-11U1
CURRENT APPLICATION UNMER: US/11/077,939
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: PCT/AU2003/001200
PRIOR FILING DATE: 2003-09-12
PRIOR FILING DATE: 2003-09-13
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin version 3.2
SEQ ID NO 5
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT ; ORGANISM: Human papillomavirus type 16 US-11-077-939-5
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; TYPE: PRT
; ORCANISM: Human papillomavirus type 16
US-10-530-253-14
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US-11-077-939-5
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PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 14
                                                                                                                                            Sequence 4, Application US/11179478 Publication No. US20050249745A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/11077939 Publication No. US20050196865A1 GENERAL INFORMATION:
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Best Local Similarity
                                                GENERAL INFORMATION:
APPLICANT: BURGER, Alexander
APPLICANT: HALLEK, Michael
TITLE OF INVENTION: FARTILLOMA VIRUS CAPSOMERE VACCINE
TITLE OF INVENTION: FORMULATIONS AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT FILING DATE:
               CORRESPONDENCE ADDRESS:
                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 98
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Pred. No. 1.8e-53;
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Pred. No. 1.8e-53;
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STREET:

3000 K Street, N.W.

Washington D.C.

U.S.A.

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PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 121
TYPE: PRT
TYPE: PRT
ORGANISM: Artificial Sequence
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                                     ; FEATURE:
; OTHER INFORMATION: fusion
US-10-267-311-12
                                                                                                                                                                                                                                                        APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE.
FILE REPERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
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Best Local Similarity
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Query Match
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PILING DATE: 13-JULY-2005
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/654,129
FILING DATE: 04-Sep-2003
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 98 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Sandercock, Colin G.
REGISTRACE 31,298
REFERENCE/DOCKET NUMBER: 37067/102
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
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SOFTWARE: Patentin Bol-
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99.0%; Score 512;
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Pred. No. 1.8e-53;
0; Mismatches 3
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DB
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Length 121;
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1909-07-08
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
NUMBER OF SEQ ID NOS: 55
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                                                                                                               APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE:
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/99/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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Publication No.
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                                                        SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 35
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                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                    LENGTH: 198
TYPE: PRT
ORGANISM: Artificial Sequence
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No. US20050089841A1
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0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 512; DB 5;
Pred. No. 2.4e-53;
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: LNDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/99/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
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PRIOR APPLICATION NUMBER: US 60/143,757
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US-10-000-903-1
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US-10-679-956-35
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; OTHER INFORMATION:
US-10-267-311-35
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Best Local S
Matches 95
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                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/10000903 Publication No. US20020182221A1
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FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
                                                                                                                              APPLICANT: Gerard, Catherin
APPLICANT: Lombardo-Benche
TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                        APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva,
APPLICANT: Delisse, Anne-b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: fusion sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95;
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                                                                                                                                                      Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
Lombardo-Bencheikh, Angela
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Pred. No. 4.4e-53;
0; Mismatches 3
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Pred. No. 4.4e-53;
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GENERAL

INFORMATION:

APPLICANT: Bruck, APPLICANT: Cabezo APPLICANT: Delise

Cabezon Silva, Teresa Delisse, Anne-Marie Eva

Fernande

Claudine

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RESULT 31
US-10-000-903-12
; Sequence 12, Application US/10000903
; Publication No. US20020182221A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP99/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 1
LENGTH: 220
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Matches
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 1
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APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 28
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TYPE: PRT
ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E7 from Human papilloma virus OTHER INFORMATION: 16)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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95; Conser
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                                                                                                                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
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Pred. No. 5e-53;
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Pred. No. 5e-53;
D; Mismatches
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; OTHER INFORMATION: Chimaeric protein (Clyta from Streptococcus; OTHER INFORMATION: pneumoniae and E7 from Human papilloma virus type; OTHER INFORMATION: 16)
US-10-899-771-12
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 12
LENGTH: 239
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-12
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LENGTH: 239
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APPLICANT: Gerard, Catherine Marie Chislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR FILING DATE: 1200-12-18
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR PILING DATE: 1999-12-18
PRIOR FILING DATE: 1997-12-24
PRIOR FILING DATE: 1997-12-24
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
                                                                                                                                                                                                  Local Similarity
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                                61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                     MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 192
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96.9%;
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Pred. No. 5.5e-53;
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                                                                                                                                                                                                                      Length 239;
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Sequence 2, Application US/11192923A

Publication No. US20060018928A1

GENERAL INFORMATION:

APPLICANT: PANO, XIAOWU

TITLE OF INVENTION: VIRUS-LIKE PARTICLE CONTAINING A DENGUE VIRUS

TITLE OF INVENTION: RECOMBINANT REPLICON

FILE REFERENCE: 116620-003

CURRENT APPLICATION NUMBER: US/11/192,923A

CURRENT FILING DATE: 2005-07-29

PRIOR APPLICATION NUMBER: CN 03115272.4

PRIOR APPLICATION NUMBER: CN 03115273.2

PRIOR APPLICATION NUMBER: CN 03115273.2

PRIOR FILING DATE: 2003-01-30

PRIOR FILING DATE: 2003-01-30

NUMBER OF SEQ ID NOS: 45

SOFTWARE: Patentin Ver. 3.3
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US-10-530-253-7
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US-11-192-923A-2
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Publication No. US20060014926A1

GENERAL INFORMATION:
APPLICANT: Casesetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Jeffrey K. Pullen
APPLICANT: SUBJECT OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: DCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NIMBREW OF SECT IT NOCE 65
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                                                                                                                                                                                                                                               LENGTH: 256
TYPE: PRT
ORGANISM: Human papillomavirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Human papillomavirus type
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                                                                                                                                                                             Local Similarity
61
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                                                                                                               1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                  CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                        MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDBIDGPAGQABPDRAHYNIVTFCCK
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CDSTLRLCVQSTHVDIRTLEDILMGTLGIVCPICSQKP 98
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Pred. No. 5.8e-53;
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Pred. No. 6e-53;
                                                                                                                                                         Mismatches
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PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR PELICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
FENCTH: 295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: AU PO 5178
PRIOR FILING DATE: 1997-02-19
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
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APPLICANT: MALLIAROS, JIM
TITLE OF INVENTION: CHARLATING IMMUNOSTIMULATING COMPLEXES
FILE REFERENCE: 017227/0149
CURRENT APPLICATION NUMBER: US/09/367,309A
CURRENT FILING DATE: 1999-08-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/AU98/00080 PRIOR FILING DATE: 1998-02-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 266
TYPE: PRT
ORGANISM: Human papillomavirus type 16
                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                Local Similarity
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Local Similarity 96.9%;
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                          MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 257
                                                                  MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                            Conservative
                                                                                                                                            99.0%;
                                                                                                                          Score 512; DB 4; Length 295; Pred. No. 7.2e-53; O; Mismatches 3; Indels
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Pred. No. 6.3e-53;
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CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FREESEQ for Windows Version 4.0
SEQ ID NO 25
LENGTH: 324
                                                                              ; FEATURE:
; OTHER INFORMATION: fusion sequence
US-10-267-311-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-267-311-25; Sequence 25, Application US/10267311; Publication No. US20030050469A1
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Best Local Similarity
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                   Query Match
Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE
FILE REFERENCE: 12071/002001
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 295
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96.9%;
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                   Score 512; DB 4;
Pred. No. 8.1e-53;
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Pred. No. 7.2e-53;
Mismatches
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US-10-472-724-10
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CURRENT APPLICATION NUMBER: US/10/679,956

CURRENT FILING DATE: 2003-10-06

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7
FILE REFERENCE: 4121-154
                                SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 334
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 10, Application US/10472724 Publication No. US20040171806A1
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LENGTH: 324
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Best Local
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
                                                                                                                                                                  NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                 PRIOR APPLICATION NUMBER: EP 01107271.7 PRIOR FILING DATE: 2001-03-23
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
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ORGANISM: Artificial Sequence
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                 OTHER INFORMATION: Synthetic Construct
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQXP 98
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vo. US20050089841A1
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96.9%;
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Pred. No. 8.1e-53;
0; Mismatches 3
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RESULT 42
US-10-899-771-6
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US-10-000-903-6
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                                                     FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1998-12-18
PRIOR FILING DATE: 1997-12-24
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SOFTWARE: FAStSEQ for Windows Version
SEQ ID NO 6
LENGTH: 371
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Best Local Similarity
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CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
                                                                                                                                                                                                                                            APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Pa
TITLE OF INVENTION: and Fusion Proteins Adjuvanted
SOFTWARE: FastSEQ
EQ ID NO 6
                                    NUMBER OF SEQ ID NOS: 28
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                     for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.0%;
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Pred. No. 8.4e-53;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 512; DB 4;
Pred. No. 9.5e-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                              Human Papilloma Virus Proteins
juvanted with a CpG Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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RESULT 44
US-10-899-771-14
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; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14
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US-10-000-903-14
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             Sequence 14, Application US/10899771
Publication No. US20050031638A1
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Hu
TITLE OF INVENTION: and Fusion Proteins Adjuv
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/10/899,771
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fei
APPLICANT: Gerard, Catherine Marie Ghi
APPLICANT: Lombardo-Bencheikh, Angela
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-899-771-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                           284 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              325 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                265
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                  1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MHGDTPTLHEYMLDLQPETTDLYXYXQLND$SEEEDBIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95;
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                                                                                                                                                                                                                                                                                                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 324
                                                                                                                                                                                                                                                                                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cabezon Silva, Teresa
Dellsse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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llarity 96.9%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               plication US/10000903
US20020182221A1
                                                          and Fusion Proteins Adjuvanted
2004-07-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 512; DB 4
Pred. No. le-52;
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Pred. No. 9.5e-53;
0; Mismatches 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 4; Length 390;
                                                          Human Papilloma Virus Proteins
juvanted with a CpG Oligonucleo
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                                                          CpG Oligonucleotide
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PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR PPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOPTWARE: FASUSEQ for Windows Version 3.0
SEQ ID NO 14
LENGTH: 390
                                                                                                                                                                                                                                            ; LENGTH: 421
; TYPE: PRT
; ORGANISM: Chimaeric
US-10-296-770-7
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US-10-899-771-14
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US-10-296-770-7
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CURRENT APPLICATION NUMBER: US/10/296,770

CURRENT FILING DATE: 2002-12-13

PRIOR APPLICATION NUMBER: PCT/EP01/06952

PRIOR FILING DATE: 2001-06-19

PRIOR FILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: GB 0015619.0

PRIOR PILING DATE: 2000-06-26

PRIOR APPLICATION NUMBER: GB 0026484.6

PRIOR PILING DATE: 2000-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/10296770 Publication No. US20030104570A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                             SEQ ID NO 7
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Best Local
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                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cabezon Silva, Teresa Elisa Virginia
APPLICANT: Delisse, Anne-Marie Eva Fernande
TITLE OF INVENTION: Triple Pusion Proteins Comprising
TITLE OF INVENTION: Ubiquitin Fused Between Thioredoxin and a
TITLE OF INVENTION: Interest
                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           344
375 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 412
                                                                              315 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCK
                                      61
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                                                                                                    1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                                                                               95;
                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 343
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                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                               (E. coli - human)
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                                                                                                                                                                                 Score 512; DB 4;
Pred. No. 1.1e-52;
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Pred. No. 1e-52;
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RESULT 46 US-10-267-311-19

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FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: PASESEQ for Windows Version 4.0

SEQ ID NO 19
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                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 19, Application US/10679956
Publication No. US20050089841A1
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Publication No. US20030050469A1
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                 -10-679-956-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randa
APPLICANT: Mizzen, Lee A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 493
TYPE: PRT
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                            OTHER INFORMATION: fusion sequence
                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: fusion sequence
                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      396 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 455
                                                               396 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 455
                         61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95; Conservative
                                                                                                                                                                                                                                                                                                                                 493
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                                                                                                                                              95; Conservative
                                                                                                                                                               Similarity
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
                                                                                           MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                               99.0%;
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                                                                                                                                            Score 512; DB 5; L
Pred. No. 1.4e-52;
0; Mismatches 3;
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Pred. No. 1.4e-52;
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APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RES
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-267-311-17
; Sequence 17, Application US/10267311
; Publication No. US20030050469A1
                                                                                                                                                                                                                                                             APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE:
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/05/613,303
PRIOR PILING DATE: 2000-07-10
PRIOR PPLICATION NUMBER: US/05/143,757
PRIOR FILING DATE: 1999-07-08
                                                                               ; FEATURE:
; OTHER INFORMATION: fusion sequence US-10-679-956-17
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US-10-679-956-17
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
  Matches
                   Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                   TENGTH: 639
TYPE: PRT
ORGANISM: Artificial Sequence
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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  95;
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milarity 96.9%;
Conservative
  Conservative
                 99.0%;
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                   Score 512; DB 5;
Pred. No. 1.9e-52;
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Pred. No. 1.9e-52;
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  Mismatches
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                                      Length 639;
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MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60

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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/99/613,303
PRIOR APPLICATION NUMBER: US/99/613,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTMARE: PastSEQ for Windows Version 4.0
SEQ ID NO 51
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US-10-679-956-51
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US-10-267-311-51
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LENGTH: 641
TYPE: PRT
ORGANISM: Artificial Sequence
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Publication No.
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE:
TILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
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                                                             LENGTH: 641
TYPE: PRT
OTHER INFORMATION: fusion sequence
                ORGANISM: Artificial Sequence
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|o. US20030050469A1
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96.9%;
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Pred. No. 1.9e-52;
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FILE REFERENCE: 12071/002001

CURRENT APPLICATION NUMBER: US/10/679,956

CURRENT FILING DATE: 2003-10-06

PRIOR APPLICATION NUMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEG ID NOS: 55

SOFTWARE: FASTSEQ for Windows Version 4.0

SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 53
US-10-679-956-53
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; OTHER INFORMATION: fusion sequence
US-10-267-311-53
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CURRENT APPLICATION NUMBER: US/10/267,311

CURRENT FILING DATE: 2002-10-09

PRIOR APPLICATION UNMBER: US/09/613,303

PRIOR FILING DATE: 2000-07-10

PRIOR APPLICATION NUMBER: US 60/143,757

PRIOR FILING DATE: 1999-07-08

NUMBER OF SEQ ID NOS: 55

SOFTWARE: FastSEQ for Windows Version 4.0
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LENGTH: 647
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Best Local Similarity
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
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Local Similarity 96.9%;
les 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          610 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 647
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647
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Pred. No. 1.9e-52;
0; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                  RESULT 55
US-10-530-253-3
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TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-10-530-253-5
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Best Local Similarity
Matches 95; Conserv
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Publication No. US20060014926A1
GENERAL INFORMATION:
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Publication No. US20060014926A1
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
CURRENT FILING DATE: 2005-04-04
       APPLICANT: Jeffry K. Pullen
APPLICANT: Jeffry K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
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SOFTWARE: PatentIn version 3.1
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PRIOR FILING DATE: 2003-10-02
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PRIOR FILING DATE: 2002-10-03
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Local Similarity 95.9%;
FILING DATE: 2002-10-03
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96.9%;
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Pred. No. 7.6e-53;
1; Mismatches 3
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Pred. No. 1.9e-52;
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SOFTWARE: PatentIn ver
SEQ ID NO 3
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LENGTH: 24
TYPE: PRT
GENERAL INFORMATION:
APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
APPLICANT: CHEN, SI-YI AND ZHAOYANG, YOU
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANTIGENS WHICH ELICIT AN
TITLE OF INVENTION: IMMUNE RESPONSE
FILE REFERENCE: TBA
CURRENT FILING DATE: 202-07-22
PRIOR APPLICATION NUMBER: US/10/201,764
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
PRIOR FILING DATE: 2000-05-05
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Publication No. US20030166140A1
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Best Local Similarity
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Best Local
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APPLICANT: Susan P. McSlhiney
TITLE OF INVENTION: HUWAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
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SOFTWARE: PatentIn version 3.1
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95.9%;

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Pred. No. 1e-52;
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; PRIOR FILING DATE: 1999-05-06
; PRIOR APPLICATION NUMBER: 60/132,750
; PRIOR FILING DATE: 1999-05-06
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 19
; LENGTH: 98
; TYPE: PRT
; ORGANISM: Human papillomavirus type E7
US-10-201-764-19
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; ORGANISM: Human papillomavirus type
US-10-681-410-19
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CURRENT FILING DATE: 2003-10-08
PRIOR APPLICATION NUMBER: US/10/201,764
PRIOR FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/566,420
PRIOR TILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: 60/132,752
PRIOR APPLICATION NUMBER: 60/132,752
PRIOR APPLICATION NUMBER: 60/132,750
PRIOR PILING DATE: 1999-05-06
PRIOR PILING DATE: 1999-05-06
PRIOR PILING DATE: 1999-05-06
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Sequence 26, Application US/10484063
Publication No. US20050048467A1
GENERAL INFORMATION:
APPLICANT: SASTRY, K. JAGANNADHA
APPLICANT: TORTOLERO-LUNA, GUILLERMO
APPLICANT: FOLLEM, MICHELE
TITLE OF INVENTION: METHODS AND COMPOSITIONS
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Publication No. US20040096426A1
GENERAL INFORMATION:
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Best Local
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Best Local :
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Similarity 95.9%;
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95.9%;
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Pred. No. 7.4e-53;
1; Mismatches 3
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Pred. No. 7.4e-53;
1; Mismatches 3
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RESULT 61
US-10-392-113-29
; Sequence 29, Application US/10392113
; Publication No. US20030224993A1
; GENERAL INFORMATION:
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; TYPE: PRT
; ORGANISM: Human papillomavirus type
US-10-484-063-26
                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Synthetic Construct US-10-472-724-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 60
US-10-472-724-4
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Best Local Similarity
Matches 94; Conserv
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LENGTH: 98
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APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/484,063
CURRENT FILING DATE: 2004-01-16
PRIOR APPLICATION NUMBER: PCT/US02/23198
PRIOR FILING DATE: 2002-07-19
PRIOR APPLICATION NUMBER: 60/306,809
PRIOR FILING DATE: 2001-07-20
PRIOR FILING DATE: 2010-7-20
NUMBER OF SEQ ID NOS: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: UTSC:560US
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 111
                                                                                                                                                                                                                                                                                                     Local Similarity 96.9 es 94; Conservative
                                                                                                                                             67
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                                                                                                                                                                  DSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
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                                                                                                                                           DSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP
                                                                                                                                                                                                                        HGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKC
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95.9%;
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Pred. No. 8.6e-53;
0; Mismatches 3;
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Pred. No. 7.4e-53;
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TITLE OF INVENTION: COMPOSITIONS THAT INHIBIT PROLIFERATION
TITLE OF INVENTION: OF CANCER CELLS
FILE REFERENCE: 21108.0005U3
CURRENT APPLICATION NUMBER: US/10/392,113
CURRENT APPLICATION NUMBER: 60/365,078
PRIOR APPLICATION NUMBER: 60/365,078
PRIOR PILING DATE: 2002-03-15
PRIOR PILING DATE: 2002-03-15
PRIOR APPLICATION NUMBER: PCT/US01/32127
PRIOR PILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 60/239,705
PRIOR APPLICATION NUMBER: 60/239,705
PRIOR PILING DATE: 2000-10-12
NUMBER: OF SEQ ID NOS: 45
SOPTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 29
LENGTH: 98
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RES
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-9
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR PILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LEEGTH: 98
LEEGTH: 98
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US-10-267-311-8
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Best Local Similarity
                                                                                                                                                                         Matches
                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: Description of Artificial Sequence:/Note OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                            1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                                                                                                                                         h 97.3%;
Similarity 95.9%;
CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 98
                                      CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                                 MDGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK
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95.9%;
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                                                                                                                                                                                           Score 503; DB 4; Length 98; Pred. No. 2.2e-52;
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APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
FRIOR APPLICATION NUMBER: US/99/613,303
PRIOR APPLICATION NUMBER: US/99/613,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 29
TENUM: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 29, Application US/10267311 Publication No. US20030050469A1 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
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                                                                    Matches
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                                                                                                            Query Match
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION UNMEER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR FILING DATE: 2003-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                            LENGTH: 648
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                                                                                        Similarity
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MHGDTFTLHEYMLDLQPETTDLYXXXQLNDSSEEBBEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                                                  97.3%;
ilarity 95.9%;
Conservative
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Pred. No. 2.2e-52;
0; Mismatches 4
                                                                Score 503; DB 4; Length 648; Pred. No. 2.3e-51; O; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 98;
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RESULT 66
US-10-267-311-41
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US-10-679-956-29
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Query Match
                                                                                                                      SEQ ID NO 41
LENGTH: 711
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
                                                                                                                                                                     APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
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PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
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APPLICANT: Chu, I
APPLICANT: Mizze
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TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
                                                                                                                                                          SOFTWARE: FastSEQ for Windows Version 4.0
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                 ORGANISM: Artificial Sequence
                                                 OTHER INFORMATION: fusion sequence
                                                                      FEATURE:
                                                                                                         TYPE: PRT
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 97.3%;
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 Score 503;
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2.3e-51;
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Length 711;
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US-10-267-311-45
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TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RE:
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
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LENGTH: 711
                                                                     SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 45
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                                                                                                                          APPLICANT: Siegel, Marvin
APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A TH1-LIKE RESPONSE IN VITRO
FILE REFERENCE: 12071/002001
CURRENT APPLICATION NUMBER: US/10/267,311
CURRENT FILING DATE: 2002-10-09
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR APPLICATION NUMBER: US/09/613,757
PRIOR FILING DATE: 2000-07-10
PRIOR FILING DATE: 1999-07-08
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                                                                                                               NUMBER OF SEQ ID NOS:
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SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Chu,
APPLICANT: Mizze
TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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Pred. No. 2.6e-51;
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PRIOR APPLICATION NUMBER: US 60/143,757
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FREUSEQ for Windows Version 4.0
SEQ ID NO 45
LENGTH: 724
TYPE: PRT
ORGANISM: Artificial Sequence
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US-10-115-440-7
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; OTHER INFORMATION:
US-10-267-311-45
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                                                                                                                                                                                                                                            Sequence 7, Application US/10115440 Publication No. US20040086845A1 GENERAL INFORMATION:
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Best Local 9
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Best Local Similarity
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APPLICANT: WU, TZYY-Choou
APPLICANT: HUNG, Chien-Fu
ITILE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLOCATION DOMAIN OF ITILE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN
FILE REFERENCE: 02240-17934
CURRENT FILING DATE: 2002-09-30
PRIOR APPLICATION NUMBER: US 60/281,003
PRIOR APPLICATION NUMBER: US 60/281,003
PRIOR APPLICATION NUMBER: PCT/US00/41422
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: PCT/US00/41422
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: WS 09/501,097
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APPLICANT: Chu, N. Randall
APPLICANT: Mizzen, Lee A.
TITLE OF INVENTION: INDUCTION OF A THI-LIKE RESPONSE
FILE REFERENCE: 12071/002001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/679,956
CURRENT FILING DATE: 2003-10-06
PRIOR APPLICATION NUMBER: US/09/613,303
PRIOR FILING DATE: 2000-07-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                               61 CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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94; Conservative
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Vo. US20050089841A1
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95.9%;
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95.9%;
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Pred. No. 2.6e-51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 724;
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RESULT 72 US-11-072-288-2

Sequence 2, Application US/11072288
Publication No. US20050159386A1
GENERAL INFORMATION:
APPLICANT: KIENY, Marie-Paule
APPLICANT: BALLOUL, Jean-Marc
APPLICANT: BIZOUARNE, Nadine

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; ORGANISM: Human papillomavirus
US-10-115-440-7
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                                                                                                                                                                                                                               ; ORGANISM: Human papillomavirus US-10-115-440-5
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US-10-115-440-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
                                                                                                                                                    Matches
                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                         SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLOCATION DOMAIN OF A TITLE OF INVENTION: SUPERIOR MOLECULAR VACCINE LINKING THE TRANSLOCATION DOMAIN OF A TITLE OF INVENTION: BACTERIAL TOXIN TO AN ANTIGEN

FILE REFERENCE: 02240-17934

CURRENT PELICATION NUMBER: US/10/115,440

CURRENT FILLING DATE: 2002-09-30

PRIOR APPLICATION NUMBER: US 60/281,003

PRIOR FILLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: PCT/US00/41422

PRIOR APPLICATION NUMBER: US 09/501,097

PRIOR FILLING DATE: 2000-02-09

PRIOR FILLING DATE: 2000-02-09

PRIOR FILLING DATE: 2000-02-09

PRIOR FILLING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                 LENGTH: 28
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: WU, Tzyy-Choou APPLICANT: HUNG, Chien-Fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2000-02-09
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234
                                                                          174 MHGDTPTLHEYMLDLQPETTDLYCYEQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 233
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                                                                                                            1 MHGDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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                                CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQ 96
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQ
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                                                                                                                                                  Conservative
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96.9%;
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96.9%;
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Pred. No. 1.9e-51;
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Pred. No. 5.2e-52;
                                                                                                                                                    Mismatches
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269
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APPLICANT: Jeffrey K. Fullen
APPLICANT: Susan P. McElhiney
FILE OPTINENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT FILING DATE: US/10/530,253
CURRENT FILING DATE: PCT/US2003/031726
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR FILING DATE: 2003-10-03
INUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 30
US-10-530-253-30
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US-11-072-288-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/11/072,288
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US/09/462,993
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: PCT/FR98/01576
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: FR 97/09152
PRIOR FILING DATE: 1997-07-18
NUMBER OF SEQ ID NOS: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30, Application US/10530253
Publication No. US20060014926A1
                                                                                                                                                         Matches
                                                                                                                                                                        Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: ANTITUMORAL COMPOSITION BASED ON IMMUNOGENIC TITLE OF INVENTION: POLYPEPTIDE WITH MODIFIED CELL LOCATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE: 017753-122
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                                                                                                                                                                          Similarity
              KCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                             MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSS-EEEDEIDGPAGQAEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP 98
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                                                                        MHGEITTLQDYVLDLEPEATDLYCYEQLCDSSEEEEDTIDGPAGQAKPDTSNYNIVTSCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVCPICSQKP 117
                                                                                                                                                       Conservative
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                                                                                                                                                                      73.8%;
73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92.5%;
                                                                                                                                                   Score 381.5; DB 5; Pred. No. 9.4e-38; 11; Mismatches 14;
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Pred. No. 5e-49;
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US-10-530-253-28
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                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Swith, Maria C.
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 98
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SEQ ID NO 29
LENGTH: 97
TYPE: PRT
                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 29, Application US/10530253
Publication No. US20060014926A1
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                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Cassetti, Maria C. APPLICANT: Smith, Larry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEBEDEIDGPAGQAEPDRAHYNIVTFCCK 60
                                                                                                56;
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CDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                              MRGHKPTLKEYVLDLYPEPTDLYCYEQLSDSSDEDEGLDRPDGQAQPATADYYIVTCCHT 60
                                                         MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCK 60
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71.1%;
                                                                                                            57.1%; Score 295; DB 5; 57.7%; Pred. No. 2.3e-27;
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Pred. No. 1.3e-36;
2; Mismatches 16
                                                                                                Mismatches
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                                                                                                                           Length 97;
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APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Susan P. McElhiney
APPLICANT: Susan P. McElhiney
ITILE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
SEQ ID NO 36
LENGTH: 98
LENGTH: 98
TYPE: PRT
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US-10-530-253-34
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Best Local Similarity 5/...
56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 36, Application US/10530253 Publication No. US20060014926A1
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 34
LENGTH: 99
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Publication No. US20060014926A1
                                                                             Matches
                                                                                                                            Query Match
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APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
PRIOR FILING DATE: 2002-10-03
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                                                                                                                                                                               ORGANISM: Human papillomavirus type 58-10-530-253-36
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                                                                                                    Local
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1 MHGDTPTLHEYMLDLQPETTDLYXYXQLNDSSEEED-EIDGPAGQAEPDRAHYNIVTFCC 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MRGDKATIKDYILDLQPETTDLHCYEQLGDSSDEEDTDGVDRPDGQAEQATSNYYIVTYC 60
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                                                                                                       Similarity
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CNTTVRLCVNSTASDLRTIQQLLMGTVNIVCPTCAQQ
                                                                          56.0%; Score 289.5; DB 5; llarity 57.1%; Pred. No. 1.1e-26; Conservative 16; Mismatches 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56.9%; Score 294; DB 5; Length 99; 57.1%; Pred. No. 3.2e-27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Indels
                                                                                                                         Length 98;
                                                                             Indels
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                                                                             Gaps
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; ORGANISM: Homo sapiens
US-10-367-057-12
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US-10-751-845-126
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                                                              ; OTHER INFORMATION: Artificial US-10-751-845-126
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                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLERIC ACIDS ENCODING
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 126
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SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 12
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                   CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-09-16
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APPLICANT: Jackson, Amanda;
APPLICANT: Lewin, David A.;
APPLICANT: Ooi, Chean Eng
TITLE OF INVENTION: Complexes and Methods
FILE REFERENCE: 21402-559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/367,057
CURRENT FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/256,911
PRIOR FILING DATE: 2002-02-14
                                                                                                    TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                   LENGTH: 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WHGRLVTLKDIVLDLQPPDPVGLHCYEQLEDSSEDEVDKVD--KQDAQPLTQHYQILTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGCDSNVRLVVECTDGDIRQLQDLLLGTLNIVCPICAPKP 98
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41.6%;
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;; Pred. No. 2.5e-21;
14; Mismatches 29
Score 215; DB 5;
Pred. No. 1.2e-17;
                                                                                    fusion sequence
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                    Length 117;
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APPLICANT: Hedley, Mary Lynne
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POLYEPITOPE POLYPEPTIDES
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-12-09
PRIOR FILING DATE: 1999-19-16
NUMBER OF SEO ID NOS: 163
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US-10-751-845-158
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PRIOR FILING DATE: 1999-09-16
NUMBER OF SEQ ID NOS: 163
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 157
LENGTH: 236
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                        Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
SEQ ID
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CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/09/664,225
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
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APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
                   SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 41.6%;
Local Similarity 52.2%;
NO 158
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o. US20050100928A1
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Pred. No. 3e-17;
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RESULT 83
US-10-530-253-32
; Sequence 32, Application US/10530253
; Publication No. US20060014926A1
; GENERAL INFORMATION:
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APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING POI
FILE REFERENCE: 08191-013001
CURRENT APPLICATION NUMBER: US/10/751,845
CURRENT FILING DATE: 2004-01-05
PRIOR APPLICATION NUMBER: US/99/664,225
PRIOR APPLICATION NUMBER: US 60/169,846
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR APPLICATION NUMBER: US 60/154,665
PRIOR FILING DATE: 1999-16
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US-10-751-845-160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Artificial fusion sequence
US-10-751-845-160
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
                                                                                                  APPLICANT: Cassetti, Maria C. APPLICANT: Smith, Larry
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SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ocal Similarity
                                                                                                                                                                                                                                                                                     126
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                                                                                                                                                                                                                                                                                                                   67 LCVQSTHVDIRTLEDLLMGTLGIVXPICSQKP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
                                                                                                                                                                                                                                                                                                                                                                                            TLHBYMLDLQPETTDLYXYXQLNDSSBEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLR 66
                                                                                                                                                                                                                                                                                                                                                                     TLHEYMLDLQPETTDLYSY--------
                                                                                                                                                                                                                                                                                     -----LLMGTLGIVCPICSQKP
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Pred. No. 3.3e-17;
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Pred. No. 3e-17;
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RESULT 84
US-10-433-091-4
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US-10-530-253-32
                                                                                                                                                        RESULT 85
Sequence 27, Application US/10530253
Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/10433091 Publication No. US20040101533A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS TYPE 18 FILE REFERENCE: 037067/0115 CURRENT APPLICATION NUMBER: US/10/433,091 CURRENT FILING DATE: 2003-11-25 PRIOR APPLICATION NUMBER: PCT/EP01/14038 PRIOR FILING DATE: 2001-11-30 PRIOR FILING DATE: 2001-11-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: MULLER, RAINER
APPLICANT: NIELAND, JOHN
APPLICANT: GABBLISBERGER, JOSEF
APPLICANT: HERBST, RUTH
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PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
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PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: DE 100 59 630.4 PRIOR FILING DATE: 2000-12-01 NUMBER OF SEQ ID NOS: 72 SOFTWARE: Patentin Ver. 2.1
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TYPE: PRT
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                                                                                                                                                                                                                                                               52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                                                                                                                                                      1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
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                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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APPLICANT: Bruck, Claudine
APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Delisse, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
ITILE OF INVENTION: Vaccine
FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT APPLICATION NUMBER: CUT/EP98/05285
PRIOR APPLICATION NUMBER: GD171953.5
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 19
SEQ ID NO 19
                                         RESULT 87
US-10-899-771-19
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SEQ ID NO 27
LENGTH: 105
Sequence 19, Application US/10899771 Publication No. US20050031638A1
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                                                                                                                                                                                                                                                                                                           Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SUSAN P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR PILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                    172
                                                                                                                                                                                                                    114 MHGPKATLQDIVLHLEPQNEIPVDLLGHQQLSDSEEENDEIDGVNHQHLPARRAEPQR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 HTMLCMCCKCEARIKLVVESSADDLRAFQQLFLNTLSFVCPWCASQ 104
                                                                                                                                                                         52 YNIVTFÇÇKÇDSTLRLCVQSTHVDIRTLEDILMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                                                           1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
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                                                                                                                                  HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCFWCASQ 217
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No. US20020182221A1
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39.6%; Pred
39.6%; 20;
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39.6%; Pred. No. 3.5e-16;
tive 21; Mismatches 32
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                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                           171
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PRIOR APPLICATION NUMBER: GB 9717953.5
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 23
LENGTH: 383
TYPE: PRT
ORGANISM: Homo sapien
US-10-000-903-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius; OTHER INFORMATION: influenzae B and mutated E7 from Human papillor; OTHER INFORMATION: virus type 18)
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US-10-000-903-23
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CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR APPLICATION NUMBER: PS777262.9
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Bruck, Claudine APPLICANT: Cabezon Silva, Te APPLICANT: Delisse, Anne-Mar APPLICANT: Gerard, Catherine APPLICANT: Lombardo-Bencheik TITLE OF INVENTION: Vaccine
                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 23, Ap
Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 19
                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
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TYPE: PRT
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    270
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              172 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52 YNIVTFCCKCDSTLRĻCVQSTHVDIRTLEDĻLMGTLGIVXPICSQK 97
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                                1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                       42;
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MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cabezon Silva, Teresa
Delisse, Anne-Marie Eva Fernande
Gerard, Catherine Marie Ghislaine
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                                                                                       Conservative
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                                                                                  38.8%; Score 200.5; DB
39.6%; Pred. No. 3e-15;
tive 20; Mismatches
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Pred. No. 1.2e-15;
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                                                                                                                              DB 4;
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                                                                                                                              Length 383;
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TITLE OF INVENTION: Enhanced Antigen Delivery and Modulation
TITLE OF INVENTION: of the Immune Response Therefrom
FILE REFERENCE: 600-1-081CONCIP1
CURRENT APPLICATION NUMBER: US/10/800,023
CURRENT FILING DATE: 2004-03-14
PRIOR APPLICATION NUMBER: 09/925,284
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 09/926,704
PRIOR APPLICATION NUMBER: 09/586,704
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 2000-06-05
PRIOR FILING DATE: 1995-01-31
PRIOR APPLICATION NUMBER: PCT/US96/01383
PRIOR FILING DATE: 1995-01-31
PRIOR APPLICATION NUMBER: 08/381,528
PRIOR FILING DATE: 1995-01-31
PRIOR FILING DATE: 1995-01-31
PRIOR FILING DATE: 1995-01-31
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US-10-899-771-23
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US-10-800-023-28
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CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 9727262.9
PRIOR FILING DATE: 1997-12-24
PRIOR FILING DATE: 1997-12-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 28, Application US/10800023 Publication No. US20040258688A1 GENERAL INFORMATION:
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Publication No.
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APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Steinman, Ralph
APPLICANT: Nussenzweig, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E6E7 fusion from Human papilloma OTHER INFORMATION: virus type 18)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          328 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hawiger, Daniel
Bonifaz, Laura
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; ORGANISM: human papilloma virus E7 protein
US-10-800-023-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 92
US-10-530-253-37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Human Papillomavirus E7
US-11-041-893-101
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                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
APPLICANT: Jeffrey K. Pullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: MAHAIRAS, Gregory G.
APPLICANT: MAHAIRAS, Gregory G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
FILE REPERENCE: 100123.401
CURRENT APPLICATION NUMBER: US/11/041,893
CURRENT FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: US 60/616,855
PRIOR PILING DATE: 2004-10-06
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Best Local Similarity
Matches 42; Conserv
                                                            SOFTWARE: PatentIn version 3.1 SEQ ID NO 37
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 37, Application US/10530253 Publication No. US20060014926A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 101
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                                                                                                                     CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/538,713 PRIOR FILING DATE: 2004-01-23
                                                                                                    NUMBER OF SEQ ID NOS: 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 105
ORGANISM: Human papillomavirus type 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 35
                                          LENGTH: 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43 GQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIR 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59 HTMLCMCCKCEARIELVVESSADDLKAFQQLFLKTLSFVCPWCASQ 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 YNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MHGDTFTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIR 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MHGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/11041893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 198.5;
Pred. No. 1.1
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. 1.1e-15;
tches 33;
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; OTHER INFORMATION: Synthetic Construct
US-10-472-724-8
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US-10-472-724-8
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                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/10000903 Publication No. US20020182221A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/10472724
Publication No. US20040171806A1
GENERAL INFORMATION:
APPLICANT: Cid-Arregui, Angel
APPLICANT: Zur Hausen, Harald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/EP02/03271
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: EP 01107271.7
PRIOR FILING DATE: 2001-03-23
NUMBER OF SEQ ID NOS: 27
                                                          FILE REFERENCE: B45107
CURRENT APPLICATION NUMBER: US/10/000,903
CURRENT FILING DATE: 2001-10-01
PRIOR APPLICATION NUMBER: PCT/EP98/05285
PRIOR FILING DATE: 1998-08-17
PRIOR APPLICATION NUMBER: GB 9717953.5
                                                                                                                                                                                                           APPLICANT: Cabezon Silva, Teresa
APPLICANT: Delisse, Anne-Marie Eva Fernande
APPLICANT: Gerard, Catherine Marie Ghislaine
APPLICANT: Lombardo-Bencheikh, Angela
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: 4121-154
CURRENT APPLICATION NUMBER: US/10/472,724
CURRENT FILING DATE: 2003-09-17
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                              TITLE OF INVENTION: Vaccine
                                                                                                                                                                                                                                                                             APPLICANT: Bruck,
APPLICANT: Cabezo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Zur Hausen, Harald
TITLE OF INVENTION: Modified HPV E6 and E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53 NIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICSQK 97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCFWCASQ 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HGPKATLQDIVLHLEPQNEIPVDLLCHEQLSDSEEENDEIDGVNHQHLPARRAEPQR--H 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HGDTPTLHEYMLDLOPET---TDLYXXXQLNDSSEEEDEIDG-----PAGQAEPDRAHY 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHGPKATLCDIVLDLEPQNYEEVDLVCYEQLPDSDSENEKDEPDGVNHPLLLARRAEPQR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 195.5; DB 4;
Pred. No. 2.8e-15;
O; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genes and proteins useful for vaccination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 11;
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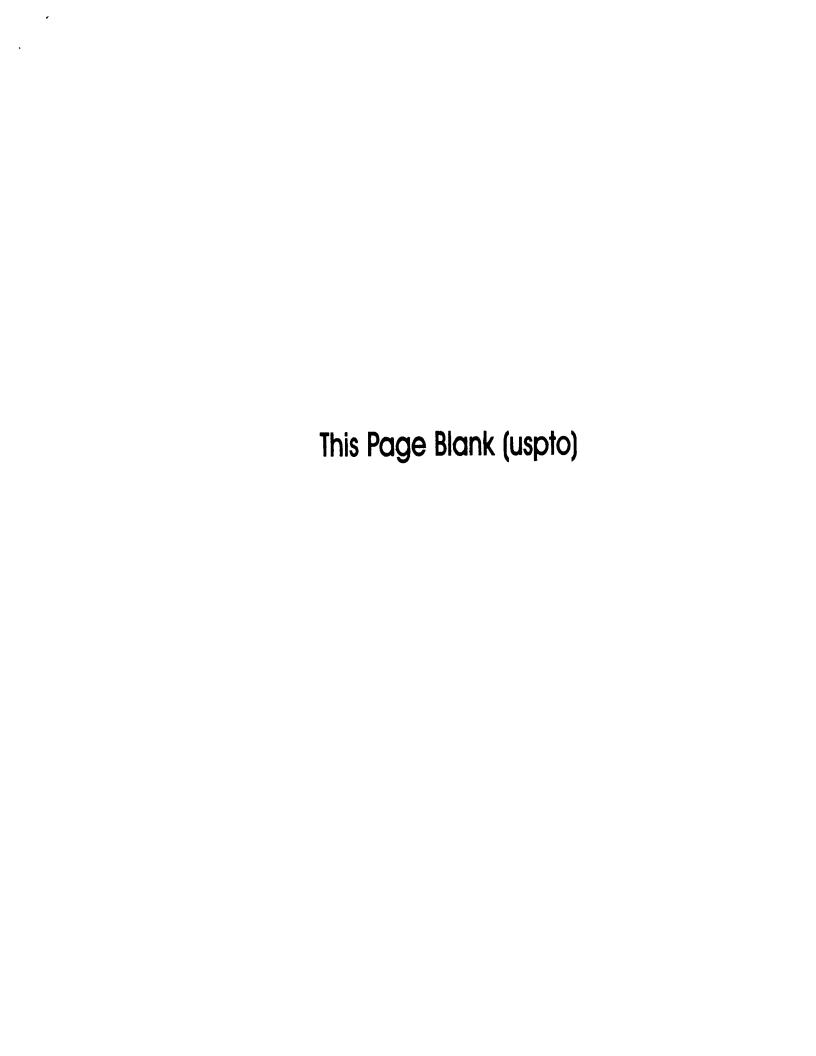
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US-10-899-771-16
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                                                                                                                                                                                                                           RESULT 96
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US-10-000-903-16
                                                                                                                             Sequence 35, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 16, Application US/10899771 Publication No. US20050031638A1
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Best Local Similarity 38.7%;
Matches 41; Conservative 2
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                APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Smith, Larry
APPLICANT: Seffrey K. Pullen
APPLICANT: Susan P. McElhiney
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/899,771
CURRENT FILING DATE: 2004-07-27
PRIOR APPLICATION NUMBER: US/09/581,976
PRIOR FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR PILING DATE: 1998-12.5
PRIOR PILING DATE: 1998-12-24
PRIOR FILING DATE: 1997-12-24
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SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OF INVENTION: Compositions Comprising Human Papilloma Virus Proteins
TITLE OF INVENTION: and Fusion Proteins Adjuvanted with a CpG Oligonucleotide
FILE REFERENCE: B45124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Chimaeric protein (protein D from Haemophilius OTHER INFORMATION: influenzae B and E7 from Human papilloma virus OTHER INFORMATION: 18)
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TYPE: PRT
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  REFERENCE:
                                                                                                                                                                                                                                                                                          172 HTMLCMCCKCEARIELVVESSADDLRAFQQLFLNTLSFVCPWCASQ 217
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                                                                                                                                                                                                                                                                                                                                                                              1 MHGDTPTLHEYMLDLQPET---TDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAH 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
00630/100M137-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.2%; Score 192.5; DB 5; 38.7%; Pred. No. 1.4e-14; tive 20; Mismatches 34;
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Pred. No. 1.4e-14;
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RESULT 98
US-10-530-253-31
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US-10-530-253-33
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                                                             Sequence 31, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 33, Application US/10530253 Publication No. US20060014926A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jeffrey K. Fullen
APPLICANT: Susan P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
PRIOR FILING DATE: 2005-04-09
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2003-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
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CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US2003/031726
PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
SOFTWARE: Patentin version 3.1
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Jeffrey K. Pullen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 10
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                            ocal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 LIHVPCCECKFVVQLDIQSTKEDLRVVQQLLMGALTVTCPLCA 102
                                                                                                                                                                                                                                            56 TECCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 NIVTECCKCDSTLRLCVQSTHVDIRTLEDILMGTLGIVXPICS 95
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                                                                                                                                                                                                                                                                                                                                                                     41;
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                                                                                                                                                                                                      APCCRCSSVVQLAVESSGDTLRVVQQMLMGELSLVCPCCA
                                                                                                                                                                                                                                                                                                                             MHGDTPTLHEYMLDLQPET-TDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAH----YNIV 55
                                                                                                                                                                                                                                                                                         MRGNVPQLKDVVLHLTPQTEIDLQCYEQF-DSSEEEDEVDNMRDQLPERRAGQATCYRIE
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                                                                                                                                                                                                                                                                                                                                                                Score 178; DB 5; L. Pred. No. 2.9e-13; Midmatches 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 178.5; DB : Pred. No. 2.7e-13
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US-10-530-253-38
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                                                                      RESULT 100
US-10-475-203A-14
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TYPE: PRT
; ORGANISM: Human papillomavirus type 39
US-10-530-253-31
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Publication No. US20060014926A1
GENERAL INFORMATION:
APPLICANT: Cassetti, Maria C.
APPLICANT: Smith, Larry
APPLICANT: Swith, Larry
APPLICANT: Susten P. McElhiney
TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT PILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: DCT/US2003/031726
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER: 2002-10-03
Sequence 14, Application US/10475203A Publication No. US20040241177A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                Query Match 31.8%; Score 164.5; DB 5; Best Local Similarity 34.0%; Pred. No. 1.4e-11; Matches 36; Conservative 20; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 38
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PRIOR FILING DATE: 2003-10-02
PRIOR APPLICATION NUMBER: US 60/415,929
PRIOR FILING DATE: 2002-10-03
NUMBER OF SEQ ID NOS: 65
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TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS
FILE REFERENCE: 00630/100M137-US2
CURRENT APPLICATION NUMBER: US/10/530,253
CURRENT FILING DATE: 2005-04-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 65
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 110
TYPE: PRT
ORGANISM: Human papillomavirus type 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8
                                                                                                                                                                                                                   50 AHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                46 EPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXPICS 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             43; Conservative
                                                                                                                                                                      61 QRHRIQCICCKCNKALQLVVEASRDNLRTLQQLFMDSLNFVCPWCA 106
                                                                                                                                                                                                                                                                                                                1 MHGDTPTLHEYMLDLQP----ETTDLYXYXQLNDSSEEEDEIDGPAGQAE------PDR 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MRGPKPTLQEIVLDLCPYNEIQPVDLVCHEQLGES---EDEIDEPDHAVNHQHQLLARRD
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                                                                                                                                                                                                                                                                     MHGPKPTVQEIVLELCPYNEIQPVDLVCHEQLGDSDDEIDEPDHAVNHHQHLLLARRDEQ 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32.9%; Score 170; DB 5 39.1%; Pred. No. 3e-12;
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                                                                                                                                                Query Match
Best Local Similarity
Matches 36; Conserv
                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.1 SEQ ID NO 14
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: AU PR4468/01 PRIOR FILING DATE: 2001-04-18 NUMBER OF SEQ ID NOS: 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/10/475,203A
CURRENT FILING DATE: 2003-10-17
PRIOR APPLICATION NUMBER: PCT/AU02/00486
PRIOR FILING DATE: 2002-04-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FRAZER, IAN
TITLE OF INVENTION: NOVEL COMPOSITIONS AND USES THEREFOR
FILE REFERENCE: E1679-00002
                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                     LENGTH: 517
489
                                                                                429 EKEKPDPYKNLSFWEVNLKEKFSSELDQYPLGRKFLLQSHGHFQIVTCCCGCDSNVRLVV
                                    70 OSTHYDIRTLEDILMGTLGIVXPICSOK 97
                                                                                                                         16 QPETTDLY---XYXQLNDSSEEEDEIDG-PAGQ--AEPDRAHYNIVTFCCKCDSTLRLCV 69
QCTETDIREVQQLLLGTLNIVCPICAPK 516
                                                                                                                                                                  Conservative
                                                                                                                                                                30.2%; Score 156; DB 5; 1
40.9%; Pred. No. 9.7e-10;
ative 13; Mismatches 33;
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Search completed: May 27, 2006, 05:37:53 Job time : 103.936 secs



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Result
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Maximum Match 100%
Listing first 100 summaries
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Match
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1. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

2. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

3. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

4. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

5. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

6. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

7. /EMC_Celerra_SIDS3/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
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1 MHGDTPTLHEYMLDLQ
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163.129 Million cell updates/sec
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PRIOR APPLICATION NUMBER: PCT/US03/12667
PRIOR FILING DATE: 2003-04-21
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PRIOR FILING DATE: 2002-04-19
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APPLICANT: Westbrook, III, Thomas F.
TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1)
FILE REFERENCE: 21108.0016U2
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CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US03/12667
PRIOR FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: 60/374,245
PRIOR FILING DATE: 2002-04-19
NUMBER OF SEQ ID NOS: 21
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TITLE OF INVENTION: E7 REGULATION OF P21 (CIP1) THROUGH AKT
FILE REFERENCE: 21108.0016U2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                       TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence:/Note OTHER INFORMATION: Synthetic Construct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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95; Conservative
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878
98.8%;
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Pred. No. 2.3e-50;
0; Mismatches 3
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US-11-293-697-3814
Score 511;
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DB
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Length 98;
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APPLICANT: Jacquet, Alain
APPLICANT: Bollen, Alex
TITLE OF INVENTION: MUTATED HPV-16 E7 POLYPEPTIDE, PHARMACEUTICAL COMPOSITION
TITLE OF INVENTION: COMPRISING IT AND ITS PREPARATION PROCESS
FILE REFERENCE: 9997.50USWO
CURRENT APPLICATION NUMBER: US/10/512,190
CURRENT FILING DATE: 2004-10-22
PRIOR APPLICATION NUMBER: PCT/BE03/00073
PRIOR FILING DATE: 2003-04-24
PRIOR APPLICATION NUMBER: US 60/410,461
PRIOR APPLICATION NUMBER: US 60/410,461
PRIOR APPLICATION NUMBER: R 0205173
PRIOR APPLICATION NUMBER: FR 0205173
PRIOR APPLICATION NUMBER: FR 0205173
PRIOR APPLICATION NUMBER: FR 0304170
PRIOR FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: FR 0304170
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin version 3.3
SEQ ID NO 2
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length CDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION UNBER: US/10/108,260
PRIOR APPLICATION UNBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 2678
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Sequence 2678, Application US/11293697
; Publication No. US20060105376A1
; GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 92
TYPE: PRT
ORGANISM: Artificial Sequence
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1; Mismatches
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Pred. No. 1.3e-46;
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Sequence 4473, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
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US-10-505-928-341
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                                                                      ) ORGANISM: Homo sapiens
US-11-293-697-4473
Query Match 11.6%;
Best Local Similarity 22.7%;
Matches 29; Conservative 1
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                                                                                                                                          SEQ ID NO 4473
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Best Local Similarity
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CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ludwig Institute for Cancer Research TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
                                                                                                                                                       PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                  APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA
                                                                                                                                                                                                                                                                   FILE REFERENCE: H1-A0106
                                                                                                         LENGTH: 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23 YXYXQLNDSSEBEDBIDGPA-----
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llarity 30.6%;
Conservative
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23.8%;
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; Score 60; DB 7; Length 468; ; Pred. No. 16; 17; Mismatches 30; Indels
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARRE: PATENTIN VERSION 3.3
SEQ ID NO 39521
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US-10-953-349-39521
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US-10-953-349-39520
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Publication No. US20060107345A1
                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.3 SEQ ID NO 39520 LENGTH: 616
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 39520, Application US/10953349
Publication No. US20060107345A1
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Best Local Similarity
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                                                                                                           Query Match
                                                                                                                                                                                                                                                        FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                  APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                       TYPE: PRT
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                                                                                         Local
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505 PAVHMASVDLKGKAYDV-----LRQNSSRFLLEDVYRNPGPLQFEGPGADSKP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 QPETTDLYXYXQLNDSSE----
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                                                                                           Similarity
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                                 PTLHEYMLDLOPETTDLYXYXQLNDSSEE---ED-----EIDGPAGQAEPDRAHYNI 54
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                                                                      Score 58.5; D
Pred. No. 32;
L5; Mismatches
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Pred. No. 23
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APPLICANT: ALEXANDROV, Nickolai et al.
FITTLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 39519
LENGTH: 646
TYPE: PRT
ORGANISM: Zea mays subsp. mays
US-10-953-349-39519
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US-10-953-349-39519
US-10-953-349-39519; Sequence 39519, Application US/10953349; Publication No. US20060107345A1; GENERAL INFORMATION:
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US-10-953-349-27425
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FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 27426
LENGTH: 233
GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al
TITLE OF INVENTION: SEQUENCE-DETERMINI
TITLE OF INVENTION: ENCONDED THERBY
                                                                                    Sequence 27425, Application US/10953349 Publication No. US20060107345A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 27426, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
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                                                                                                                                                                                                                                                                                                                        Similarity
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SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES ENCONDED THERBY
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27.6%; Pred. No. 14;
tive 11; Mismatches
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Pred. No. 33;
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; TYPE: PRT
; ORGANISM: Triticum aestivum
US-10-953-349-27425
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US-10-953-349-39537
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US-10-953-349-27424
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                                                                                                                                        ; ORGANISM: Zea mays subsp. mays US-10-953-349-39537
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 39537
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40752
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27424
LENGTH: 353
TYPE: PRT
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27425
LENGTH: 296
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Best Local Similarity 27.6%;
                                                              Matches
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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                                                                                                                                                                               LENGTH: 446
TYPE: PRT
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Local Similarity 27.6%;
                                                                              Match 11.1%; Score 57.5; Local Similarity 23.8%; Pred. No. 29;
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6 PTLHEYMLDLQPETTDLYXXXQLNDSSEEED-
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                                                              Conservative
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                      -- EIDGPAGQAEPDRAHYNIVTF 57
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                                                                                                 Length 446;
                                                              Indels 29;
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RESULT 14
US-10-953-349-39536
(Sequence 39536, Application US/10953349
; Publication No. US20060107345A1
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; FILE REFERENCE: 2750-1579PUS2
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                                                                                                                                                                                                                                                                                                                             ; TYPE: PRT ; ORGANISM: Arabidopsis thaliana US-10-953-349-3781
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US-10-953-349-39536
                                                                             RESULT 16
US-10-953-349-3780
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               Sequence 3780, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 2004-09:
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 3781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3781, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOPTWARE: PatentIn version 3.3 SEQ ID NO 39536
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                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
APPLICANT: ALEXANDROV, Nickolai et al.
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                                                                                                                                                                                                                                                                                                                                                                                            ENGTH: 499
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24;
                                                                                                                                                                13
                                                                                                                                                                                                    28 LNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCC-KCDST-----LRLCVQSTH 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 PTLHEYMLDLQPETTDLYXYXQLNDSSEEED-----EIDGPAGQAEPDRAHYNIVTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCKCDSTLRLCVQSTHV--DIRTLEDLLMGTLGIVXPICSQ 96
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                                                                                                                                                                LNDDDDDDDDCDW-----EPVQAPMEFVKWCCVNCTMSNPGDMVHCCICGEH 59
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23.8%;
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Pred. No. 33;
8; Mismatches
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Pred. No. 30;
15; Mismatches
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CURRENT APPLICATION NUMBER: US/11/242,111
CURRENT FILING DATE: 2005-09-29
PRIOR APPLICATION NUMBER: 60/614,746
PRIOR FILING DATE: 2004-09-30
PRIOR APPLICATION NUMBER: 60/651,344
PRIOR FILING DATE: 2005-02-08
PRIOR FILING DATE: 2005-02-08
VANDBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.3
SEQ ID NO 23
LENGTH: 300
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TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PAtentin version 3.3
SEQ ID NO 3780
LENGTH: 552
TYPE: PRT
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SOFTWARE: PACENTIN VERSION
SEQ ID NO 39535
LENGTH: 618
TYPE: PRT
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Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30

CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                          Sequence 23, Application US/11242111
Publication No. US20060088862A1
GENERAL INFORMATION:
APPLICANT: Lee, Nancy M
TITLE OF INVENTION: OR COLORECTAL CANCER: REAGENTS, METHODS, AND KITS THEREOF
FILE REFERENCE: NLEE-01001US1 MCF/MLB
FILE REFERENCE: NLEE-01001US1 MCF/MLB
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23.8%;
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Pred. No. 41
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Pred. No. 36;
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US-10-953-349-23406

J Sequence 23406, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA

TITLE OF INVENTION: ENCONDED THERBY

TILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252
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; ORGANISM: HUMAN
US-11-242-111-23
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US-09-981-845-1
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SEQ ID NO 23406
LENCTH: 286
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ashkar, Samy

IIILE OF INVENTION: Osteopontin-Coated Surfaces and Methods of 
FILE REFERENCE: CMCC 779

CURRENT APPLICATION NUMBER: US/09/981,845

CURRENT FILING DATE: 2001-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US 60/327,273
PRIOR FILING DATE: 2001-10-05
NUMBER OF SEQ ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/241,248
PRIOR FILING DATE: 2000-10-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Children's Medical Center Corporation APPLICANT: Ashkar, Samy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 314
TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               y Match 11.0%; Score 57; DB 1; Length 314; Local Similarity 24.4%; Pred. No. 22; hes 11; Conservative 12; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 11.0%; Score 57; DB Local Similarity 24.4%; Pred. No. 21;
                                                                                                Local Similarity
188 KVDGPGGWSYGIKVRYSVQGNDEFCGACEATAGTC 222
                                    37 EIDGPAGQAEPDRAHYNIV---TFCCKCDSTLRLC 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  82 HDHMDDMDDEDDDDHVDSQDSIDSNDSDDVDDTDDSHQSDESHHS 126
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                                                                               Conservative
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                                                                                                Score 55.5;
Pred. No. 30;
                                                                               Mismatches
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                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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CURRENT APPLICATION NUMBER: US/10/
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5452
LENGTH: 538
TYPE: PRT
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US-10-953-349-5451
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US-10-953-349-23405
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              Sequence 5451, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT FILING APPLICATION NUMBER: US/10/953,349
CURRENT FILING APPLICATION NUMBER: US/10/953,349
NUMBER OF SEQ ID NOS: 40252
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23405
LENGTH: 293
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Publication No. US20066107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
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publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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SOFTWARE: PatentIn version 3.3
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les 11; Conserv
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Pred. No. 30;
7; Mismatches
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Pred. No. 59
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Sequence 32, Application US/10468193

; Publication No. US20060100416A1

; GENERAL INFORMATION:
   APPLICANT: Palli, Subba R.

; APPLICANT: Cress, Dean E.

; APPLICANT: Kumar, Mohan B.

; TITLE OF INVENTION: Receptor-Based Inducible Gene Expression System

; FILE REFERENCE: A01247-US

; CURRENT APPLICATION NUMBER: US/10/468,193

; CURRENT APPLICATION NUMBER: US 60/313,925

pRIOR APPLICATION NUMBER: PCT/US02/05090

pRIOR APPLICATION NUMBER: 2002-02-20

; PRIOR APPLICATION NUMBER: DCT/US02/05090

pRIOR APPLICATION NUMBER: 2002-02-20

; PRIOR APPLICATION NUMBER: 2002-02-20

; PRIOR APPLICATION NUMBER: 2002-02-20

; PRIOR PILING DATE: 2002-02-20

; PRIOR APPLICATION NUMBER: 2002-02-20

; PRIOR PILING DATE: 2002-02-20
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 5450
LENGTH: 574
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US-10-468-193-32
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US-10-953-349-5450
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LENGTH: 544
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 32
LENGTH: 878
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27.7%; Pred. No. 63;
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; ORGANISM: Drosophila melanogaster
US-10-468-193-32
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US-10-525-126-215
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GENERAL INFORMATION:

APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA

APPLICANT: NATIONAL RESEARCH COUNCIL OF LORINIFICATION OF NOVEL BROAD-SPECTRUM

TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM

TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH

TILE REFERENCE: 6899-6/PAR

CURRENT APPLICATION NUMBER: US/10/525,126

CURRENT FILING DATE: 2005-02-18

PRIOR APPLICATION NUMBER: PCT/CA03/01323

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR APPLICATION NUMBER: 60/404,922

PRIOR TILING DATE: 2002-08-22
                                                                                                                                                                                                                                                                                 Sequence 215, Application US/10525126
Publication No. US2006093596A1
GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
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SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 177
                                                                 SOFTWARE: PatentIn Ver. 3.2 SEQ ID NO 215
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                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2002-08-22
                                                                                                              NUMBER OF SEQ ID NOS: 329
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ORGANISM: Unknown Organism
FEATURE:
ORGANISM: Salmo salar
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                                             ENGTH:
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27; Conserv
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22.2%;
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24.8%; Pred. No. 10
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Pred. No. 6.
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APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NO
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT APPLICATION NUMBER: PCT/CA03/01323
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR FILING DATE: 2003-08-22
PRIOR FILING DATE: 2003-08-22
PRIOR FILING DATE: 2003-08-22
PRIOR FILING DATE: 2003-08-22
PRIOR FILING DATE: 2003-08-22
VMMBER OF SEQ ID NOS: 329
SOFTMARE: PATENT DATE: 2007-08-22
VMMBER OF SEQ ID NOS: 329
SOFTMARE: PATENT DATE: 2007-08-22
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US-10-525-126-174
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TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REPERENCE: 6899-6/PAR
CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
SOPTWARE: Patentin Ver. 3.2
  Query Match
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                                                                 OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                  TYPE: PRT
ORGANISM: Unknown Organism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Description of Unknown Organism: Hepcidin peptide OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
                                                                                                               FEATURE:
                                                                                                                                                                              LENGTH: 88
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                                                                 Description of Unknown Organism: Hepcidin peptide sequence
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Pred. No. 6
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Pred. No. 11;
Score 54.5;
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DB 6;
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FILE REFERENCE: 6899-6/PAR
CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
SOFTWARE: Patentin Ver. 3.2
SEQ ID NO 212
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; ORGANISM: Hippoglossus hippoglossus
US-10-525-126-212
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US-10-525-126-212
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TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
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                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity les 10; Conserv
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                         32 SEEEDEIDGPAGQAEPD------RAHYNIVTFCCKC
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                                                    10;
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                                                                Similarity
TEEVESIDSPYGEHQQPGGTSMNLPMHFRFKRQSHLSLCRWCCNC
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o. US20060093596A1
                                                    Conservative
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                                                                Score 54.5;
Pred. No. 11;
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Pred. No. 11;
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                                                                                                                         US-10-525-126-300
                                                                                                                                               RESULT 34
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US-10-525-126-299
Sequence 300, Application US/10525126
publication NO. US20060093596A1
GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 299
LENGTH: 88
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publication No. US20060093596A1
GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
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Best Local (
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CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2002-08-22
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CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH FILE REFERENCE: 6899-6/PAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Unknown Organism: Type1 Hepcidin OTHER INFORMATION: sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                              Match 10.5%;
Local Similarity 22.2%;
es 10; Conservative
                                                                                                                                                                                                                     32 TEEVESIDSPYGEHQQPGGTSMNLPMHFRFKRQSHLSLCRWCCNC 76
                                                                                                                                                                                                                                                                  32 SEEEDEIDGPAGQAEPD-------RAHYNIVTFCCKC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32 TEEVESIDSPVGEHQQPGGTSMNLPMHFRFKRQSHLSLCRWCCNC 76
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D. US20060093596A1
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llarity 22.2%;
Conservative
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Pred. No. 11;
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Pred. No. 11;
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); Mismatches
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                                    US-10-953-349-20548
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 20549
LENGTH: 255
                                                                                            FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 20548
LENGTH: 269
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
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NUMBER OF SEQ ID NOS: 329
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 300
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Query Match
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PRIOR FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: 60/404,922
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CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
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                                                     TYPE: PRT
ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Salmo salar
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Pred. No. 34;
  Score 54.5;
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Pred. No. 11;
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  Length 269;
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US-11-293-697-2988
                                                                                                                                                                                                                                         ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                           APPLICANT: ALEXANDROV, NICKOIAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 1526
LENGTH: 278
TYPE: PRT
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APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
FILE REFERENCE: H1-A0106
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LENGTH: 489
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CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                        / Match 10.4%; Score 54; DB Local Similarity 27.4%; Pred. No. 42; es 20; Conservative 10; Mismatches
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                                     67 LCVQSTHVDIRTL 79
                                                                             62 TLNEPTIGDKLESLDLLNGEKVN--SEESNRDSAPGDDKPPTAASVNV--
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                                                                                                                  7 TLHEYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8 LHEYMLDLQPETTDLYXXXQLNDSSEEEDBIDGPAGQAEPDRAHYNIVTFCCKCDSTLRL 67
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LLRQALHADDRSL 120
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24.7%; Pred. No. 69;
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                                                                                                                                                                                                  DB 6; Length 278;
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                                                                                                                                                          29; Indels
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 35808
LENGTH: 630
TYPE: PRT
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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CURRENT FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PA 2002 0092
PRIOR FILING DATE: 2002-06-17
NUMBER OF SEQ ID NOS: 8
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APPLICANT: Maarten van den Brink, Johannes
APPLICANT: Harboe, Marianne K.
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APPLICANT: Rahbek-Nielsen, Henrik
TITLE OF INVENTION: IMPROVED METHOD OF PRODUCING
TITLE OF INVENTION: A RECOMBINANT HOST ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: P1031US00
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TYPE: PRT
ORGANISM: Bos taurus
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                                         71 STH 73
                                                                                32 VELRAETDSDEVYAQIMLQPQTEQSEPTSPDPEPPEPERC--NIHSFC--
                                                                                                                                                                 l Similarity
18; Conserv
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STH 88
                                                                                                                     LDLOPET -- TDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQ 70
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                                                                                                                                                                 10.4%; Score 54; DB 6; ilarity 28.6%; Pred. No. 1e+02; Conservative 10; Mismatches 2
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                                                                                                                                                                   27;
                                                                                                                                                                                                        Length 630;
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                                                                                  -KTLTASDT 85
                                                                                                                                                                 Gaps
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RESULT 41 US-10-953-349-35807 ; Sequence 35807, Application US/10953349

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RESULT 42
US-10-953-349-31198
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; Sequence 23351, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
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US-10-953-349-35807
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US-10-953-349-31198
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 31198
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Publication No. US20060107345A1
GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35807
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23351
LENGTH: 639
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Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
EILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
                                                                           APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
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Pred. No. 97;
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Sequence 23349, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRA
TITLE OF INVENTION: BNCONDED THERBY
FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 23349

LENGTH: 664
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FR.
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 23350
                                                                                                                                                                                                                                                                                                       ; TYPE: PRT; ORGANISM: Glycine max US-10-953-349-23349
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-23350
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                                                           RESULT 46
US-10-953-349-34172
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US-10-953-349-23349
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US-10-953-349-23350
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Best Local S
Matches 16
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Best Local Similarity
Matches 16; Conserv
Sequence 34172, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
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                                                                                                                                          44 EEEEEEEEVWDDWEGEDEGERESEFVCLFCDSRYSSCGSLFDHCASLHRFDFHTIRTTL 102
                                                                                                                                                                                30 DSSEEEDEI-DGPAGQAEPDRAHYNIVTFC----CKCDSTLRLCVQSTHVDIRTLEDLL 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       36 EEEEEEEVWDDWEGEDEGERESEFVCLFCDSRYSSCGSLFDHCASLHRFDFHTIRTTL 94
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                                                                                                                                                                                                                         7; Mismatches
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Pred. No. 1.2e+02;
7; Mismatches 31;
                                                                                                                                                                                                                           Score 53.5; DB 6;
Pred. No. 1.2e+02;
7; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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Sequence 34171, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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US-10-953-349-34170
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US-10-953-349-34171
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT PAPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 34172
LENGTH: 263
TYPE: PRT
                                                                                                                                                       Sequence 34170, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PATENTIN VERSION 3.3
SEQ ID NO 34171
LENGTH: 283
TYPE: PRT
SOFTWARE: PatentIn version 3.3 SEQ ID NO 34170
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                 FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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                                                                                                     APPLICANT: ALEXANDROV, Nickolai et al. TITLE OF INVENTION: SEQUENCE-DETERMINED DNA TITLE OF INVENTION: ENCONDED THERBY
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                                                                                                                                                                                                                                                                                                                                                        52 OVSDALRLHDEIMOPGGSLEPKAAIALIEHIRTEGELDRMHOLLDGLNDSNSWFDGCGRV 111
                                                                                                                                                                                                                                                                                                                                                                                           27 QLNDSSEEEDEIDGPAGQAEP------
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                                                                                                                                                                                                                                                                                                                                                                                                                                25;
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Pred. No. 55;
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Pred. No.
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                                                                                                                          FRAGMENTS AND
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; LENGTH: 286
; TYPE: PRT
; ORGANISM: Zea mays subsp.
US-10-953-349-34170
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 12021
LENGTH: 377
Type:
                                                                                                                                                                             Query Match
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DI
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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Best Local Similarity
                                                                                                                                                                                                                                                  NAME/KEY: misc feature LOCATION: (325) (325) OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                             LOCATION: (314)..(314)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: misc_feature
LOCATION: (228)...(228)
OTHER_INFORMATION: Xaa
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ORGANISM: Glycine max
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LOCATION: (314) ... (314)
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NAME/KEY: misc feature
LOCATION: (252)..(252)
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LGVPLP
                          LGIVXP 92
                                                      TEWELDFCSRPILDARGKKVWELVVCDKTLSL--QYTKYFPNNVINSITLKDAIVAVSDQ 15:
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                                                                                                                                              TPT-LHEYMLDLQPETTDLYXYXQL-----NDSSEEEDEIDGPAGQ-----AEPDRA
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Pred. No. 56;
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US-10-953-349-15959
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US-11-293-697-3292
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US-11-293-697-3292
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SOFTWARE: PatentIn 3.2
SEQ ID NO 443
LENGTH: 749
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PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3292
LENGTH: 423
TYPE: PRT
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Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
                Sequence 15959, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND
TITLE OF INVENTION: ENCONDED THERBY
PILE REFERENCE: 2750-1579PUS2
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Best Local Similarity
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CURRENT FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: US 60/363,019
PRIOR FILING DATE: 2002-03-07
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CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ludwig Institute for Cancer Research et al. TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES FILE REFERENCE: 28967/39178
  CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
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US/10/953,349
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Pred. No. 86;
10; Mismatches
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Pred. No. 1.6e+02;
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                                                        CORRESPONDING POLYPEPTIDES
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 11222
LENGTH: 288
TYPE: PRT
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CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3886
LENGTH: 275
TYPE: PRT
Query Match
Best Local Similarity
Watches 15; Conserva
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-953-349-15959
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US-10-953-349-11222
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Publication No. US/20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: Novel full length cDNA
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NUMBER OF SEQ ID NOS:
SOFTWARE: PatentIn ver
SEQ ID NO 15959
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18; Conserv
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            10.2%;
ilarity 27.8%;
Conservative
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              Score 52.5; D. Pred. No. 64; 9; Mismatches
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Pred. No. 61;
8; Mismatches
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Pred. No. 22;
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                                                                                                                                                                                                                                                                            DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
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                                                 Length 288;
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9

19;

Indels

11;

Gaps

N

δ

15

LOPETTDLYXYXQLNDSSEEEDEIDG-----PAGQAEPDRAHYNIVTFC

58

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RESULT 56
US-10-525-126-296
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                                                                                           ; ORGANISM: Oryzias latipes
US-10-525-126-296
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US-10-511-937-2561
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US-10-511-937-2561
                                                                                                                                                                                                                                                                                                                                           Sequence 296, Application US/10525126
Publication No. US20060093596A1
GENERAL INFORMATION:
APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
CURRENT APPLICATION NUMBER: US/10/525,126
CURRENT FILING DATE: 2005-02-18
CURRENT FILING DATE: 2005-02-18
Query Match
Best Local Similarity
Matches 13; Conserv
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LENGTH: 1912
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                                                                                                                                                                                    SEQ ID NO 296
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CURRENT APPLICATION NUMBER: US/10/511,937
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR APPLICATION NUMBER: PCT/US2003/012946
PRIOR PILING DATE: 2003-04-24
PRIOR FILING DATE: 2003-04-24
PRIOR FILING DATE: 2002-04-24
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APPLICANT: Wohlgemuth, Jay
APPLICANT: Fry, Kirk
APPLICANT: Woodward, Robert
APPLICANT: Ly, Ngoc
APPLICANT: Prentice, James
APPLICANT: Morris, MacDonald
                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
NUMBER OF SEQ ID NOS: 329
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/CA03/01323 PRIOR FILING DATE: 2003-08-22
                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 3.2
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SOFTWARE: PatentIn ver
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                                                                                                                                        LENGTH: 90
TYPE: PRT
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tes 16; Conservative
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Rosenberg, Steven
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                     10.1%;
Score 52; DB
Pred. No. 20;
8; Mismatches
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Pred. No. 5.1e+02;
9; Mismatches 14;
                                           DB 6; Length 90;
24;
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Indels
20;
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Sequence 21799, Application US/10953349

Publication No. US20060107345A1

GENERAL INFORMATION:
APPLICAUT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 21799

LENGTH: 324

TYPE: DET
RESULT 59
US-10-953-349-21798
; Sequence 21798, Application US/10953349
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US-10-953-349-15960
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 15960
LENGTH: 97
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14; Conserv
                                                                                              EEKHTEVDLQSSSQSGSLG 171
                                                                                                                                  OSTHVDIRTLEDLLMGTLG 88
                                                                                                                                                                      EHKLDWDPTASETKSF-----KKHEDLLNDP-
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23.7%;
                                                                                                                                                                                                                                        10.1%; Score 52; DB 21.5%; Pred. No. 83; tive 13; Mismatches
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RESULT 61

US-10-953-349-31968
; Sequence 31968, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
wnmber OF SEQ ID NOS: 40252
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US-10-953-349-21797
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 21797
LENGTH: 352
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 10.1%; Score 52; DB Local Similarity 21.5%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                177
                                                                                                                                                                                                                                                                                                                                                                                              181 EEKHTEVDLQSSSQSGSLG 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137 EHKLDWDPTASETKSF----KKHEDLLNDP---
                                                                                                                                                                                                                                                                                                                                                                                                                                    70 QSTHVDIRTLEDLLMGTLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 EYMLDLQPETTDLYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCV 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17;
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Pred. No. 90;
                                                                                                                                                                                                                                                                                                                                                                                                                                      88
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: PAtentIn version 3.3
SEQ ID NO 31967
LENGTH: 405
TYPE: PRT
ORGANISM: Triticum aestivum
US-10-953-349-31967
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                                                   US-10-953-349-31966
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                                                                                                    CURRENT APPLICATION NUMBER: US/11
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31966
LENGTH: 475
                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: ALEXANDROV, NICKOLAI et al.
APPLICANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                            Sequence 31966, Application US/10953349
Publication No. US20060107345A1
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SEQ ID NO 31968
LENCTH: 357
TYPE: PRT
Query Match
Best Local Similarity
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                     TYPE: PRT ORGANISM: Triticum aestivum
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19; Conserv
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10.1%;
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Pred. No. 92;
9; Mismatches
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 Score
Pred.
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Pred. No. 1.1e+02;
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 No ;
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92;
   DB 6;
1.3e+02;
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FILE REFERENCE: 05508-2210
CURRENT APPLICATION NUMBER: US/10/514,462
CURRENT FILING DATE: 2004-11-12
PRIOR APPLICATION NUMBER: 60/381,557
PRIOR FILING DATE: 2002-05-17
NUMBER OF SEQ ID NOS: 11
SOPTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 507
TYPE: DET.
                                                                                                                                                                                                                                                     APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NOVEL full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 3174
LENGTH: 634
TYPE: PRT
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US-11-293-697-3174
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; ORGANISM: RVFV GC
US-10-514-462-4
                                                                                                                                                                                                                        ; ORGANISM: Homo sapiens
US-11-293-697-3174
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                                                                                                                                              Query Match
Best Local S
Matches 21
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Publication No. US20060088909A1
GENERAL INFORMATION:
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Best Local Similarity 30.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Emory University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     329 EVDFVGAAVSCDAAFLNL-TGCYSCNAGARVCLSITSTGTGSLSAHNKD---GSLHIVLP 384
242 E 242
                                                                      183 HEMMEEEEEIPKPKSVVAPPGAPKKEHVNVV-FIGHVDAGKSTIGGQIMYLIGMVDKRTL 241
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                                     80
E
                                                                                                       29 NDSSEEEDEIDGP----AGQAEPDRAHYNIVTFCCKCD---STL--RLCVQSTHVDIRTL 79
                                                                                                                                                21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
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                                                                                                                                                                 Similarity
                                     80
                                                                                                                                                Conservative
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                                                                                                                                            Score 52; DB 7; Lo
Pred. No. 1.7e+02;
9; Mismatches 21;
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                                                                                                                                              Indels
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; NAME/KEY: MOD_RES
; LOCATION: (55)
; OTHER INFORMATION: Variable amino acid
US-10-525-126-302
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US-10-514-462-2
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Publication No. US20060088909A1

GENERAL INFORMATION:

APPLICANT: Emory University

ITILE OF INVENTION: Virus-Like Particles, Methods of Preparation, And Immunogenic TITLE OF INVENTION: Compositions

FILE REFERENCE: 050508-2210

CURRENT APPLICATION NUMBER: US/10/514,462

CURRENT FILING DATE: 2004-11-12

PRIOR FILING DATE: 2004-05-17

NUMBER OF SEQ ID NOS: 11

SOFTWARE: PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NATIONAL RESEARCH COUNCIL OF CANADA
TITLE OF INVENTION: A GENOMIC APPROACH TO IDENTIFICATION OF NOVEL BROAD-SPECTRUM
TITLE OF INVENTION: ANTIMICROBIAL PEPTIDES FROM BONY FISH
FILE REFERENCE: 6899-6/PAR
CURRENT FILING DATE: 2005-02-18
PRIOR APPLICATION NUMBER: PCT/CA03/01323
PRIOR FILING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR APPLICATION NUMBER: 60/404,922
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2002-08-22
PRIOR FILING DATE: 2002-08-22
SEQ ID NO 302
SOFTWARE: PATENTIN Ver. 3.2
SEQ ID NO 302
LENGTH: 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 302, Application US/10525126 Publication No. US20060093596A1 GENERAL INFORMATION:
                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                       NAME/KEY: MOD RES
LOCATION: (37)
OTHER INFORMATION: V
FEATURE:
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TYPE: PRT
                                                                                                                                                                                                                                                                                                                                       ORGANISM: Oncorhynchus mykiss
                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37 EIDGPAGOAEPDRAHYNIVTFCCKCDSTLRLCVOSTHVDIRTL----EDLLMGTLGIVXP 92
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                                     32 SEEEDEIDGPAGQAE---
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5 TEEVGSIDSPVGEHQQPGGESMRLPEHFRFKRXSHLSLCRWCCNC 49
                                                                             Conservative
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                                                                                                                                                                                                                                                          Variable amino
                                                                                             10.0%;
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Pred. No. 3e+02;
9; Mismatches 2
                                                                           Score 51.5; D
Pred. No. 15;
8; Mismatches
                                       ----PDR-----AHYNIVTFCCKC
                                                                                                                                                                                                                                                          acid
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                                                                                                                  Length 61;
                                                                             Indels
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RESULT 68 US-10-953-349-6871

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RESULT 70
US-11-297-160-7
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US-10-953-349-6870
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Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30
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SOPTWARE: PatentIn version 3.3
SEQ ID NO 6870
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 6871
LENGTH: 145
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                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/11297160 Publication No. US20060088888A1 GENERAL INFORMATION:
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Best Local :
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Best Local S
                                                                                                                                                                                 APPLICANT: Wang, Xin wei APPLICANT: Harris, Curtis C. APPLICANT: Fornace Jr., Albert J. APPLICANT: Coursen, Jill D. APPLICANT: Zhan, Qimin APPLICANT: Zhan, Qimin for the
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REPERENCE: 2750-1579PUS2
                                                            APPLICANT: The Government of the United States of America APPLICANT: as represented by the Secretary of the APPLICANT: Department of Health and Human Services TITLE OF INVENTION: Methods for Identifying Inhibitors of GADD45 TITLE OF INVENTION: Polypeptide Activity, and Inhibitors of Such REPERENCE: 015280-367100US
                     CURRENT APPLICATION NUMBER: US/11/297,160
CURRENT FILING DATE: 2005-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/953,349
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  NUMBER:
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US/10/600,158
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                                                                                      and Inhibitors of Such Activity
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US-10-953-349-24840
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 24841
LENGTH: 315
TYPE: PRT
ORGANISM: Glycine max
                                                   Sequence 24840, Application US/10953349
publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 24841, Application US/10953349
Publication No. US20066107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Best Local :
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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NUMBER OF SEQ ID NOS: 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2003-06-20
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No. 91;
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Pred. No. 43;
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Sequence 195, Application US/11121154

Publication No. US20060105914A1

GENERAL INFORMATION:
APPLICANT: TAYLOR, LARRY EDMUND
APPLICANT: WEINER, RONALD M.
APPLICANT: WEINER, RONALD M.
APPLICANT: EKBORG, NATHAN A.
APPLICANT: EKBORG, NATHAN A.
APPLICANT: HOWARD, MICHAEL
TITLE OF INVENTION: PLANT WALL DEGRADATIVE COMPOUNDS AND SYSTEMS
FILE REFERENCE: 108172-00121
CURRENT APPLICATION NUMBER: US/11/121,154
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,971
PRIOR APPLICATION NUMBER: 60/567,971
PRIOR APPLICATION NUMBER: 2005-04
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US-10-953-349-22956
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; ORGANISM: Glycine max
US-10-953-349-24840
                                                                                                                                                           Sequence 22956, Application US/10953349

Publication No. US20066107345A1

GENERAL INFORMATION:

APPLICANT: ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT APPLICATION NUMBER: US/10/953,349

CURRENT FILING DATE: 2004-09-30
                                                                                           NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 22956
LENGTH: 155
 Query Match
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SOFTWARE: PatentIn version 3.3
SEQ ID NO 195
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Best Local Similarity
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                                                      ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                  219 EHTLRIAVQAGNFNINWLELLLAGTQQPDMLGV 251
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23.5%;
   9.98;
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Pred. No. 1.5e+02;
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   Score 51;
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Length 155;
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 16871
LENGTH: 549
TYPE: PRT
ORGANISM: Glycine max
US-10-953-349-16871
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US-10-953-349-22955
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CURRENT FILING DATE: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 22955
LENGTH: 171
TYPE: PRT
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APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 16871, Application US/10953349 Publication No. US20060107345A1 GENERAL INFORMATION:
                                                                       Matches
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Matches 20; Conservative
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478
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                                22 LYXYXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQST 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 SSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQ--STHVDIRTLEDLLMGTL-
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                                                                                        Similarity
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tive 10; Mismatches
                                                                                                       9.9%;
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                                                                   Score 51; DB 6;
Pred. No. 1.9e+0;
7; Mismatches
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Pred. No. 53;
 -NNNIVINACKCLSRDRTCDPSS 518
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                                                                                        1.9e+02
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                                                                                                       Length 549;
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RESULT 77

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SOFTWARE: PatentIn version 3.3
SEQ ID NO 16869
LENGTH: 585
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 16870
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                                                                                                                                                                                                                                                                                     Sequence 4398, Application US/11293697 Publication No. US20060105376A1 GENERAL INFORMATION:
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Best Local Similarity
                                                            NUMBER OF SEQ ID NOS: 5458
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 4398
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                                                                                                                                CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR PILING DATE: 2002-03-28
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TITLE OF INVENTION: ENQUENCE-DETERNY
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                      APPLICANT: HELIX RESEARCH INSTITUTE TITLE OF INVENTION: Novel full length cDNA FILE REFERENCE: H1-A0106
TYPE: PRT
ORGANISM: Homo sapiens
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                                            LENGTH: 764
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ilarity 31.4%;
Conservative
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ilarity 31.4%;
Conservative
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Pred. No. 1.9e+02;
7; Mismatches 18
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US-10-953-349-23159
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Best Local S
Matches 18
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOCTWARE: Patentin version 3.3
SEQ ID NO 13813
LENGTH: 176
                                                                                                                                                                                                                                                             Sequence 23159, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV:
ALEXANDROV SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: Patentin version 3.3
SEQ ID NO 23159
LENGTH: 218
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TYPE: PRT
ORGANISM: Glycine max
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                                   30
61 LIDTAGCOMEEKKDEEDSTFNEGEAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MHGDTPTLHEYMLDL---QPETTDLYXXXQLNDSSEEBDEIDGPAGQAEPDRAHYNIVTF 57
                                                                                                           1 MHGDTPT-----LHEYMLD-----
                                                                                                                                                             Similarity
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                                 -----DSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLED 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LHNENPGIHNLLLSLYAKQEDDSSLLRFLQSKFGKGPE---NGPEFFYDPKYA----LRL 60
                                                                     MYGDEITSMLTIQYRMHELIMDWSSKELYNSKIKAHPSVTAHMLYDLEGVKRTNSTEPTL 60
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25.0%; Pred. No. 62;
                                                                                                                                          13; Mismatches
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Pred. No.
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Pred. No. 79;
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                                                                                                                                          Indels 59;
 -VTVTHAKRLVQSG 100
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; Sequence 36028, Application US/10953349
                    US-10-953-349-36028
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                                       RESULT 84
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US-10-953-349-23158
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US-10-953-349-36029
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Publication No. US20060107345A1

GENERAL INFORMATION:

APPLICANT; ALEXANDROV, Nickolai et al.

TITLE OF INVENTION: SEQUENCE DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

TITLE OF INVENTION: ENCONDED THERBY

FILE REFERENCE: 2750-1579PUS2

CURRENT FILING DATE: 2004-09-30

NUMBER OF SEQ ID NOS: 40252

SOFTWARE: Patentin version 3.3

SEQ ID NO 23158
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LENGTH: 235
TYPE: PRT
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Best Local
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Best Local
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-15799US2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40352
NUMBER OF SEQ ID NOS: 40352
SOFTWARE: Patentin version 3.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 3
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Local Similarity 28.6%;
                                                                                                                                                                                                                                                          126 MYGDEITSMLTIQYRMHELIMDWSSKELYNSKIKAHPSVTAHMLYDLEGVKRTNSTEPTL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 VLPSDIGIITPYAAQ 115
                                                                                                                                                                              186 LLIDTAGCDMEEKKDEEDSTFNEGEAE--
                                                                                                                                                                                                                 30 -----DSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLED 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50 HLLDRPKEAAASVSFRRLDPKAEEEEDEDMDEGGSSSEDSAH 91
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                                                                                                                                                                                                                                                                                                                                                        h 9.8%; Score 50.5; DB 6; Similarity 19.3%; Pred. No. 1.3e+02;
                                                                                                  VLPSDIGITTPYANO 240
                                                                                                                                     riwgricivxbicso 96
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Pred. No. 85;
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RESULT 86

US-10-953-349-9399

; Sequence 9399, Application US/10953349
; Publication No. US20060107345A1
; GENERAL INFORMATION:
; APPLICANT: ALEXANDROV, Nickolai et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
; TITLE OF INVENTION: ENCONDED THERBY
; FILE REFERENCE: 2750-1579PUS2
; CURRENT APPLICATION NUMBER: US/10/953,349
; CURRENT FILING DATE: 2004-09-30
; NUMBER OF SEQ ID NOS: 40252
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US-10-953-349-23157
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 36038
LENGTH: 369
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT ENTLING DATE: 2004-09-30
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 23157
LENGTH: 382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local Similarity
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Best Local
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TYPE: PRT
ORGANISM: Zea mays subsp. mays
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 MYGDEITSMLTIQYRMHELIMDWSSKELYNSKIKAHPSVTAHMLYDLEGVKRTNSTEPTL 224
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28.6%;
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Pred. No. 1.5e+02;
3; Mismatches 37;
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Pred. No. 1.4e+02;
9; Mismatches 20;
                                                                                                              DNA FRAGMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 382;
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                                                                                                                 AND CORRESPONDING POLYPEPTIDES
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                                                                                                                                                                                                                                                                                                                           RESULT 88
US-10-953-349-27383
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US-10-953-349-9398
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                                                 ; TYPE: PRT; ORGANISM: Triticum aestivum US-10-953-349-27383
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                       Sequence 27383, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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SEQ ID NO 9398
LENCTH: 81
TYPE: PRT
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SEQ ID NO 9399
LENGTH: 57
TYPE: PRT
                                                                                              NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27383
LENGTH: 205
Query Match
Best Local Similarity
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                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10 CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                     APPLICANT: ALEXANDROV, Nickolai et al. TITLE OF INVENTION: SEQUENCE-DETERMINED TITLE OF INVENTION: ENCONDED THERBY FILE REFERENCE: 2750-1579PUS2
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Local Similarity 24.6%;
Les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GDTPTLHEYMLDLQPETTDLYXXXQLNDSSEEEDEIDGPAGQAEPDRAHYNIVTFCCKCD 62
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ilarity 24.6%;
Conservative
9.7%;
21.3%;
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Score 50;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 50; DB Pred. No. 30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                         DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
DB
84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 81;
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                9
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                Length 205;
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NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 27382
LENGTH: 231
TYPE: PRT
ORGANISM: Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : LENGTH: 211
; TYPE: PRT
; ORGANISM: Zea mays subsp. mays
US-10-953-349-38511
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
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Publication No. US20060107345A1
GENERAL INFORMATION:
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCOUNED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                  Local
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93 VDRILYSSVVYPHNYGFVPRTLCEDGDPIDVLVL 126
                               47 PDRAHYNIVTFCCKCDSTLR-LCVQSTHVDIRTL 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73 GQAEREFRVEVEAIGRVRHKNIJVRLIGYCAEGAQRIIJVYEYVDNGNIEQWIHGDVGAVSP 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 PDRAHYNIVTFCCKCDSTLR-LCVQSTHVDIRTL 79
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                                                                                                 4 DTPTLHEYM-----
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                                                                                                                                                  Similarity
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                                                              DAPKLNORMVSSLSKRTAAAHSWHDLEIGPEAPLIFNAVVEITKGSKVKYELDKKTGMIK 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VDRILYSSVVYPHNYGEVPRTLCEDGDPIDVLVL 100
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                                                                                                                                 Conservative
                                                                                                                                                9.7%;
21.3%;
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                                                                                                                                 16; Mismatches
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                                                                                                                                               Score 50; DB 6; Length 231; Pred. No. 95;
                                                                                                 -LDLQPETTDLY-XYXQLNDSSEEEDEIDGPAGQAE 46
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86;
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FILE REFERENCE: 506612000104

CURRENT FILING DATE: 2004-10-19

CURRENT FILING DATE: 2004-10-19

PRIOR APPLICATION NUMBER: US/10/511,937

CURRENT FILING DATE: 2003-04-24

PRIOR PILING DATE: 2003-04-24

PRIOR PILING DATE: 2003-04-24

PRIOR FILING DATE: 2002-04-24

PRIOR FILING DATE: 2002-04-24

PRIOR FILING DATE: 2002-04-24

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR APPLICATION NUMBER: US 10/325,899

PRIOR PILING DATE: 2002-12-20

NUMBER OF SEQ ID NOS: 3117

SOFTWARE: PACENTIN VETSION 3.2

SEQ ID NO 2618
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US-10-511-937-2618
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOPTWARE: Patentin version 3.3
SEQ ID NO 12546
                                                                                                                                   Query Match
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APPLICANT: ROSENDETS, Steven
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING
TITLE OF INVENTION: AND MONITORING TRANSPLANT REJECTION
                                                                                                                                                                                                                      TYPE: PRT
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TYPE: PRT
                                                                                                        Local Similarity 28.1%;
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Local Similarity 25.4%;
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      18
                                        17 PETTDLYXYXQLNDSSEEED----EIDGPAGQAEPDRAHYNIVTFCCKCDSTLRLCVQST 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       65 LRL 67
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PENTSI-----DRNNEKNAGMVEFVSPNGE-----VFICKSDLEIGICHODK 59
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                                                                                       Conservative
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Pred. No. 1.2e+02;
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Pred. No. 1.1e+02;
9; Mismatches 22
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Sequence 38510, Application US/10953349
PUDDICATION NO. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 38510
LENGTH: 343
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SOFTWARE: Patentin version 3.3
SEQ ID NO 8835
LENGTH: 438
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APPLICANT: ALEXANDROV, NICKOLAI et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
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CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
                                                                                                                                                                                                                                                                            TYPE: PRT
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nes 19; Conserv
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                                                                           118 LSVEMPEIEFARALDDAEEAIFYRHFKPEVVWKMQRLIGVGAELKLKRAHAIFDRVCSKC 177
178 IASKRDEI-SQGIDSSSSKDLLMSSINV 204
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                                    62 DSTLRLCVQSTHVDIRTLEDLLMGTLGI 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43 GQAEPD-----RAHYNIVTFCCKCDSTLRLCVQSTHVDIRTLEDLLMGTLGIVXP
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27.9%;
                                                                                                                                                                         9.7%; Score 50;
21.6%; Pred. No.
                                                                                                                                                        17;
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Pred. No. 1.5e+02;
7; Mismatches 27;
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                                                                                                                                                                                             DB 6;
                                                                                                                                                                                         Length 438
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RESULT 95 US-10-953-349-8834 ; Sequence 8834, Application US/10953349

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RESULT 96
US-10-953-349-8833
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US-10-953-349-13398
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: Patentin version 3.3
SEQ ID NO 8834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PATENTIN VERSION 3.3
SEQ ID NO 8833
LENGTH: 516
                                                       Sequence 13398, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
PILE REFERENCE: 2750-1579PUS2
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Publication No. US20060107345A1
GENERAL INFORMATION:
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: ENCONDED THERBY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT APPLICATION NUMBER: US/10/953,349
CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
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Pred. No.
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Pred. No. 2.3e+02;
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ORGANISM: Glycine max
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9)...(9)
OTHER INFORMATION: Xaa can be any naturally occurring amino US-10-953-349-13398
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NAME/KEY: misc feature
LOCATION: (30)...(30)
OTHER INFORMATION: Xaa can be any naturally occurring amino US-10-953-349-13397
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Publication No. US20060107345A1
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
                                                                                               Sequence 13396, Application US/10953349
Publication No. US20060107345A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2004-09-30
NUMBER OF SEQ ID NOS: 40252
SOFTWARE: PatentIn version 3.3
SEQ ID NO 13397
LENGTH: 548
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SEQ ID NO 13398
LENGTH: 527
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Best Local Similarity
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Best Local Similarity
APPLICANT: ALEXANDROV, Nickolai et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA
TITLE OF INVENTION: ENCONDED THERBY
FILE REFERENCE: 2750-1579PUS2
CURRENT APPLICATION NUMBER: US/10/953,349
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Pred. No. 2.3e+02;
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CURRENT FILING DATE: 2004-09-30 NUMBER OF SEQ ID NOS: 40252 SOFTWARE: PatentIn version 3.3

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Sequence 3814, Application US/11293697
Publication No. US20060105376A1
GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
FITLE OF INVENTION: NOVEl full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/11/293,697
CURRENT FILING DATE: 2005-12-05
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR APPLICATION NUMBER: US/10/108,260
PRIOR FILING DATE: 2002-03-28
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3814
LENGTH: 878
TYPE: PRT
Search completed: May 27, 2006, 05:38:15 Job time: 8.69076 secs
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; LENGTH: 634
; TYPE: PRT
; ORGANISM: Glycine max
; PEATURE:
; NAME/KEY: misc feature
; LOCATION: (116)...(116)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-953-349-13396
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US-11-293-697-3814
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US-11-293-697-3814
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Local Similarity 24.3%; Pred. No. 4.1e+02;
1es 25; Conservative 15; Mismatches 39; Indels
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